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Evaluation of Biostimulant Products for the Control of *Phytophthora capsici* (Peronosporales, Peronosporaceae) in Pepper

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Resumen

Los bioestimulantes de plantas son productos que "contienen sustancias y/o microorganismos cuya función cuando se aplican a las plantas o la rizosfera es estimular los procesos naturales para mejorar/beneficiar la absorción de nutrientes, la eficiencia de nutrientes, la tolerancia al estrés abiótico y la calidad del cultivo (EBIC, 2012). Con el objetivo de cumplir con las regulaciones legales de la Unión Europea, una empresa de protección de cultivos facilitó una selección de productos bioestimulantes para determinar su posible fungitoxicidad y eficacia en el control de oomicetos. Estos productos se han preparado comercialmente para el control de las enfermedades causadas por *Phytophthora*. Los componentes de su formulación están codificados como L01-L13 y los bioestimulantes como A y B. En este estudio, titulado 'Evaluación de productos bioestimulantes para el control de *Phytophthora capsici* en pimiento', los productos y los componentes de su formulación se estudiaron *in vitro* y mediante ensayos de invernadero. En los experimentos *in vitro* se estudió la posible fungitoxicidad frente a los organismos fitopatógenos *P. capsici* y *P. citrophthora*, *Fusarium solani*, *Verticillium dahliae*, así como *Alternaria alternata*. Los patógenos se expusieron a diferentes concentraciones de producto y los resultados de la inhibición del crecimiento se analizaron mediante curvas dosis-respuesta y, cuando fue posible, se calcularon también los valores de EC_{50} (concentración efectiva media). L01-L13 no indujeron en ningún caso una reducción del 50% del crecimiento de los organismos. Lo mismo ocurrió con los bioestimulantes A y B. Los resultados del estudio *in vitro* indican que ninguno de estos dos productos, ni los componentes de su formulación, resultaron fungitóxicos para los organismos incluidos en el experimento. Los ensayos de invernadero tuvieron como objetivo evaluar la eficacia de los productos A y B para el control de *P. capsici* en pimiento. Las plántulas se cultivaron durante dos meses y se pulverizaron foliarmente con los productos. Posteriormente se inocularon con *P. capsici* mediante inmersión de las raíces en una suspensión de zoosporas. La severidad de la enfermedad se evaluó semanalmente hasta la muerte de las plántulas. Los datos de severidad se analizaron mediante modelos de regresión ordinal, calculando los correspondientes odds ratios con las plantas inoculadas no tratadas como nivel de referencia. Todos los productos evaluados presentaron odds ratios entre 0 y 1, concluyendo que ninguno ellos fue efectivo para el control de *P. capsici* en pimiento bajo las condiciones del experimento. El posible efecto de control de estos productos habría quedado enmascarado por un estrés excesivo de la plantas, inducido por las condiciones extremadamente agresivas de la inoculación, unido a posibles problemas de fitotoxicidad. Por lo tanto, en el futuro sería necesario explorar otras metodologías para evaluar la eficacia de los bioestimulantes A y B en el control de *P. capsici* en pimiento.

Palabras clave: curva dosis-respuesta, valor absoluto de EC_{50}, regresión ordinal, evaluación de enfermedad, piraclostrobin, fungitoxicidad, diseño experimental

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Abstract

Plant biostimulants are products which "contain substance(s) and/or micro-organisms whose function when applied to plants or the rhizosphere is to stimulate natural processes to enhance/benefit nutrient uptake, nutrient efficiency, tolerance to abiotic stress, and crop quality" (EBIC, 2012). Aiming to comply with the legislative regulations of the European Union, a plant protection company submitted a selection of biostimulating products to studies of fungitoxicity and oomycete control efficacy. These products are aimed for the control of Phytophthora diseases. The product components were coded L01-L13 and the biostimulants A and B. In this investigation, titled 'Evaluation of biostimulant products for the control of *Phytophthora capsici* in pepper', the products themselves as well as their formulation components were studied *in vitro* and through greenhouse trials. The *in vitro* experiments involved the target oomycetes *P. capsici* and *P. citrophthora*, the soil-borne fungi *Fusarium solani* and *Verticillium dahliae* as well as the foliar fungal pathogen *Alternaria alternata*. The pathogens were exposed to different product concentrations and the results of growth inhibition were analyzed by dose-response curves and, wherever possible, EC_{50} values (half maximal effective concentration) were calculated. None of the product components (L01-L13) reached an effect of 50% growth reduction. The same was true for biostimulants A and B, and since the results were significant, these products and their components were not considered fungitoxic to the organisms of the study. The greenhouse trials were conducted in parallel and aimed at evaluating the efficacy of products A and B in preventing *P. capsici* from infecting pepper seedlings. Seedlings were grown for two months, were foliarly sprayed with the products and were subsequently inoculated with *P. capsici* by root submersion in a zoospore suspension. Disease severity was assessed weekly, until seedling death, and the data were analyzed through ordinal regression models and the calculation of odds ratios. The comparisons were done using inoculated non-treated plants as the reference group. All odds ratios ranged from 0 to 1 suggesting that none of the products achieved to significantly increase the chances of disease control under the conditions tested. It is speculated that the potential benefits of the products against disease were masked by the negative impact that inoculation aggressiveness and phytotoxicity had on plant status. Thus, exploring other methodologies in future trials will be the next step in investigating the topic further and achieving a comprehensive understanding of the efficacy and capacity that biostimulants A and B have in preventing pepper infection from *P. capsici*.

Keywords: dose-response curve, absolute EC_{50} value, ordinal regression, disease evaluation, pyraclostrobin, fungitoxicity, experimental design

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Abbreviations

$CI_{0.95}$	95% confidence interval
EC_{50}	Half maximal effective concentration
GR	Percentage of growth reduction
IPM	Integrated Pest and Disease Management
IR	Irrigation
IVIA	Valencian Institute of Agricultural Investigation
R	Daily radial growth
RD	Root Dipping

1. Introduction

1.1 The pathogen *Phytophthora capsici*

The oomycete genus *Phytophthora*, the second largest genus of the Peronosporaceae family, was first described by de Bary (1876) and has been given extensive attention by the scientific community due to its large number of phytopathogenic species, known to cause important diseases in a considerable variety of crops. When infecting a host, members of this genus initially feed on living cells (biotrophic phase) before killing them and absorbing nutrients from dead plant tissue (necrotrophic phase). Being hemibiotrophic is, thus, a contradicting point when comparing *Phytophthora* spp. with other oomycetes such as most downy mildews, which are biotrophic, or the usually necrotrophic *Pythium* spp. (Thines, 2013). Currently, there are more than 100 *Phytophthora* spp., a number which is continuously growing (Érsek and Ribeiro, 2010). The genus *Phytophthora* is most notorious due to *P. infestans* (Mont.) de Bary, the causal agent of the potato blight, which was part of the factors that led to the Irish Potato Famine during the 19th century (Thines, 2013).

Another species of the same genus, *P. capsici* Leonian is a destructive broad-host-pathogen of vegetables and a causal agent of root, crown, foliar and fruit rot. It attacks many economically important vegetable crops, including members of the Cucurbitaceae family like pumpkin, squash, cucumber and melon as well as of the Solanaceae family like pepper, tomato and eggplant (Erwin and Ribeiro, 1996). Some crop members of the families Amaranthaceae (e.g. beet and spinach), Fabaceae (e.g. snap beans and lima beans) and Brassicaceae (e.g. radish and turnip) can also act as hosts of *P. capsici*, while the pathogen also has the ability to survive on certain weeds like *Solanum nigrum* which is a member of the Solanaceae family and commonly found on pumpkin fields, for instance (SMART, 2018; Tian and Babadoost, 2004).

This oomycete species was first recovered from chili pepper plants in 1918 in New Mexico (Leonian, 1922) and was soon reported on many other crops as well (Lamour *et al*., 2012). Morphological, physiological and molecular evidence proves the high genetic diversity of *P. capsici*, while multiple studies have shown that isolates are not host-specific and can, thus, infect different types of crops (Sanogo and Bosland, 2013). The species managed to spread across North and South America, Asia, Africa and Europe and being problematic for the cultivation of various important crop families, made it a popular research subject with relation to epidemiology, genetics and pathogen virulence (Lamour *et al*., 2012).

The thallus of *P. capsici* is made up of coenocytic (nonseptate) mycelium from which sporangia can rise on top of long caduceus pedicels (stalks from which sporangia can be detached) (Bernhardt and Grogan, 1982). Spread of Phytophthora blight is most likely to occur during July and August and most rapid reproduction is witnessed under warm, (25-30 ^{o}C), wet and humid conditions, in which sporangia production is the highest (SMART, 2018).

Sporangia are lemon-shaped and although non-motile, if detached from their pedicels, they can move passively by rain splash or moving water and cause infection through direct germination. Additionally, when immersed in free water, a sporangium can differentiate and produce and release 20-40 zoospores which either swim short distances or passively move in water and, thus, move from the soil to a plant or from plant to plant. Zoospores are asexual spores and the main source of inoculum in an infected field since they can take advantage of soil water to reach plant roots, after which they become attached to them and infect them (Hausbeck and Lamour, 2004). For their production, only a single isolate of *P. capsici* is required, which is another factor making zoospores abundant. Infection by zoospores requires their attachment to the body of the host, a step which varies depending on the host plant under attack as well as factors such as the existence of wounds in the roots and the amount of free water available. Wounding of shoot organs, such as fruits has also been shown to enhance infection by the oomycete (Sanogo and Bosland, 2013).

However, since they can only survive a few days if not in contact with a host, *P. capsici* relies on its oospores for long-term survival. Oospores form inside infected plant tissue, only when mating types A1 and A2 are paired and can survive for more than a year, thus, allowing the pathogen to remain in an infected field from one growing season to the next (SMART, 2018). Mating of the two different types allows sexual recombination and is, thus, a source of genetic diversity for *P. capsici*. They are amphigynous (the antheridium encircles the oogonial stalk), have thick walls which consist of multiple layers of β-glucan and cellulose and require being dormant for a period of at least one month before either directly germinating or forming sporangia (Bernhardt and Grogan, 1982).

1.2 Phytophthora blight symptomatology

Phytophthora blight caused by *P. capsici* produces symptoms both in the root as well as the shoot, thus, compromising the function of the host in multiple manners. Although below-ground symptoms are more common, fields in which sprinkler irrigation is used and areas experiencing summer rains will also exhibit above-ground symptoms including symptoms on the leaves, stems and fruits. This is related to the movement of water increasing the dispersal rate of soil inoculum and is also related to the overall increase in soil moisture, since inoculum production is also increased under these conditions (Sanogo and Bosland, 2013). Warm and wet conditions, in the field, allow infections on the root and crown of plants which may lead to permanent wilt and plant death (Hausbeck and Lamour, 2004). Although temperature and humidity are the factors dictating whether infection is possible or not, salinity has also been studied as part of the environmental factors affecting this pathosystem. It has been demonstrated that increasing salinity leads to a decrease in the number of sporangia formed as well as of zoospores contained in them (Sanogo, 2004).

Depending on the host plant, infected plant part and environmental conditions, disease symptoms may vary considerably. This investigation will focus on pepper as a host of *P. capsici*. The pathogen can infect pepper plants at any growth stage, although seedlings are more vulnerable to the disease than adult plants (Tian and Babadoost, 2004). Damping off can occur pre- or post-emergence; in young pepper plants infected through the root it is expressed as stunting, wilting and eventually death. Plants infected at a later stage, may exhibit shoot wilt, stem lesions at the soil line, fruit rot and root necrosis (Lamour *et al.*, 2012). Nonetheless, since water is indispensable for this pathogen, water-soaked conditions are a great advantage for it and, thus, entire fields of adult pepper plants can be devastated if the soil becomes water-saturated by intense rainfall or poorly managed flood irrigation practices, for instance (Hausbeck and Lamour, 2004). At initial stages of an outbreak, most diseased plants are found at the lower areas of an inclined field, where water tends to accumulate after rain or extensive irrigation. In such cases, plant stunting or plant death in this part of a field may be blamed on waterlogging, while Phytophthora blight may be the cause. After the pathogen penetrates the host, a 3- to 6-day period usually passes before symptoms start to be visible. This lagging period can lead to the harvest of seemingly healthy vegetables and fruits which exhibit rotting soon after. Symptoms are seen as water-soaked brown to black discoloured roots and/or crowns. Fruit rot is another symptom of the disease, although less common, and it is manifested as brown to black lesions extending over the vegetables as disease progresses. These dark, water-soaked lesions are eventually covered by a layer of sporangia-full mycelium, which gives them a 'powdered-sugar' appearance (Hausbeck and Lamour, 2004).

1.3 Control strategies against *Phytophthora capsici*

As a plant pathogen, *P. capsici* is undoubtedly important owing to its ability to infect a broad range of hosts, produce oospores which are long-living dormant sexual spores and spread at a high speed through asexual cycles in which large number of zoospores are formed (Lamour *et al.*, 2012). Its extensive genotypic diversity and documented resistance to commonly used fungicides are pressuring the scientific community and plant protection industry to invest in diverse control strategies (Matheron and Porchas, 2014).

Since the disease is soilborne and connected to high soil moisture, cultural control is fundamental in preventing it, especially on fields which have suffered previous outbreaks. Spores of the pathogen may be moved by humans, animals or field equipment which may carry infected soil or dead plant material and, thus, field hygiene needs to be consistent; worker shoes and machinery tires for instance need to be cleaned before moving from one field to another and infected fruits or plant material needs to be disposed far away from the field. Efficient soil drainage, the use of drip irrigation or low-frequency furrow irrigation can all reduce Phytophthora blight incidence. Planting the crop in raised beds to avoid soil water saturation in the rhizosphere is also essential. The beds are recommended to be high, dome-shaped and mulched, since otherwise they

may deteriorate throughout the season and fail to ensure sufficient drainage during summer when *P. capsici* outbreaks may occur (SMART, 2018).

With relation to crop rotation, host plants should be rotated with crops which do not belong to families that are affected by the oomycete. In case of disease, the field should be sown with crops that don't belong to the Cucurbitaceae or Solanaceae family for at least three years. Since the oomycete can also survive on certain weeds, managing those is also part of managing Phytophthora blight (SMART, 2018).

These practices can be combined with chemical control for better results. Preventive fungicide treatments are considered efficient, such as the commonly used product mefenoxam (Matheron and Porchas, 2014). Nonetheless, when considering a system of Integrated Pest and Disease Management (IPM), chemical products need to be used in moderation and in combination with other methods (Van den Bergand and Jiggins, 2007). Additionally, *P. capsici* has been developing resistance to different active ingredients and mode of actions with the passage of time since these have often been abused in agriculture. Thus, new and up-to-date control strategies are constantly demanded against this pathogen (Matheron and Porchas, 2014).

The use of resistant cultivars is considered a sustainable, environmentally-friendly and cost-effective means of avoiding disease in a field. Nonetheless, in the case of breeding for *Phytophthora*-resistant pepper cultivars, the fact that *P. capsici* attacks and can simultaneously cause various disease syndromes in different parts of the host (root rot, foliar blight, fruit rot and stem blight) makes genetic resistance complex and difficult. This complexity is also linked to the high genetic diversity within and between *P. capsici* populations, which makes the breeding of a universal resistant cultivar improbable. Nowadays, various *P. capsici* resistance genes are used in combination, aiming to convey resistance to various isolates of a certain geographic region (Sanogo and Bosland, 2013). Thus, area-specific solutions can be available based on gene pyramiding as seen in investigations similar to that of Thabuis *et al*. (2004).

In the sector of biological control, multiple bacteria-based biofungicides and extracts of plant tissues, such as garlic extract, have been assessed over the years for their efficacy in preventing and controlling *P. capsici* through seed, soil and plant treatments (Sanogo, 2008; Sanogo and Liess, 2010). Promising treatments proved to be those with oleoresins of *Capsicum* spp. as well as with by-products of pecan (*Carya illinoinensis*) (Sanogo and Bosland, 2013). Additionally, companies are now exploring the use of biostimulants for the prevention of Phytophthora blight in pepper.

1.4 Legislative context on the release of biostimulant products

In an effort to comply with the latest legislative regulations of the European Union (Directive 2009/128/EC) and make plant protection more sustainable, modern management strategies are shifting towards Integrated Pest and Disease Management techniques (European Parliament, 2009). This change is accompanied by an increased

use of biostimulant products and the subsequent creation of a market niche for products of this category (Calvo *et al*., 2014). Plant biostimulants have been defined by the European Biostimulants Industry Council (EBIC, 2012) as products which "contain substance(s) and/or micro-organisms whose function when applied to plants or the rhizosphere is to stimulate natural processes to enhance/benefit nutrient uptake, nutrient efficiency, tolerance to abiotic stress, and crop quality" (Calvo *et al*., 2014). The expansion of the global market for such products is expected to continue increasing and is forecasted to exceed $3,000 million by 2022 (Sessitsch *et al*., 2018).

These products cannot be commercialised following the same regulations as fungicides or fertilizers since they are not considered to comply with the description of any of these two categories. Owing to this, establishing a legal framework for regulating and commercializing such products became necessary and, thus, companies participating in this market sector are now faced with the obligation of submitting their products together with a dossier of experiments and information about the way these products achieve plant protection. Part of this process is proving that the products do not have any direct fungitoxic effect to the pathogen of interest, while the products are also commonly evaluated for disease control or prevention efficacy through greenhouse trials. This process is beneficial since it directs attention to the sector of biostimulants and also allows the circumvention of legislative procedures relating to pesticides (Regulation (EC) No 1107/2009), which tend to be more time-consuming and expensive. Finally, not being considered pesticides, may lead to biostimulants becoming fundamental to future IPM systems (European Parliament, 2009a; Calvo *et al*., 2014).

2. Objectives

Being a Mediterranean country with favourable climatic conditions, Spain is a key producer of vegetables such as pepper (e.g. sweet bell pepper *Capsicum annuum* L.) within Europe (FAO, 2017). As a result, the topic of plant protection within the field of Spanish agriculture maintains the interest of the phytosanitary industry and scientific community, especially with regards to establishing new strategies of controlling biotic stresses, such as Phytophthora blight, caused by *P. capsici*.

Given the above, a Spanish plant protection company submitted a selection of biostimulating products, which are used for the control of Phytophthora diseases, to studies of fungitoxicity and oomycete control efficacy. The products themselves as well as their formulation components were studied *in vitro* and through greenhouse trials, under code names for non-disclosure purposes. The overall objective of this study was the evaluation of these products as new strategies for the control of *P. capsici* in pepper. Specifically, the study aimed to (1) examine the potential fungitoxicity of the tested products and their components through *in vitro* experiments and (2) to evaluate the product efficacy of these products against *P. capsici* in pepper through greenhouse trials.

3. Materials and Methods

3.1 Products used

Apart from the two products, A and B, submitted to efficacy trials, four commercially used products were also used in *in vitro* experiments and two of these were also used in the greenhouse trials for comparison. Fosetyl-al and commercial product C were used both in the *in vitro* experiments as well as the greenhouse trials, while mefenoxam and pyraclostrobin were only used in the *in vitro* experiments. The formulation components of products A and B, namely components L01-L13 were also tested *in vitro* (Table 1).

Table 1: List of tested products. The concentrations in which the products were initially available are also given. With the exceptions of fosetyl-al, mefenoxam and pyraclostrobin all other products are presented under code names.

Product	Concentration (%)
L01	100
L02	100
L03	100
L04	100
L05	100
L06	100
L07	100
L08	100
L09	100
L10	100
L11	100
L12	100
L13	100
A	100
B	100
Fosetyl-al (F)	80
C	40
Mefenoxam	48
Pyraclostrobin	25

3.2 *In vitro* experiments

The *in vitro* experiments were conducted to assess the potential fungitoxicity against phytopathogenic organisms. They involved the target oomycetes *P. capsici* and *P. citrophthora* (R.E. Sm. and E.H. Sm.) Leonian, the foliar fungal pathogen *Alternaria alternata* (Fr.) Keissl., as well as the soil-borne fungi *Fusarium solani* (Mart.) Sacc. and *Verticillium dahliae* Kleb. (Table 2), all of which are available as part of the culture collection of the Mycology Unit of the Valencian Institute of Agricultural Investigation (IVIA). The pathogens were exposed to different product concentrations and the results of growth inhibition were statistically analysed.

The five pathogens were initially grown on potato dextrose agar (PDA) plates until covering the entire plate and for a maximum of 14 days, at 25 ^{o}C, in the absence of light. Agar discs of 0.5 cm diameter, colonized by a pathogen, were then taken from these plates and placed, facing downward, in the centre of PDA plates which included different concentrations of the products tested. All plates were incubated at 25 ^{o}C, in the absence of light. The products were diluted in order to obtain a range of increasing concentrations, namely, 0 ppm, 0.01 ppm, 0.1 ppm, 1 ppm, 10 ppm and 100 ppm. Excluding 0 ppm, these concentrations correspond to a logarithmic scale of $\log_{10}$ including the $\log_{10}$(concentration) values of -2, -1, 0, 1 and 2. Products L01, L02, L03, L04, L05, L06, L07, L08, L09, L10, L11, L12, L13, A and B were provided at a 100% dose. Fosetyl-al, C, mefenoxam and pyraclostrobin were provided at different doses (Table 1) but were used in the same concentrations. Pathogen handling, media preparation and isolations were all executed in sterile conditions.

Table 2: Oomycete and fungal isolates evaluated *in vitro* with a series of products.

Pathogen species	Isolate code	Host	Location	Year
Alternaria alternata (Fr.) Keissl.	A190	Pomegranate	Elx	2016
Fusarium solani (Mart.) Sacc.	V015	Pepper	Almeria	2013
Phytophthora capsici Leonian	-	Pepper	El Perelló	2015
P. citrophthora (R.E. Sm. and E.H. Sm.) Leonian	-	Sweet orange	Borriana	2013
Verticillium dahliae Kleb.	V094	Almond	Llíria	2017

Plates were repeated four times for each pathogen-product-concentration and two randomly chosen perpendicular diameters would be measured on each colony, thus, leading to the acquisition of eight data points per concentration, for each product-pathogen combination. For every product-pathogen combination, colony growth would be measured for all plates when one of the colonies isolated on 0 ppm would cover or nearly cover the petri dish. This happened within 6 to 11 days of incubation, for all pathogens with the exception of *V. dahliae* which is a slow growing fungus; data for *V. dahliae* were collected after 10 to 15 days of incubation, even though it would have still only achieved covering half of the plate in that time.

In continuation, the data were statistically analysed using statistical software R 3.4.3 (R Core Team, 2013). The multcomp package for R (Hothorn *et al*., 2017) was used to perform regression analyses (generalized linear model) for the data sets of each product-pathogen combination. In those combinations where increasing product concentrations would significantly reduce the growth of the oomycete or fungus, the data would be examined further. Anomalies were also examined more thoroughly.

In total, 95 product–pathogen combinations were tested. These were comprised of the five pathogens of the experiment (Table 2), being tested separately against each of the 19 products of the study (Table 1). The 95 data sets produced (Annex I) were all examined for data normality and homoscedasticity and since they lacked both in the majority of cases, Analysis of Variance and Simple Lineal Regression were both considered unsuitable for analysing the data. They were, thus, analysed through a generalized lineal model which is more flexible than an ordinary linear regression and, thus, useful for dependent variables with a non-normal distribution (Rawlings *et al*., 2001). The regressions conducted with the generalized lineal model, aimed to detect whether product concentration as an independent variable had a significant effect on colony growth (diameter). At an initial stage, the analysis included colony growth expressed as diameter instead of expressed as growth reduction to avoid the handling of an excessive amount of zeros which could have reduced model fit. Given that the dependent variable (diameter) is a continuous variable of positive values, it is assumed that it follows a Gamma distribution: $y_i \sim$ Gamma (a, b) (for which mean E(y)=a/b and variance Var(y)= a/b^2) (Bretz *et al*., 2016). Thus, the generalized lineal models used employ a link function which inversely connects the lineal predictor to the average response value. This results in positive b_2 coefficient values representing negative slopes and vice versa. At the same time, the value of the b_2 coefficient is also informative with regards to the magnitude of the effect of concentration on the dependent variable. For instance, $b_2 = 0.00001$ represents a smaller slope and, thus, a smaller effect in comparison to $b_2 = 0.001$ which would represent a gradient that is 100 times steeper.

$$\frac{1}{\mu_i} = b_1 + b_2 * x_i \quad \text{i= 1, …, 6} \qquad (1)$$

where:

μ_i is the average diameter value of concentration group i
x_i is the value of the independent variable (concentration) which corresponds to group *i*
b_1 is the intercept
b_2 represents the slope, as the expected change in the inverse function of μ_i per unit change of the predictor *x*

The data collected were also used for the calculation of daily radial growth (R) as cm day^{-1}. In the case of the control treatment of 0 ppm, the data were averaged. In all calculations 0.5 cm were subtracted from diametrical colony growth since this is the diameter of the agar disc initially placed in the plates. The factor 'days of incubation' differed between product-pathogen combinations from 6 to 15 days. Daily radial growth was then used for the calculation of the percentage of growth reduction (GR) in comparison to average control conditions for each data point. In this way, a data set of GR values was generated for each fungicide-pathogen combination.

$$R = \frac{Diameter - 0.5cm}{2 * Days\ of\ Incubation} \quad (2)$$

$$GR = \frac{R(control_{mean}) - R(x)}{R(control_{mean})}, \text{ where x = diameter} \quad (3)$$

The calculation of the half maximal effective concentration (EC_{50}) value was only possible for treatments with data sets that satisfied certain criteria. Apart from confirming that concentration had a significant effect on colony diameter, a 50% growth reduction had to be within the range of growth reduction levels observed. In other words, the conclusions drawn from a toxicology study cannot be extrapolated to concentrations outside the range included in the experiments. Dose-response curves were created and the EC_{50} values were calculated through the functions of the nplr package for R (Commo and Bot, 2015) for the data sets meeting these requirements. The package is used for n-parameter logistic regression models and, since it allows fixing specific parameters manually, it was used for three-parameter logistic regressions.

$$\mu_i = \frac{T}{1+10^{\,b(x_{mid}-x_i)}} \quad (4)$$

where:
μ_i is the average GR value of concentration group i
T is the value of the upper asymptote
x_i is the value of the independent variable (concentration) which corresponds to group i
x_{mid} is the absolute EC_{50} value
b is the Hill slope

3.3 Greenhouse trials

The greenhouse trials aimed to determine the efficacy of A and B in peppers inoculated with *P. capsici*. The trials were conducted on sweet bell pepper plantlets of the variety ΄California Wonder΄, which was specifically chosen for its susceptibility to the pathogen. Using a susceptible variety allowed the rapid development of severe disease symptoms and a faster plant death. Seeds were sown in 16 cm^2 alveoli filled with a substrate of peat and sand (2:1 vol/vol) and grown for approximately two months. The greenhouse was periodically ventilated and temperature ranged from 18 °C to 24 °C during the period of February 2018– May 2018.

Two independent trials, named 2.1 and 2.2, were conducted, each including 12 treatments (Table 3). Products were foliarly sprayed 7 or 14 days pre-inoculation, at a 0.3% dose; every alveoli tray bearing 104 plantlets was sprayed with 125 ml of product diluted in water. The treatments also included positive and negative controls, in which plants were sprayed with water. The positive control plants were inoculated with *P. capsici*, while negative control plants were not. An excess of seeds was sown and, subsequently, only uniform plantlets of approximately 20 cm shoot length were selected for the trials. In trial 2.1, 50 plants per treatment were periodically evaluated from the time of inoculation, while in trial 2.2 plants available and used per treatment varied from 50 to 140. No fungicides were used for seed coating or soil application to avoid possible interference with the experimental results. Plantlets of trial 2.2 were sprayed once with insecticide (Chlorpyrifos 7.2%) on 22/06/2018 to control an aphid infestation in the greenhouse.

For the inoculation, a suspension of 10^5 zoospores ml^{-1} was prepared from the same reference *P. capsici* isolate used in the *in vitro* experiments. The isolate was grown in darkness on V8 juice agar for nine days, at 25 ^oC. The mycelium-covered agar was then cut in approximately 1 cm stripes, half of which were transferred on empty sterile petri dishes (Figure 1a). All petri dishes were then filled with approximately 25 ml of soil suspension, which was prepared by mixing distilled water with soil and filtering out the larger soil particles. Petri dishes were left under constant light at 23 ^oC for five days. In continuation, the oomycete colonies were observed for the presence of zoospore-filled sporangia (Figure 1b) and were cold shocked in 8 ^oC for an hour. Following that and after being left for two hours at room temperature, the oomycete colonies were observed again for released zoospores and emptied sporangia. The contents of the petri dishes were passed through a sieve with the aim to collect the zoospore suspension, the concentration of which was subsequently deduced by sampling 20 drops in a haematocytometer. Finally, water was added to the suspension in order to achieve the desired concentration of 10^5 zoospores ml^{-1}.

Table 3: Details of the treatments evaluated in the greenhouse experiments. Treatment codes include the product codes, an acronym referring to the inoculation method (RD – Root dipping, IR – Irrigation) and a number referring to the days pre-inoculation (7 or 14) when plants were sprayed with the products.

Inoculation method	Application timing (days pre-inoculation)	Treatment group	Treatment code	Product	Dose (%)
Root dipping (RD) Trial 2.1	7	RD-7	ARD-7	A	0.3
			BRD-7	B	0.3
			FRD-7	Fosetyl-al (F)	0.3
			CRD-7	C	0.3
			PCRD-7	Positive control	non-treated/inoculated
			NCRD-7	Negative control	non-treated/non-inoculated
	14	RD-14	ARD-14	A	0.3
			BRD-14	B	0.3
			FRD-14	Fosetyl-al (F)	0.3
			CRD-14	C	0.3
			PCRD-14	Positive control	non-treated/inoculated
			NCRD-14	Negative control	non-treated/non-inoculated
Irrigation (IR) Trial 2.2	7	IR-7	AIR-7	A	0.3
			BIR-7	B	0.3
			FIR-7	Fosetyl-al (F)	0.3
			CIR-7	C	0.3
			PCIR-7	Positive control	non-treated/inoculated
			NCIR-7	Negative control	non-treated/non-inoculated
	14	IR-14	AIR-14	A	0.3
			BIR-14	B	0.3
			FIR-14	Fosetyl-al (F)	0.3
			CIR-14	C	0.3
			PCIR-14	Positive control	non-treated/inoculated
			NCIR-14	Negative control	non-treated/non-inoculated

Inoculation was done either by root dipping (trial 2.1) or irrigation (trial 2.2). In root dipping, the pepper plantlets were carefully removed from the alveoli and were manually manipulated until most of the substrate would fall off the root system. In continuation, plantlets were inoculated with the oomycete by submersing the roots in the zoospore suspension for 48 hours (Erwin and Ribeiro, 1996). Inoculation took place in non-transparent buckets, to avoid exposing the root system and inoculum to sunlight. Once inoculation was completed, the plantlets were transplanted in 50 cm^2 individual pots filled with a substrate of peat and sand (2:1 vol/vol) where they were kept until the completion of the trial. In trial 2.1, inoculation by root dipping was performed on 30/04/2018, which was considered the time point T_0. Treatments RD-7 were done on 23/04/2018 (7 days before the inoculation) and treatments RD-14 on 16/04/2018 (14 days before the inoculation).

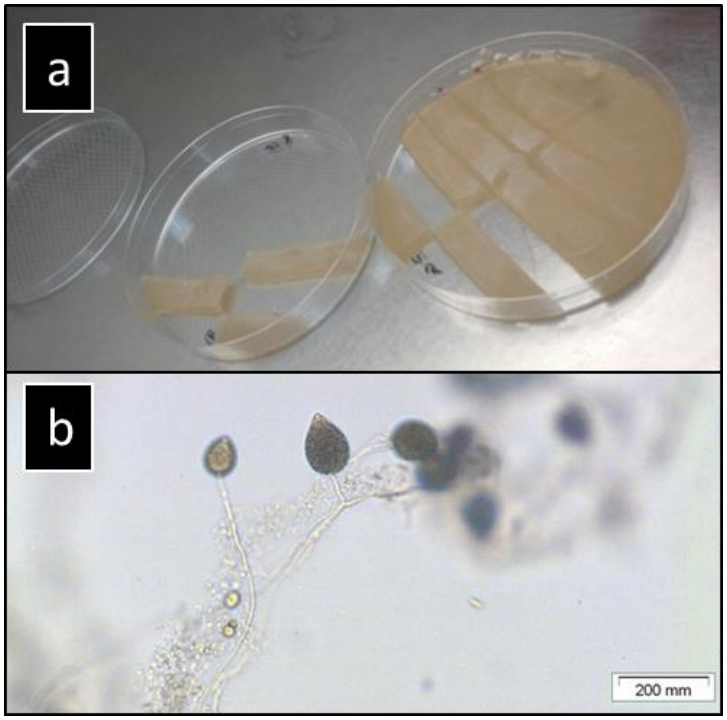

Figure 1: *Phytophthora capsici* zoospore suspension preparation. a) mycelium-covered agar is cut in stripes, half of which were transferred on an empty sterile petri dish. b) zoospore-filled sporangia observed under the microscope after the stripes were immersed in soil suspension and left under constant light at 23 ^{o}C for five days.

Inoculation by irrigation (trial 2.2) consisted of irrigating the plantlets with the zoospore suspension without removing them from the alveoli. Each tray of 104 alveoli was irrigated with 1.4 L of 10^5 zoospores ml^{-1} suspension, using a watering can with an extended neck. In trial 2.2, inoculation by irrigation was performed on 02/07/2018, which was considered the time point T_0. The plantlets were inoculated again on 24/07/18. Treatments IR-7 were done on 25/06/2018 (7 days before the inoculation of T_0) and treatments IR-14on 18/06/2018 (14 days before the inoculation of T_0.). Plantlets had nine true leaves at the time of inoculation in both trials. Before inoculation, a record of visual phytotoxicity symptoms such as leaf burning was kept by visually observing treated plants.

The inoculated plants were kept in the greenhouse, in controlled conditions (temperature fluctuating as detailed above) and periodic evaluations of disease severity were carried out for a minimum of 20 days. Treatments RD-7 and RD-14 were evaluated on 07/05/18, 09/05/18, 11/05/18, 14/05/18, 16/05/18, 18/05/18 and 21/05/18. Treatments IR-7 and IR-14 were evaluated on 09/07/18 and 16/07/18; evaluations continued sporadically after the second inoculation took place.

Disease severity was evaluated following an ordinal scale of four categories. These are: category 0 = healthy/symptomless plants, category 1 = mild to moderate wilting, category 2 = severe wilting and category 3 = dead plants (Figure 2). In more detail, healthy plants (category 0) were considered those that presented no disease symptoms at the time of evaluation. They did not suffer chlorosis, stem bending, petiole collapse or wilt and they also did not present any browning or lesion at the stem. Mildly or moderately wilted plants (category 1) were those in which petioles would start to collapse, initial signs of wilting would be seen, and/or a brown lesion would surround the stem, while, however, the plant would remain standing upright. Severely wilted plants (category 2) were those that apart from collapsed petioles and a wilted appearance would also bend downward due to a collapsing stem. Finally, plants would be considered dead (category 3) once dry and chlorotic.

At the end of trial 2.1, the presence or absence of *P. capsici* in the plants was confirmed by isolation of *P. capsici* from roots on PARB selective culture medium (Erwin and Ribeiro, 1996). Roots from still alive plants were arbitrarily collected for each treatment, washed with tap-water and left in sterile water for 24 hours. Small root fragments were plated in PARB petri dishes and incubated at 25 ^{o}C for 3 days. Colonies on these plates were then identified as *P. capsici*. Trial 2.2 remained open at the end of this investigation and, thus, no re-isolation was attempted.

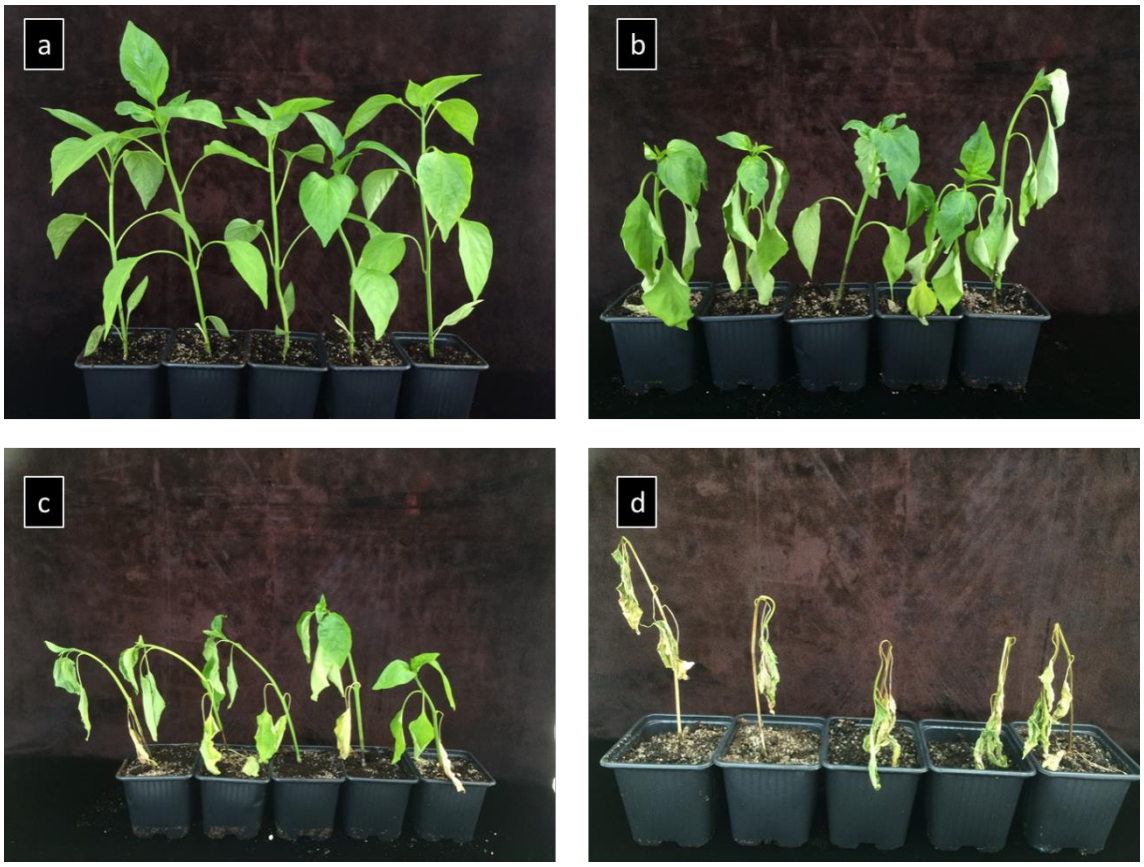

Figure 2: Ordinal scale of disease severity on 'California Wonder' pepper plants inoculated with *Phytophthora capsici*: a) category 0 = healthy/symptomless plants; b) category 1 = mild to moderate wilting; c) category 2 = severe wilting; and d) category 3 = dead plants.

All data of the greenhouse trials were statistically analysed using the statistical software R 3.4.3 (R Core Team, 2013). Since disease severity was evaluated along an ordinal scale, it was considered an order factor and was modelled through a proportional odds logistic regression model using the vglm function of the VGAM package for R (Wee, 2010), which is a function used to fit vector generalized linear models.

$$logit[P(Y_i \leq j)] = \beta_{j0} + \beta_1 x_{1i} + \cdots + \beta_k x_{ki} \qquad \text{j = 1, …, J-1, i = 1, …, n.} \qquad (5)$$

where $P(Y_i \leq j)$ is the cumulative probability between 0 and 1 for category j of Y_i, with J representing the categories of disease severity and j =1, …, J-1; β_{j0} denotes the intercepts of the severity categories, β_1, …, β_k are the coefficients for the k treatments evaluated ($X_1 \ldots X_k$) and n is the total number of plants evaluated.

The proportional odds logistic regression model is based on two assumptions. It assumes that the logit of the cumulative probabilities changes linearly as the explanatory variables change, and that the slope of this relationship is the same regardless of the severity category. This model is usually preferred when accounting for an ordered multinomial response, such as a disease severity scale, like in this case. Nonetheless, note that, due to its assumptions, this model treats the slope regression parameters as constant over the response categories. Hence, the proportional odds logistic regression model does not allow the regression parameters to vary across the levels of Y (Bilder and Loughin, 2015).

In this analysis, the inoculated/non-treated control was used as the reference level and the odds ratio for each product treatment was calculated as e^{β} based on the cumulative probabilities. Accepting the proportional odds assumption implies that the odds ratio for each product treatment stays the same no matter how disease severity is divided into two levels. For the evaluation of the proportional odds assumption, the proportional odds model and the non-proportional odds model were compared through the Likelihood Ratio Test (LRT) (Tutz, 2011) using the lrtest function of the VGAM package for R (Wee, 2010). The goodness of fit was assessed by observing the ratio of the residual deviance and degrees of freedom (df) of each model; well-fitted models should have a deviance/df ratio approximating a 1:1 ratio. The effect of a factor was considered significant when the 95% confidence interval of the odds ratio did not overlap with the null value of 1 (Bilder and Loughin, 2015).

3.4 Statistical analysis

All data, whether ordinal or ratio, produced in the *in vitro* experiments and greenhouse trials, were statistically analysed in R with the use of suitable statistical tests and methods. A detailed presentation of the analysis, R commands and outputs can be found in Annex II.

4 Results

4.1. *In vitro* experiments

Out of the 95 product-pathogen combinations examined, product concentration had an effect on colony growth in 47 combinations at a significance level of $\alpha = 0.05$ (Table 4). Growth reduction was calculated for these combinations and maximum growth reduction exceeded the level of 50% in 9 combinations (Annex III).These combinations are: (1) product C – *P. citrophthora*, (2) product C – *P. capsici*, (3) product C – *V. dahliae*, (4) mefenoxam – *P. citrophthora*, (5) mefenoxam – *P. capsici*, (6) pyraclostrobin – *P. capsici*, (7) pyraclostrobin – *A. alternata*, (8) pyraclostrobin – *F. solani* and (9) pyraclostrobin – *V. dahliae*. For these 9 data sets, three-parameter logistic regressions were conducted, using growth reduction as the dependent variable. The regressions were done using the nplr function of the nplr package. The regressions had a fixed lower asymptote of zero, conveying that the dose-response curves are asymptotic to the x axis. The $\log_{10}$ of product concentration was the independent variable. Products A, B and L01-L13 did not yield a growth reduction of 50% on any of the pathogens tested and were, thus, not examined further. The same was true for fosetyl-al.

The dose-response curves created for these combinations (Figure 3) allowed for the absolute EC_{50} value of each product on the respective organism to be derived (Table 5). The absolute EC_{50} value is defined as the concentration which causes 50% growth reduction as compared to the control treatment and is consistent with the EC_{50} value defined by FRAC (Lamour *et al*., 2018). Specifically, product C had an EC_{50} value of 11.61 ppm against *P. citrophthora*, an EC_{50} = 48.41 ppm against *P. capsici* and an EC_{50} = 97.26 ppm against *V. dahliae*. Mefenoxam had an EC_{50} value of 0.48 ppm against *P. citrophthora* and an EC_{50} = 0.08 ppm against *P. capsici*. Lastly, pyraclostrobin had an EC_{50} = 0.33 ppm against *A. alternata*, an EC_{50} = 0.11 ppm against *F. solani* and an EC_{50} = 0.21 ppm against *V. dahliae*. The pyraclostrobin – *P. capsici* data set was inconclusive and thus the EC_{50}value could not be calculated.

The dose-response curves are presented using the response variable 'growth reduction proportion' which can range from 0 to 1 and is equivalent to growth reduction (%) divided by 100. This parameter was chosen to facilitate the statistical analysis which is also why the corresponding graphs are presented in the same way. The deviance residuals of models based on growth reduction proportion remained within the recommended range of -2.00 to 2.00. At the same time, the goodness of fit of these models was examined by contrasting the residual deviance of each model against the saturated model through a chi-square (χ^2) test and since all χ^2 tests conducted resulted in p-value > 0.05, good model fit can be assumed for all models. The same was true for the 95 models based on diameter.

Table 4: The effect of an increasing product concentration on the colony growth (diameter) of the pathogens *Phytophthora capsici*, *P. citrophthora*, *Fusarium solani*, *Verticillium dahliae* and *Alternaria alternata*. Concentrations tested ranged from 0 ppm to 100 ppm. The asterisk (*) denotes that there is an effect of concentration on colony growth that is significant at the $\alpha = 0.05$ level. The dagger (†) marks the data sets for which maximum growth reduction exceeded 50%. Negative glm coefficient b_2 signs indicate an increase in growth with increasing product concentration and vice versa.

Product	Pathogen	glm coefficient b_2
L01	*Phytophthora citrophthora*	0.00000
L01	*Phytophthora capsici*	0.00002*
L01	*Alternaria alternata*	-0.00001
L01	*Fusarium solani*	-0.00002*
L01	*Verticillium dahliae*	0.00001
L02	*Phytophthora citrophthora*	0.00000
L02	*Phytophthora capsici*	-0.00001*
L02	*Alternaria alternata*	0.00000
L02	*Fusarium solani*	0.00003*
L02	*Verticillium dahliae*	0.00002*
L03	*Phytophthora citrophthora*	0.00002*
L03	*Phytophthora capsici*	-0.00002*
L03	*Alternaria alternata*	-0.00002*
L03	*Fusarium solani*	-0.00001
L03	*Verticillium dahliae*	0.00000
L04	*Phytophthora citrophthora*	0.00001
L04	*Phytophthora capsici*	0.00001
L04	*Alternaria alternata*	0.00001
L04	*Fusarium solani*	0.00000
L04	*Verticillium dahliae*	-0.00001
L05	*Phytophthora citrophthora*	0.00000
L05	*Phytophthora capsici*	0.00000
L05	*Alternaria alternata*	0.00003*
L05	*Fusarium solani*	-0.00001
L05	*Verticillium dahliae*	0.00000
L06	*Phytophthora citrophthora*	0.00000
L06	*Phytophthora capsici*	-0.00001*
L06	*Alternaria alternata*	0.00000
L06	*Fusarium solani*	0.00000
L06	*Verticillium dahliae*	0.00000
L07	*Phytophthora citrophthora*	0.00000*
L07	*Phytophthora capsici*	-0.00001
L07	*Alternaria alternata*	0.00001
L07	*Fusarium solani*	0.00001*
L07	*Verticillium dahliae*	-0.00001

Table 4 (Cont.)

Product	Pathogen	glm coefficient b_2
L08	*Phytophthora citrophthora*	0.00002*
L08	*Phytophthora capsici*	-0.00001*
L08	*Alternaria alternata*	0.00001*
L08	*Fusarium solani*	0.00000
L08	*Verticillium dahliae*	0.00003*
L09	*Phytophthora citrophthora*	0.00001*
L09	*Phytophthora capsici*	0.00001
L09	*Alternaria alternata*	-0.00001*
L09	*Fusarium solani*	0.00000
L09	*Verticillium dahliae*	0.00001*
L10	*Phytophthora citrophthora*	0.00000
L10	*Phytophthora capsici*	0.00001*
L10	*Alternaria alternata*	-0.00002*
L10	*Fusarium solani*	-0.00001
L10	*Verticillium dahliae*	0.00000
L11	*Phytophthora citrophthora*	0.00000
L11	*Phytophthora capsici*	0.00000
L11	*Alternaria alternata*	-0.00002*
L11	*Fusarium solani*	-0.00002*
L11	*Verticillium dahliae*	0.00001
L12	*Phytophthora citrophthora*	0.00001*
L12	*Phytophthora capsici*	0.00001*
L12	*Alternaria alternata*	-0.00001
L12	*Fusarium solani*	0.00000
L12	*Verticillium dahliae*	0.00000
L13	*Phytophthora citrophthora*	0.00000
L13	*Phytophthora capsici*	0.00001
L13	*Alternaria alternata*	-0.00001
L13	*Fusarium solani*	0.00000
L13	*Verticillium dahliae*	0.00001
A	*Phytophthora citrophthora*	0.00000
A	*Phytophthora capsici*	-0.00001*
A	*Alternaria alternata*	0.00001
A	*Fusarium solani*	0.00000
A	*Verticillium dahliae*	0.00001*
B	*Phytophthora citrophthora*	0.00000
B	*Phytophthora capsici*	0.00001
B	*Alternaria alternata*	-0.00002*
B	*Fusarium solani*	0.00000
B	*Verticillium dahliae*	0.00002*

Table 4 (Cont.)

Product	Pathogen	glm coefficient b_2
Fosetyl-al	*Phytophthora citrophthora*	0.00009*
Fosetyl-al	*Phytophthora capsici*	0.00002*
Fosetyl-al	*Alternaria alternata*	-0.00001*
Fosetyl-al	*Fusarium solani*	-0.00002*
Fosetyl-al	*Verticillium dahliae*	0.00001
C	*Phytophthora citrophthora*	0.00056*†
C	*Phytophthora capsici*	0.00064*†
C	*Alternaria alternata*	0.00006*
C	*Fusarium solani*	0.00008*
C	*Verticillium dahliae*	0.00030*†
Mefenoxam	*Phytophthora citrophthora*	0.00044*†
Mefenoxam	*Phytophthora capsici*	0.00139*†
Mefenoxam	*Alternaria alternata*	0.00006*
Mefenoxam	*Fusarium solani*	0.00004*
Mefenoxam	*Verticillium dahliae*	0.00001
Pyraclostrobin	*Phytophthora citrophthora*	0.00003*
Pyraclostrobin	*Phytophthora capsici*	-0.00008*†
Pyraclostrobin	*Alternaria alternata*	0.00059*†
Pyraclostrobin	*Fusarium solani*	0.00007*†
Pyraclostrobin	*Verticillium dahliae*	0.00142*†

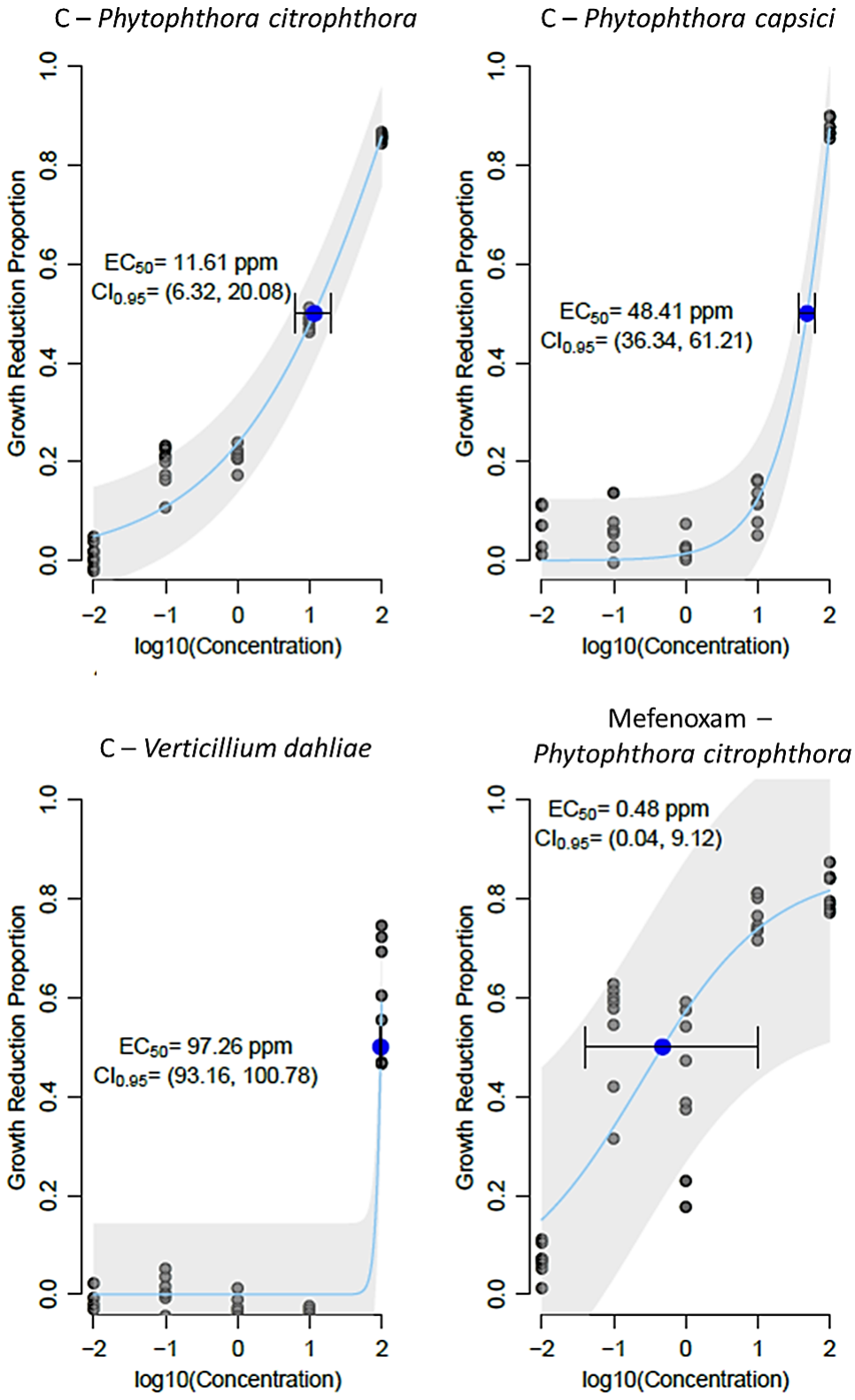

Figure 3: Proportion of growth reduction of different pathogens achieved by increasing concentrations of different products. Growth reduction is calculated in comparison to the control treatment (0 ppm). The grey dots designate the data points, the blue dot on each graph the half maximal effective concentration (EC_{50}) value (error bars: 95% confidence interval along the x axis). The grey area surrounding the regression line is the 95% confidence interval of the line.

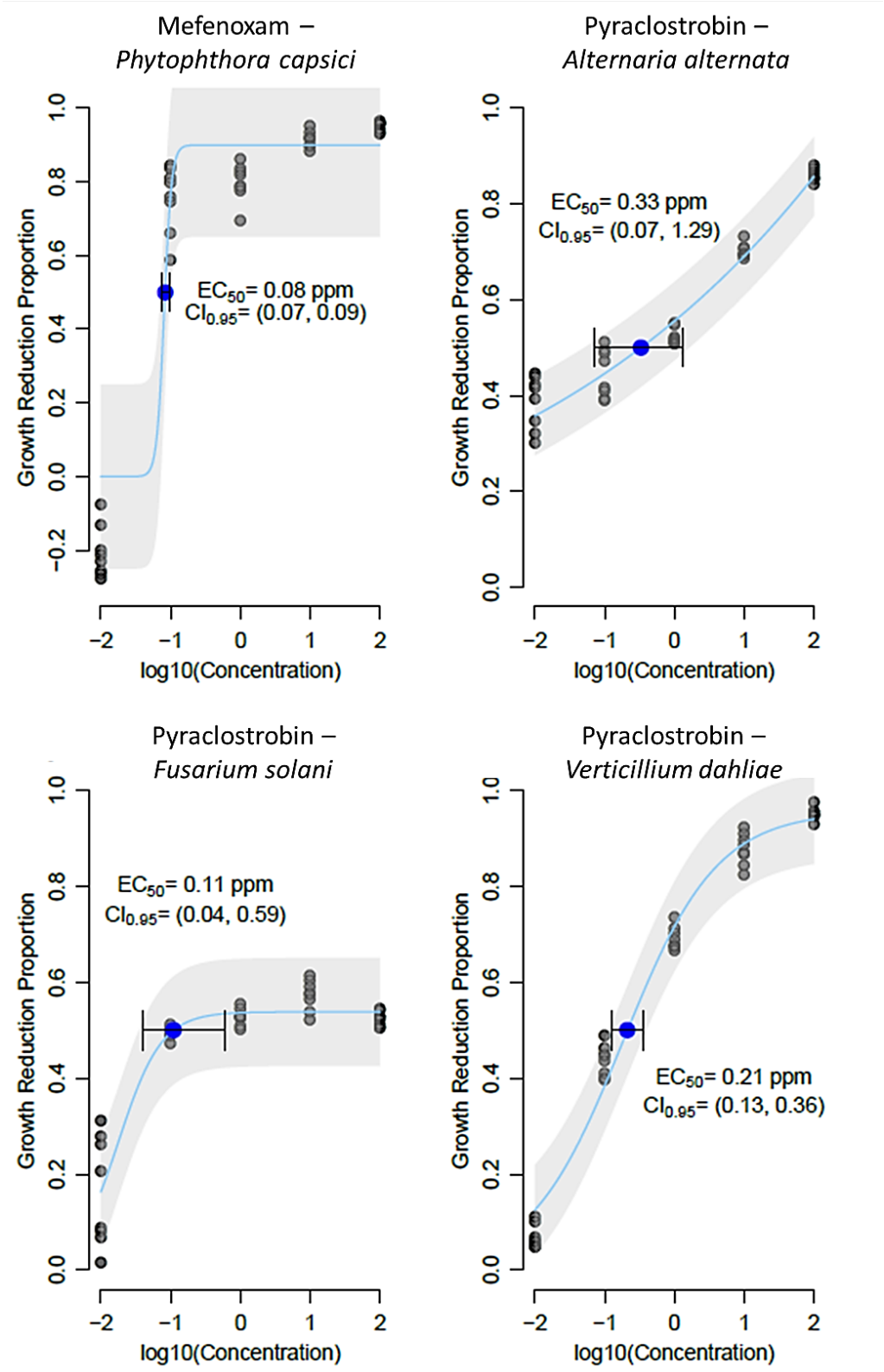

Figure 3 (Cont.)

Table 5: Half maximal effective concentration (EC_{50}) values calculated through three-parameter logistic regressions for eight product-pathogen combinations in which growth reduction exceeded the level of 50%. The parameters *T* (upper asymptote) and *b* (Hill slope) are also given.

Product	Pathogen	EC_{50} (ppm)	*T*	*b*
C	*Phytophthora citrophthora*	11.61 (6.32 – 20.08)[a]	2.14	0.36
C	*Phytophthora capsici*	48.41 (36.43 – 61.21)	3.36	0.96
C	*Verticillium dahliae*	97.26 (93.16 – 100.78)	2.39	7.81
Mefenoxam	*Phytophthora citrophthora*	0.48 (0.04 – 9.12)	0.86	0.49
Mefenoxam	*Phytophthora capsici*	0.08 (0.07 – 0.09)	0.90	8.18
Pyraclostrobin[b]	*Phytophthora capsici*	-	-	-
Pyraclostrobin	*Alternaria alternata*	0.33 (0.07 – 1.29)	16.79	0.10
Pyraclostrobin	*Fusarium solani*	0.11 (0.04 – 0.59)	0.54	1.41
Pyraclostrobin	*Verticillium dahliae*	0.21 (0.13 – 0.36)	0.96	0.65

[a] In brackets 95% confidence interval.

[b] The pyraclostrobin – *Phytophthora capsici* data set was inconclusive.

The EC_{50} value of pyraclostrobin against *P. capsici* could not be calculated due to an anomaly of the data. Pyraclostrobin inhibited the growth of *P. capsici* by more than 30% at 0.1 ppm and 10 ppm at a significance level of $\alpha = 0.05$. Similarly, at 1 ppm, it inhibited the oomycete by more than 50%. However, in comparison to control condition (0 ppm), there was no significant growth reduction when *P. capsici* grew on 100 ppm. To further examine these results, the study was repeated for the combination of pyraclostrobin – *P. capsici*, in order to confirm that the inconclusive results in this product-pathogen combination were recurrent and not caused by human error. Fresh media (PDA + pyraclostrobin at different concentrations) was prepared again and growth on pyraclostrobin was compared between that of the original *P. capsici* isolate and of a *P. capsici* isolate recovered after growing on media with 100 ppm pyraclostrobin. The isolates will be referred to as non-previously-exposed and exposed respectively. Pyraclostrobin inhibited the growth of both isolates by more than 50% at concentrations of 1 ppm and 10 ppm at a significance level of $\alpha = 0.05$. Lower concentration levels also had growth inhibiting effects, yet, to a lower extent but these inhibitions were still significant at a significance level of $\alpha = 0.05$. However, growing in 100 ppm pyraclostrobin did not have any substantial effect in the growth of either of the two isolates, in comparison to growth in the absence of pyraclostrobin (0 ppm) (Annex II). These results did not significantly differ from the results acquired the first time *P. capsici* was grown on pyraclostrobin (Annex I).

4.2. Greenhouse trials

In trial 2.1, where root dipping inoculation was used, the percentage of healthy plants (severity category 0) ranged from 0% in various treatments to 58% in the inoculated, non-treated control 7 days post inoculation (dpi). More specifically, no plants were found in category 0 on all evaluation dates for treatments CRD-7 and ARD-14. The same was true in most of the evaluation dates for treatments BRD-7 (9, 14, 16 and 21 dpi), FRD-7 (9, 11, 14, 16, 18 and 21 dpi), BRD-14 (11, 14, 18 and 21 dpi), CRD-14 (9, 11, 14, 16, 18 and 21 dpi) and PCRD-14 (11, 14, 16, 18 and 21 dpi) (Figure 4). On the other hand, plants in the severity category 3 (dead) ranged from 0% in all treatments until 11 dpi to 100% in treatment CRD-7 21 dpi (Figure 4).

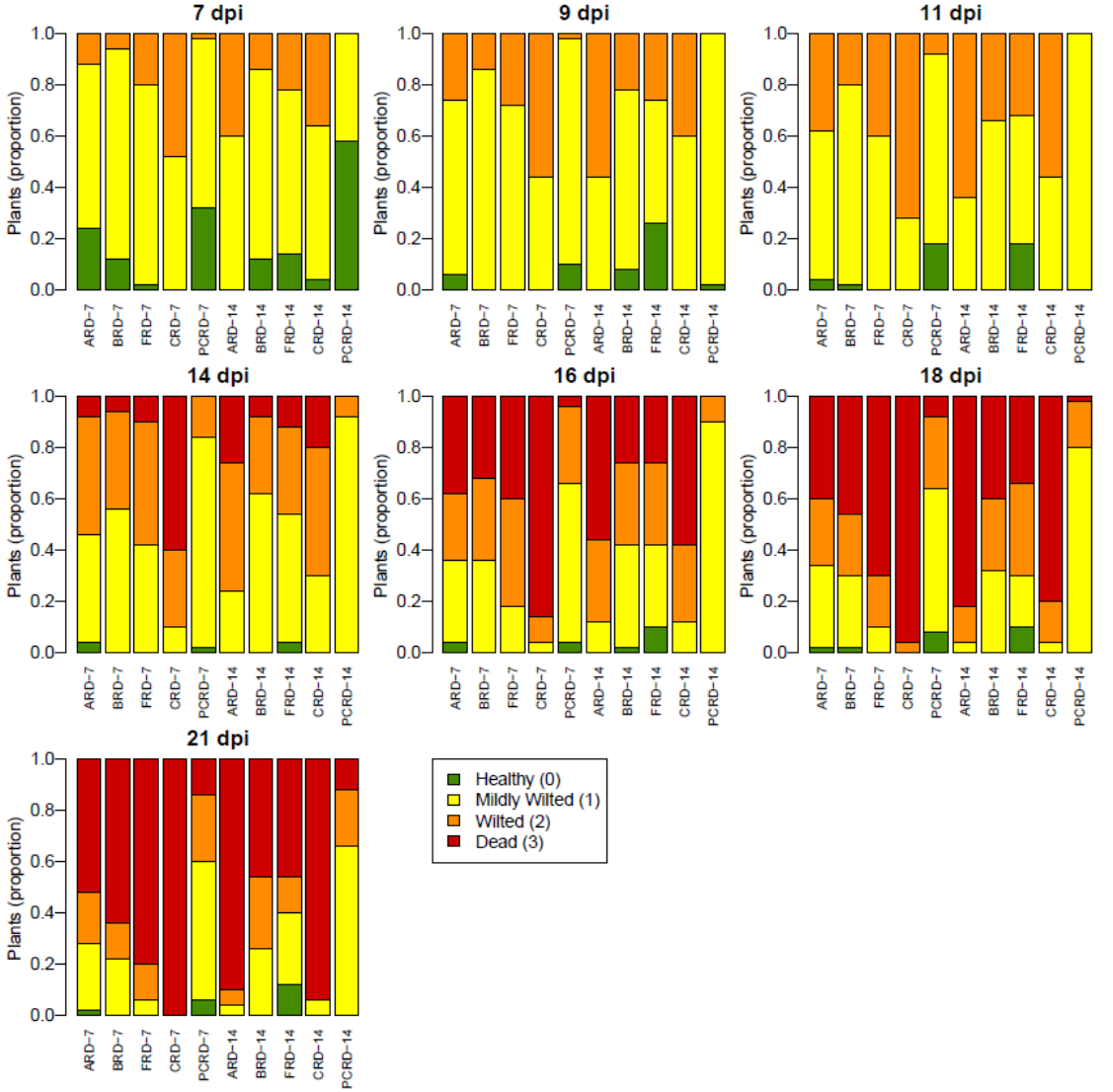

Figure 4: Disease severity on 'California Wonder' pepper plants inoculated with *Phytophthora capsici* by root dipping inoculation on 30/04/2018 (treatments RD-7 were done 7 days pre-inoculation and treatments RD-14 were done 14 days pre-inoculation; products used: A, B, F = Fosetyl-al and C; PC= inoculated/non-treated control). Bar plots reflect severity as recorded 7, 9, 11, 14, 16, 18 and 21 days post-inoculation (dpi), expressed as proportion of plants found in each disease severity category.

The proportional odds assumption was not rejected by the χ^2-test ($P > 0.05$) in the ordinal logistic regression of disease severity in most evaluation dates of trial 2.1. The goodness of fit was satisfactory for the same evaluation dates that satisfied the proportional odds assumption, with deviance/df ratios from 0.64 to 3.56. The evaluation dates with poor model fit were the ones that did not meet the proportional odds assumption. Poor goodness of fit was evident by the fact that the residual deviance/df ratio would exceed the value of 10. These data sets correspond to the evaluations of the treatments of group RD-14 (product treatments done 14 days before the inoculation) on 9, 11, 16, 18 and 21 dpi.

Products A, B, fosetyl-al and C significantly increased ($p < 0.05$) disease severity compared with the inoculated, non-treated control in all evaluation dates, with the exceptions of treatment ARD-7 7 dpi, BRD-14 and FRD-14 9 dpi and FRD-7 11 dpi (Table 6).

In group RD-7 (product treatments done 7 days before the inoculation), the estimated odds of disease severity being below a given category changed from 0.021 times with ARD-7 down to 0.00 times with CRD-7 at 21 dpi. Odds ratio values between 0 and 1 imply a negative relationship or, in other words, that the odds are against the evaluated treatment. For instance, an odds ratio of OR = 0.021 for ARD-7 at 21 dpi, suggest that plants of the ARD-7 treatment are (1 – 0.021)*100= 97.9% less likely to be healthy. The predicted probabilities for the severity category 0 in the inoculated/non-treated control ranged from 0.036 at 14 dpi to 0.325 at 7 dpi. With product A, the probability for the same severity category ranged from 0.007 at 14 dpi to 0.185 at 7 dpi and with product B from 0.008 at 21 dpi to 0.137 at 7 dpi. With fosetyl-al the predicted probabilities ranged from 0.003 at 21 dpi to 0.045 at 7 dpi and with product C from 0.000 at 21 dpi to 0.014 at 7 dpi. In fact, at 21 dpi in treatment ARD-7, the predicted probability of severity category 3 (plant death) was 1.000 since all 50 plants had already died.

In group RD-14 (product treatments done 14 days before the inoculation), the estimated odds of disease severity being below a given category changed from 0.037 times with FRD-14 down to 0.02 times with CRD-14 at 21 dpi. The predicted probabilities for the severity category 0 in the inoculated/non-treated control ranged from 0.028 at 14 dpi to 0.587 at 7 dpi. With A, the probability for the same severity category ranged from 0.001 at 18 dpi to 0.031 at 7 dpi and with B from 0.005 at 14 dpi to 0.122 at 7 dpi. With fosetyl-al the predicted probabilities ranged from 0.004 at 14 dpi to 0.122 at 9 dpi and with C from 0.001 at 14, 18 and 21 dpi to 0.039 at 7 dpi.

Table 6: Probabilities and odds ratios of the proportional odds logistic regression model for disease severity on 'California Wonder' pepper plants inoculated with *Phytophthora capsici* by root dipping inoculation (treatments RD-7 were done 7 days before inoculation and treatments RD-14 14 days before inoculation; products used: A, B, F = Fosetyl-al and C; PC = inoculated/non-treated control).

	Probabilities[a]				
Evaluation dates and products	Sev. 0	Sev. 1	Sev. 2	Sev. 3	Odds ratio
7 dpi[b]					
ARD-7	0.185	0.759	0.056	0.000	0.47 (0.20-1.12)[c]
BRD-7	0.137	0.785	0.078	0.000	0.33 (0.13-0.81)
FRD-7	0.045	0.734	0.221	0.000	0.10 (0.04-0.26)
CRD-7	0.014	0.499	0.487	0.000	0.03 (0.01-0.08)
PCRD-7	0.325	0.648	0.027	0.000	
ARD-14	0.031	0.551	0.419	0.000	0.02 (0.01-0.06)
BRD-14	0.122	0.736	0.142	0.000	0.10 (0.04-0.24)
FRD-14	0.095	0.726	0.179	0.000	0.07 (0.03-0.18)
CRD-14	0.039	0.601	0.360	0.000	0.03 (0.01-0.07)
PCRD-14	0.587	0.397	0.016	0.000	
9 dpi					
ARD-7	0.014	0.762	0.224	0.000	0.11 (0.03-0.40)
BRD-7	0.021	0.821	0.158	0.000	0.17 (0.05-0.62)
FRD-7	0.010	0.703	0.287	0.000	0.08 (0.02-0.29)
CRD-7	0.003	0.435	0.561	0.000	0.03 (0.01-0.09)
PCRD-7	0.111	0.858	0.032	0.000	
ARD-14	0.015	0.419	0.566	0.000	0.10 (0.04-0.24)
BRD-14	0.068	0.722	0.210	0.000	0.48 (0.20-1.19)
FRD-14	0.122	0.756	0.122	0.000	0.92 (0.37-2.27)
CRD-14	0.026	0.558	0.416	0.000	0.18 (0.07-0.44)
PCRD-14	0.131	0.755	0.114	0.000	
11 dpi					
ARD-7	0.020	0.613	0.367	0.000	0.11 (0.04-0.30)
BRD-7	0.041	0.742	0.217	0.000	0.22 (0.08-0.62)
FRD-7	0.017	0.573	0.410	0.000	0.09 (0.03-0.25)
CRD-7	0.005	0.274	0.721	0.000	0.02 (0.01-0.07)
PCRD-7	0.161	0.781	0.058	0.000	
ARD-14	0.006	0.351	0.642	0.000	0.06 (0.02-0.16)
BRD-14	0.021	0.626	0.354	0.000	0.20 (0.07-0.52)
FRD-14	0.042	0.752	0.206	0.000	0.41 (0.16-1.10)
CRD-14	0.009	0.427	0.564	0.000	0.08 (0.03-0.22)
PCRD-14	0.097	0.806	0.097	0.000	

Table 6 (Cont.)

Evaluation dates and products	Probabilities				Odds ratio
	Sev. 0	Sev. 1	Sev. 2	Sev. 3	
14 dpi					
ARD-7	0.007	0.474	0.431	0.087	0.19 (0.08-0.47)
BRD-7	0.010	0.547	0.377	0.066	0.26 (0.11-0.63)
FRD-7	0.006	0.417	0.469	0.108	0.15 (0.06-0.37)
CRD-7	0.000	0.060	0.358	0.582	0.01 (0.00-0.04)
PCRD-7	0.036	0.792	0.153	0.018	
ARD-14	0.001	0.247	0.483	0.268	0.04 (0.01-0.11)
BRD-14	0.005	0.608	0.316	0.071	0.18 (0.07-0.52)
FRD-14	0.004	0.543	0.362	0.091	0.14 (0.05-0.39)
CRD-14	0.001	0.309	0.477	0.212	0.05 (0.02-0.15)
PCRD-14	0.028	0.868	0.090	0.014	
16 dpi					
ARD-7	0.011	0.303	0.364	0.322	0.22 (0.10-0.48)
BRD-7	0.012	0.323	0.363	0.301	0.24 (0.11-0.53)
FRD-7	0.007	0.215	0.345	0.432	0.14 (0.06-0.30)
CRD-7	0.001	0.034	0.106	0.859	0.02 (0.01-0.05)
PCRD-7	0.048	0.626	0.231	0.095	
ARD-14	0.003	0.137	0.290	0.570	0.03 (0.01-0.08)
BRD-14	0.012	0.395	0.354	0.239	0.14 (0.06-0.33)
FRD-14	0.014	0.424	0.345	0.217	0.16 (0.07-0.38)
CRD-14	0.003	0.129	0.282	0.586	0.03 (0.01-0.08)
PCRD-14	0.082	0.749	0.127	0.042	
18 dpi					
ARD-7	0.020	0.297	0.303	0.38	0.24 (0.11-0.51)
BRD-7	0.016	0.254	0.295	0.435	0.19 (0.09-0.41)
FRD-7	0.005	0.102	0.19	0.703	0.06 (0.03-0.14)
CRD-7	0.001	0.011	0.028	0.960	0.01 (0.00-0.03)
PCRD-7	0.079	0.583	0.212	0.127	
ARD-14	0.001	0.046	0.131	0.821	0.02 (0.01-0.04)
BRD-14	0.010	0.270	0.351	0.369	0.13 (0.06-0.29)
FRD-14	0.012	0.312	0.354	0.322	0.16 (0.07-0.36)
CRD-14	0.001	0.052	0.144	0.803	0.02 (0.01-0.05)
PCRD-14	0.071	0.681	0.178	0.070	

Table 6 (Cont.)

Evaluation dates and products	Probabilities				Odds ratio
	Sev. 0	Sev. 1	Sev. 2	Sev. 3	
21 dpi					
ARD-7	0.013	0.249	0.233	0.506	0.21 (0.10-0.46)
BRD-7	0.008	0.172	0.197	0.624	0.13 (0.06-0.29)
FRD-7	0.003	0.078	0.114	0.805	0.05 (0.02-0.13)
CRD-7	0.000	0.000	0.000	1.000	0.00 (0.00-Inf)
PCRD-7	0.056	0.566	0.197	0.180	
ARD-14	0.002	0.041	0.057	0.900	0.03 (0.01-0.08)
BRD-14	0.018	0.277	0.214	0.491	0.24 (0.11-0.52)
FRD-14	0.027	0.361	0.223	0.389	0.37 (0.17-0.77)
CRD-14	0.001	0.025	0.036	0.938	0.02 (0.00-0.06)
PCRD-14	0.070	0.565	0.177	0.189	

[a]0 = healthy/symptomless plant, 1 = mild to moderate wilting, 2 = severe wilting and 3 = dead plant.

[b]dpi = days post inoculation.

[c]In brackets 95% confidence interval.

Some of the plantlets treated with B, C or fosetyl-al exhibited symptoms of phytotoxicity which appeared as leaf spots of burnt tissue. The symptoms were more evident in plants treated with C. Plants of group RD-7 (product treatments done 7 days before the inoculation) were the most affected (Figure 5).

Figure 5: Leaf spots of burnt tissue as seen on 'California Wonder' pepper plants treated on 16/04/2018 with products B, C and F (fosetyl-al). Photos taken on 24/04/2018.

5 Discussion

5.1. *In vitro* experiments

Products commercialized under the term biostimulant should not have fungitoxic effects but, instead, enhance plant defence against pests and diseases indirectly by benefiting the plant (Calvo *et al*., 2014). Apart from two oomycetes, the *in vitro* study included three fungal species. This broadens the spectrum of pathogens tested and aims to give more robustness to the conclusions of the study by examining the effects of the products on non-target pathogenic fungal species as well. *Fusarium* and *Verticillium* are soil-borne pathogens and, like *Phytophthora*, infect the plant via the root (Mace, 2012). Thus, they were chosen based on having a similar infection route with *Phytophthora*. On the other hand, *Alternaria* is the causal agent of foliar diseases (Kustrzeba *et al*., 2014) and was chosen based on being less similar to the other two fungi.

Only a single strain of each oomycete and fungus is included in the study, since the effects of within-species genetic diversity are not a focal point of the objectives. Representing each pathogen with a single strain allows more time, labour and resources to be allocated to the investigation of fungitoxicity on different species of pathogens instead of different genotypes of few of them. In this study, it is considered more productive to investigate the variability of product toxicity between-species rather than within-species. Since the products and their formulation components are expected to be non-fungitoxic, it is unlikely for differences to be observed between genotypes of a single species. In other words, proving fungitoxicity levels to be zero for single strains of different species offers more robust evidence of a product being non-fungitoxic. Given that, more focus is put in examining whether non-target pathogens, such as *F. solani*, *V. dahliae* and *A. alternata*, are also not affected by the products, instead of creating a more elaborate study on *Phytophthora* strains.

Based on the results of the *in vitro* experiments, it can be concluded that all products and formulation components submitted for examination (L01- L13, A and B) are not fungitoxic to any of the five pathogens tested. In some occasions, the effect of concentration (slope) was statistically significant, yet, the value of the slope in the regression was extremely low and thus growth reduction was not considered biologically relevant, being more associated with the inherent experimental variability. For instance, L01 affects *P. capsici* by significantly decreasing colony growth. Nonetheless, within the tested L01 concentration, the maximum growth reduction achieved did not exceed the level of 4% (data not shown). The same is true for statistically significant growth increases, with the exception of the combination of pyraclostrobin – *P. capsici*, which will be discussed later. In product-pathogen combinations in which growth is induced when a product is applied, the effect may be statistically significant for a given probability ($\alpha = 0.05$) but remains extremely low and thus biologically irrelevant. For example, L01 affects *F. solani* by significantly increasing colony growth; yet, this increase did not exceed the level of 3% (data not shown). It is also important to note that most of these statistically significant differences are due to data collected from colony growing in 100 ppm, which is the maximum

concentration used. In fact, fungitoxicity studies do not tend to use concentrations exceeding that of 100 ppm since effects observed could also be connected to an osmotic effect due to the presence of a solute in such amounts. Similarly, here, it is possible that these statistically significant, yet biologically irrelevant events are related to a chemical change of the medium on which the pathogens grew slightly better with a specific amount of solutes. Thus, taking all the above in consideration, this study provides robust evidence to support that the products L01 – L13, A and B do not have any substantial fungitoxic or fungal-growth-promoting properties.

Fosetyl-al, C, mefenoxam and pyraclostrobin are commercially used fungicides of known fungitoxic effects and were expected to inhibit the growth of their target organisms. Fosetyl-al did not inhibit the growth of any of the pathogens above the level of 50%, suggesting that it has no substantial fungitoxic properties. The same was true for a few more product-pathogen combinations regarding commercially available fungicides. These combinations are C against *A. alternata* and *F. solani*, mefenoxam against *A. alternata*, *F. solani* and *V. dahliae* as well as pyraclostrobin against *P. citrophthora* (Table 3). Observing that commercially available products do not have an effect on certain pathogens may be due to the fact that the products are not specific for such pathogens or that the strains used, were resistant to the products.

Fosetyl-al, which degrades into phosphonic acid, is used as preventive and curative fungicide against *Phytophthora* spp. in apples, avocados, ornamentals, peaches and pineapples (BAYER CROP SCIENCE, 2018). It is a phosphonate with FRAC code P7 and acts by host plant defence induction (FRAC, 2018). In Spain, it is labelled for citrus but not for pepper crops, so in this later case it may be possible that it is not expected to control *P. capsici* (BAYER CROP SCIENCE, 2018). Having used a phosphate-rich medium may have been connected to the reduced effects observed against *P. capsici* and *P. citrophthora*, since earlier *in vitro* studies had shown that the activity of fosetyl-al and most importantly, of phosphonic acid, is most prominently seen *in vitro*, in phosphate-poor media (Fenn and Coffey, 1984). Fosetyl-al achieved a maximum of 7% growth inhibition against *P. capsici* and a 40% growth inhibition against *P. citrophthora* at 100 ppm. An effect on *P. capsici* may have not been expected, yet based on past literature, *P. citrophthora* isolates have been observed to reach the level of 50% growth reduction (Fenn and Coffey, 1984; Coffey and Bower, 1984; Smillie *et al.*, 1989). The lack of high levels of fungitoxicity, however, does not deem fosetyl-al ineffective in controlling Phytophthora diseases, since there is evidence of both direct and indirect modes of actions; in the case of the latter, the product is seen to have an effect *in vivo* even if the isolates used were not affected *in vitro* (Smillie *et al.*, 1989; Fenn and Coffey, 1985; Guest, 1984; Fenn and Coffey, 1984). In the case of citrus crops, which are hosts of *P. citrophthora* for instance, fosetyl-al and phosphonic acid increase the concentration of scoparone, a phytoalexin which confers resistance to Phytophthora (Afek and Sztejnberg, 1989). At the same time, fosetyl-al is not labelled for use against *F. solani*, *V. dahliae* or *A. alternata*; hence, not affecting the growth of these fungi was foreseen.

Similarly, C targets *Phytophthora* spp. and thus, not affecting *F. solani* or *A. alternata* was foreseen. Interestingly, the growth of *V. dahliae* was significantly affected, although at high product concentrations (EC_{50} = 97.26 ppm), suggesting that C might also be effective against this pathogen, but being a vascular pathogen, its field performance may be rather limited.

Mefenoxam specially targets oomycetes, thus, only affecting *P. capsici* and *P. citrophthora* was expected (SYNGENTA, 2018). It is a phenylamide of FRAC Group A, affecting the RNA-polymerase I of its targets (FRAC, 2018). Cases of *P. capsici* isolates which have acquired resistance to mefenoxam have been recorded over time; yet, this requires exposure to the fungicide in the field (Café-Filho and Ristaino, 2008; Parra and Ristaino 2001), a requirement not fulfilled by the *P. capsici* isolate used in this study.

Lastly, pyraclostrobin is a broad-spectrum fungicide and all species were expected to be affected by it (BASF CORPORATION, 2003). It is a methoxy-carbamate (C3 fungicide) and affects its target organisms through acting on the respiratory complex III: cytochrome bc1 (ubiquinol oxidase) at Qo site (cyt b gene) (FRAC, 2018). Indeed, the growth of all five pathogens was significantly inhibited by the fungicide (Table 4), yet, in the case of *P. citrophthora*, growth inhibition did not exceed the level of 40% for the concentrations tested (Annex II). The data regarding *P. capsici* grown in the presence of pyraclostrobin are also interesting. So far, there are no records of *Phytophthora* spp. being resistant to pyraclostrobin and the oomycete isolates of this study were recovered from fields which had not been previously treated with pyraclostrobin. Nonetheless, low growth inhibition levels for *P. citrophthora* suggest that pyraclostrobin has lost its effect to inhibit the growth of this strain.

At the same time, the fact that *P. capsici* grew normally at the presence of 100 ppm pyraclostrobin, even though lower concentrations affected its growth, might be an indicator of a special case of resistance. Fungicide resistance is usually seen more prominently when low fungicide concentrations are applied (Ma and Michailides, 2005) and even though there are multiple cases of resistance discussed in the literature, the case of this *P. capsici* isolate is rare. Nonetheless, it is not unique between *Phytophthora* spp.; a sensitive *P. infestans* isolate became tolerant after a single passage on mefenoxam-containing medium (Childers *et al.*, 2014) in this same way. The isolates studied had upregulated various genes (a phospholipase "Pi-PLD-like-3," two ATP-binding cassette superfamily [ABC] transporters, and a mannitol dehydrogenase) which were speculated to be involved in the mechanism behind this type of resistance development. It is hypothesised that the *P. capsici* isolate used in this study possesses one or more genetic traits that allow it to activate resistance only in the presence of high concentrations of pyraclostrobin. In this way, growing slower in concentrations below 100 ppm while maintaining resistance inactivated, gives the isolate the advantage of avoiding the metabolic fitness cost of resistance in the absence of high levels of pyraclostrobin. Such assumption would also coincide with the finding of Childers *et al.*

(2014) that acquiring resistance to mefenoxam came with the cost of growing slower in mefenoxam-free medium. The effects of fosetyl-al, C, mefenoxam and pyraclostrobin were not in the core of this study, yet, results such as the growth rates of the two oomycetes in pyraclostrobin should be investigated further through a pathogen resistance point of view.

Given the above, it can be concluded that products L01 –L13, A and B were not fungitoxic to *P. capsici*, *P. citrophthora*, *F. solani*, *V. dahliae* and *A. alternata*.

5.2. Greenhouse trials

The greenhouse trials aimed at evaluating the efficacy of the biostimulant products A and B in preventing *P. capsici* from infecting pepper plantlets. Fosetyl-al and C were also used for comparison. Overall in trial 2.1, plantlets were observed to become progressively affected and deteriorate rapidly, thus, moving from one severity category to the next in a fairly short period of time. Out of the 500 inoculated plants across all treatments, only 79 were healthy 7 dpi, a number which was reduced to 10 when data were collected 21 dpi. Designing an experiment in which plant death occurs rapidly is advantageous with regards to optimising time and resources invested, however, a very aggressive infection may not always be representative of the epidemic of a disease in field conditions and, thus, treatment effect may be jeopardized.

The root dipping inoculation was chosen on the basis of existing protocols used in such trials when working with pepper plantlets and their root-infecting pathogens (Akgül and Mirik 2008; Bhat and Subbarao 1999; Nemec and Strandberg 1996; Van Steekelenburg 1980; Wang *et al*., 2013). Similarly to those, *P. capsici* infects the plant through the root system and is favoured by the presence of either natural or mechanically caused wounds (Lamour *et al*., 2012). Root dipping inoculation is thought to be particularly successful due to the formation of mechanical wounds during the process of uprooting the plantlets before submersing their roots in the zoospore suspension. Wishing to make the inoculation more aggressive, the dipping period was pro-longed to 48 hours. This amount of time was chosen based on the empirical knowledge that the research team had collected by working on citrus plants. The suitability of inoculation duration, however, is also related to the characteristic of the different plants. On the one hand, citrus plantlets are more rigid, have thicker and more resilient roots while on the other hand, pepper plantlets have a generally softer shoot and root tissue. Given this, it can be expected that the damage experienced by uprooted pepper plantlets is larger than that experienced by uprooted citrus plantlets. It is apparent that a root dipping inoculation of 48 hours may be moderate when working with citrus, yet, considerably aggressive for pepper plantlets. Across the literature (Akgül and Mirik 2008; Bhat and Subbarao 1999; Nemec and Strandberg 1996; Van Steekelenburg 1980; Wang *et al*., 2013), root-dipping for pepper and other vegetables is only momentary before transplanting. At the same time, the fact that pepper plantlets are generally of soft tissue may also cause them to be more sensitive to the stress of transplantation. Evidently, pepper plantlets (including the

non-inoculated/non-treated control) needed a week to recover from the stress of being transplanted which is why no data were collected during that period.

Epidemiological studies often use disease incidence as their response variable; data are recorded by dichotomizing the plants into affected and not-affected and can, thus, be analysed with a binomial logistic regression. Handling binomial data is clearly simpler than ordinal data since the number of model parameters is lower, yet, disease incidence may oversimplify experimental results and thus lead to less informative results. Evaluating plants as either affected or not-affected by a disease suggests that plants with very few symptoms are grouped along with those heavily affected, completely defoliated or dead plants. Evidently, this eliminates a large amount of informative variability from the results, especially when consecutive evaluations are done along a period of time. On the other hand, disease severity is a response variable of multiple levels, chosen according to the symptoms of the specific disease evaluated and based on few and clearly defined categories. The ordinal data retrieved from a disease severity evaluation may be harder to analyse, yet, they can be more fruitful when interpreting their analysis (Kranz and Rotem, 2012). Given the above, even though not all data sets met the proportional odds assumption of the proportional odds ratio, the data were maintained on an ordinal scale instead of being rearranged in a binomial format (merging categories 1, 2 and 3 into a single one).

In relation to the treatments of group RD-14, the data sets corresponding to the evaluations done 9, 11, 16, 18 and 21 dpi rejected the proportional odds assumption, which may happen even if the data deviate only slightly from it (O'Connell, 2006). In this case, rejecting the assumption is probably a result of the reference group data (positive control treatment) having minimal or null variability. In the case of the 11 dpi evaluation, all plants of the positive control were scored as mildly wilted (category 1). Additionally, 9, 14 and 16 dpi, reference group plants were found in only two categories and more than 90% of them were scored as mildly wilted. The evaluations done 18 and 21 dpi do appear to include more variability (plants found in 3 out of the 4 categories), yet, the data sets still do not fulfil the assumption. This suggests that it may be more suitable to use the non-proportional odds model, which relaxes this assumption. In this model, the regression parameters are allowed to vary across the levels of Y and probability and odds ratio estimates differ due to the extra parameters. In other words, the different levels of a single treatment do not share a single coefficient and, thus, have different slopes. This makes model interpretation quite difficult and model parameters poorly informative. It has been seen that using smaller models with a minor defect may give probability and odds ratio estimates that approach the reality more than a much larger model without a defect (Bilder and Loughin, 2015). In this analysis, non-proportional odds models were examined for the group RD-14 evaluations 9, 11, 16, 18 and 21 dpi and were all deemed unsuitable; the goodness of fit was very poor and the odds ratio estimates mostly had a value of OR = 0.00 and $CI_{0.95} = (0.00, +\infty)$. Another possibility would have been to compare each application with the positive control on

separate logistic regressions, yet, this would not allow comparisons to be done between applications and was thus disregarded.

The data sets of all evaluations were analysed with the proportional odds logistic regression model. The poor model fit of the the group RD-14 evaluations 9, 11, 16, 18 and 21 dpi data sets is seen as a result of contradicting the proportional odds assumption and is, hence, also disregarded. The proportional odds assumption could have possibly been met after restructuring the data and pooling NT_{RD-7} and NT_{RD-14} (the two inoculated/non-treated controls) into one group which would be then used as reference for all treatments. However, the χ^2-test conducted to examine whether NT_{RD-7} and NT_{RD-14} could be considered a single group, showed that there is a significant difference between the means of the two data sets which is evidence against the merge of the two groups. Regarding the data sets fullfilling the assumption and having a good model fit, failing to reject the proportional odds assumption is not evidence that the assumption holds true. However, it does bring certain assurance that a proportional odds model would yield a reasonable approximation to true relationships between Y and the explanatory variable(s) (Bilder and Loughin, 2015).

In the statistical analysis of the data, the inoculated/non-treated control was used as reference in order to compare the outcome of the different treatments with the progression of the disease on non-treated plantlets, assuming that those would supposedly have lower chances of surviving against the infection. As seen in Table 6, however, all odds ratios ranged from 0 to 1 suggesting that none of the treatments achieved to significantly increase the chances of controlling the disease. Additionally, the 95% confidence intervals of most odds ratios do not overlap with the value of 1, demonstrating that in these cases, the odds are even against said treatments, or in other words, that these treatments resulted in a significant reduction of likelihood of controlling the disease. These results suggest that none of the products used were effective in preventing or impeding infection and disease progression by *P. capsici* under the experimental conditions tested.

At the same time, it is important to explain the possible reasons causing those treatments to give adverse results and disadvantage the plantlets. In the cases of using fosetyl-al and C, spots of burning were visible on some plantlets of each application group within a few days after application; plantlets treated with B also exhibited some leaf burning but the incidence was much lower (Figure 5). The plantlets were grown in greenhouse conditions, yet, having been sown in February may have been the cause of the plants growing slowly and not as robust as they would have done under other circumstances. Thus, even though product dosages were used as recommended and plants were not exposed to intense sunlight after product application, being weak may have made the plantlets more prone to leaf burning. Additionally, phytotoxicity incidence cannot be quantified since it may have been manifested in other ways as well, which could have went unnoticed. For example, biostimulant A did not cause any visible leaf burning at all, yet, also caused adverse effects on treated plantlets and, thus, it would be logical to hypothesise that it could have affected the plantlets through

causing phytotoxicity in a non-visible way. Nonetheless, it must be noted that since the extreme aggressiveness of the inoculation process had already created a very poor plant status, it is likely for phytotoxicity to be the result of the products applied in interaction with this poor status in a way that would have not been observed if plants had remained physiologically robust throughout the experiment.

The physiological side effects of fungicides on plants have been discussed in various studies in the literature. These regard various plant species and different types of fungicides, yet, since they are based on few physiological parameters, reviewing them can lead to controversial conclusions regarding the exact ways in which plants exposed to fungicides are physiologically harmed (Dias, 2012). Nonetheless, adverse effects on plant health are commonly attributed to the consequence that a product application can have on the photosynthetic rates of a plant's green tissue and it can be speculated that this is the likely physiological base of poor plant status in this study as well (Saladin and Clément, 2005). In the case of fosetyl-al, for example, pulverizing tomato plants with the chemical has proved to increase the amount of closed and abnormal stomata in the leaves, thus, causing adverse physiological effects especially when using an increased fungicide concentration (İlkay, 2009). The recommended dose of Aliette WG 800 (80% fosetyl-al) is 0.2% and İlkay (2009) found that stomata suffer especially when doubling that dose to 0.4%.

The results from treatments ARD-7 7 dpi, BRD-14 9 dpi, FRD-14 9 dpi and FRD-14 11 dpi did not differ significantly from those of the non-treated groups (NTRD-7 and NTRD-14) (Table 6). This finding and the fact that such results are dispersed between data sets of different evaluation dates could imply that plantlets had the ability to recover to a certain extent and, thus, not follow a progressively deteriorating disease pattern, but rather initially go through a phase of fluctuating between disease severity categories. This is also evident when observing an increase in healthy plants (category 0) from one evaluation date to the next (e.g. treatment FRD-14 scored 9 healthy plants 7 dpi and 13 healthy plants 9 dpi) (Figure 4).

Considering all information regarding the methodology used in trial 2.1 as well as the results of the statistical analysis, it is concluded that the most likely explanation causing all treatments to significantly increase the incidence of more heavily diseased plants might be a result the excessive stress during inoculation interacting with phytotoxicity. The fact that plantlets were sown in winter should also be taken into account, as an additional stress factor. Therefore, the consideration of a different experimental design became necessary. In trial 2.2, plantlets were sown in spring and thus grew to be more rigid when being on the same leaf stage with those inoculated in trial 2.1. This could also suggest that they would, thus, be more resilient to phytotoxicity. Most importantly, however, trial 2.2 was based on inoculation via irrigation which is considered much less aggressive and is also commonly used in similar studies (Padley *et al*., 2008; Polach and Webster, 1972; Reifschneidbr *et al*., 1986; Van Steekelenburg 1980). Plants were neither uprooted nor transplanted and, thus, no wounds were induced which greatly reduces the stress levels experienced by the plantlets. During inoculation, the soil was

saturated with the zoospore suspension and the *P. capsici* zoospores were allowed to infect the plantlets via natural wounds in the root system, such as, for example, those created at the point of lateral root emergence.

Plantlets of trial 2.2 had to be inoculated twice due to the absence of disease symptoms after the first inoculation. The time limits of this investigation did not allow the completion of the trial nor the analysis of its data, thus, trial 2.2 is not extensively discussed here. Nonetheless, a further trial is planned following a methodology adjusted to the plant-pathogen system studied. More specifically, plantlets will be sown in late summer-early autumn to grow in temperate temperatures and develop robustly. The plantlets will be inoculated via irrigation after letting the substrate dry for at least 24 hours in order to make it as absorbent as possible. Apart from reducing soil water content, this slight water stress will make the plantlets more prone to be infected by the oomycete. Plantlets will either be inoculated when having nine true lives and then transplanted in more spacious alveoli, with minimal additional wounds, or will be inoculated at an earlier growth stage and be kept in the 16 cm^2 alveoli until the completion of the evaluation period. Implementing these amendments to the methodology of the greenhouse trial is expected to yield comprehensible results regarding the efficacy of products A, B, fosetyl-al and C when used in the greenhouse. It would also be advised for one more products to be included in the trial, such as azoxystrobin or dimethomorph for example since studies have shown that other fungicides may be more effective in control *P. capsici* than fosetyl-al (Matheron and Porchas, 2000a; Matheron and Porchas, 2000b). Such addition would serve in obtaining a more spherical view of potential product effect on disease progression in pepper plantlets infected with *P. capsici* and allow to accurately evaluate the efficacy of products A and B.

6 Conclusions

-In the *in vitro* experiments, product C proved to be fungitoxic to *P. citrophthora*, *P. capsici* and *V. dahliae*, mefenoxam to *P. citrophthora* and *P. capsici* and pyraclostrobin to *P. capsici*, *A. alternata*, *F. solani* and *V. dahliae*, while products L01, L02, L03, L04, L05, L06, L07, L08, L09, L10, L11, L12, L13, A, B and fosetyl-al were not fungitoxic to any of the oomycetes and fungi evaluated. Data regarding the effects of pyraclostrobin on *P. capsici* were inconclusive.

-In the greenhouse trials, in trial 2.1, the potential benefits of A and B in preventing *P. capsici* from infecting pepper plantlets seemed to have been masked by the negative impact that inoculation aggressiveness and phytotoxicity had on plant status. The same was true for fosetyl-al and C. Along the 21 days of evaluation, disease was even more severe on inoculated/treated plantlets than on inoculated/non-treated plantlets. Trial 2.2 was also inconclusive.

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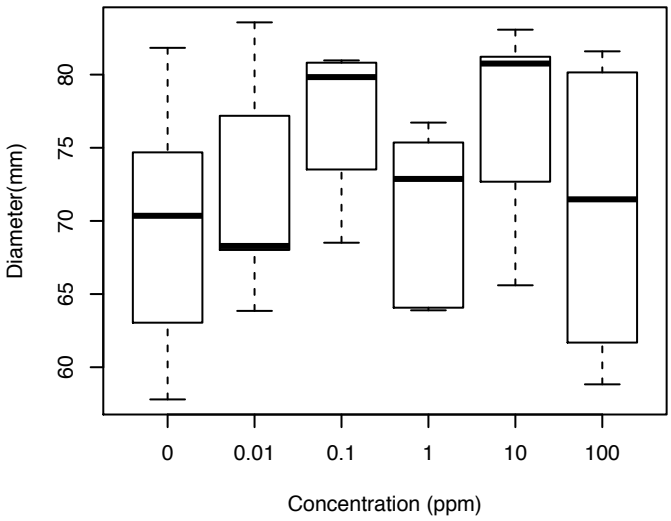
Annex I

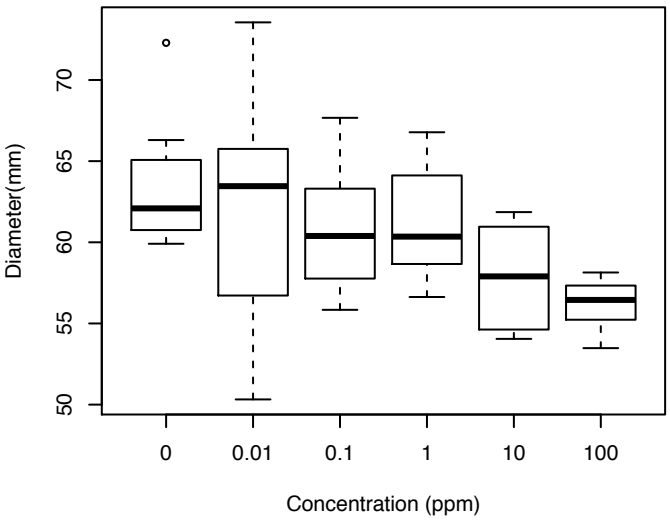
Descriptive data of colony growth (diameter) of the pathogens *Phytophthora capsici*, *P. citrophthora*, *Fusarium solani*, *Verticillium dahliae* and *Alternaria alternata* when grown in different product concentrations. Concentrations tested ranged from 0 ppm to 100 ppm.

L01

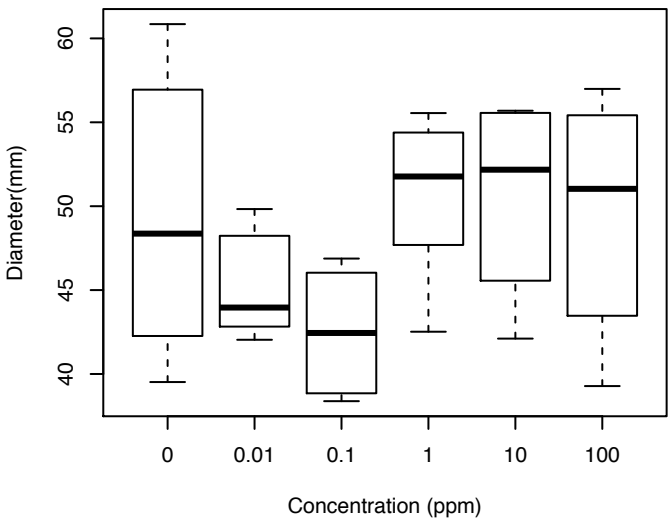
Phytophthora citrophthora



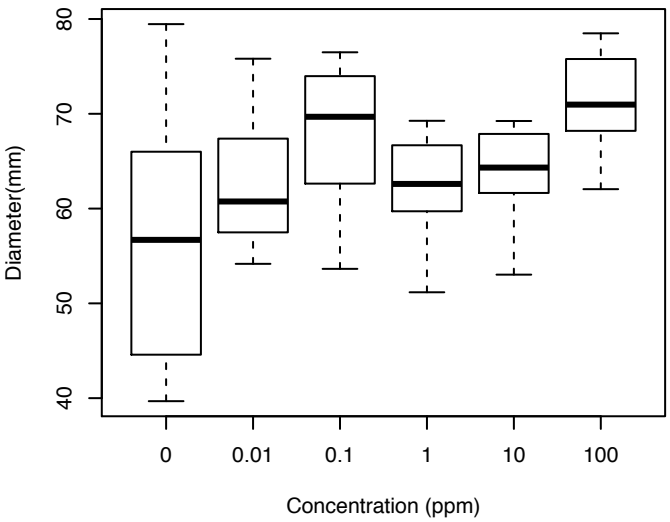
Phytophthora capsici



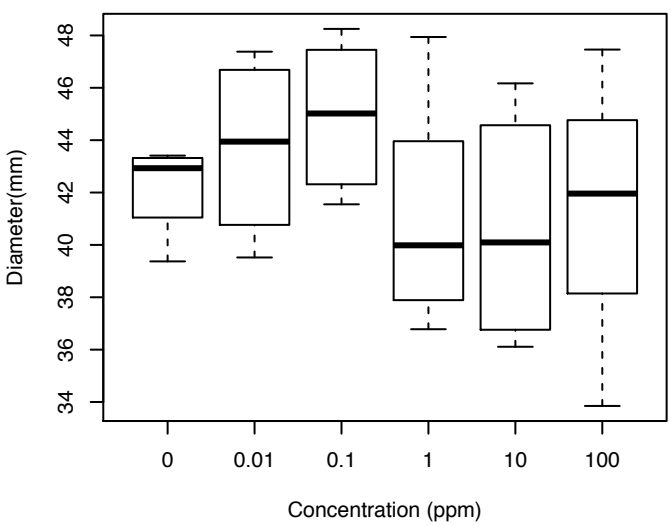
Alternaria alternata



Fusarium solani



Verticillium dahliae



L02

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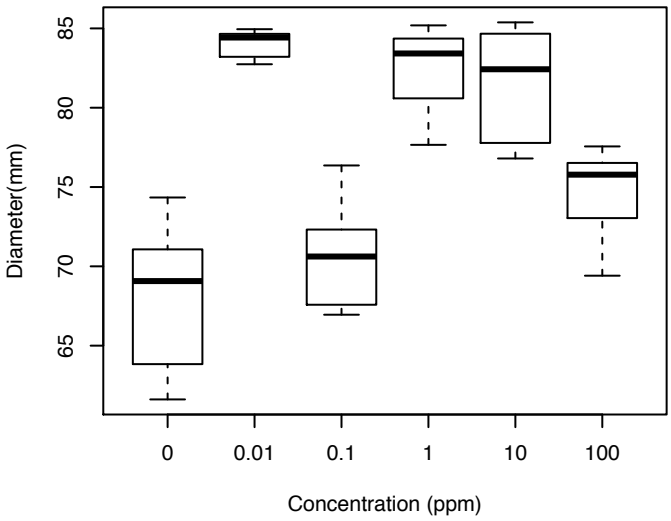
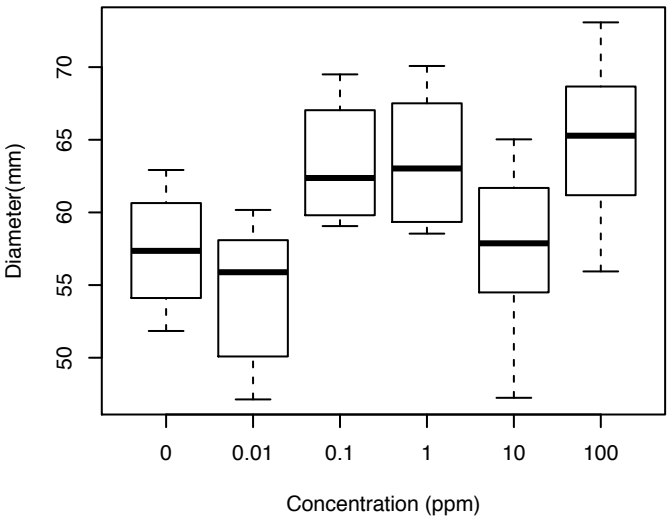
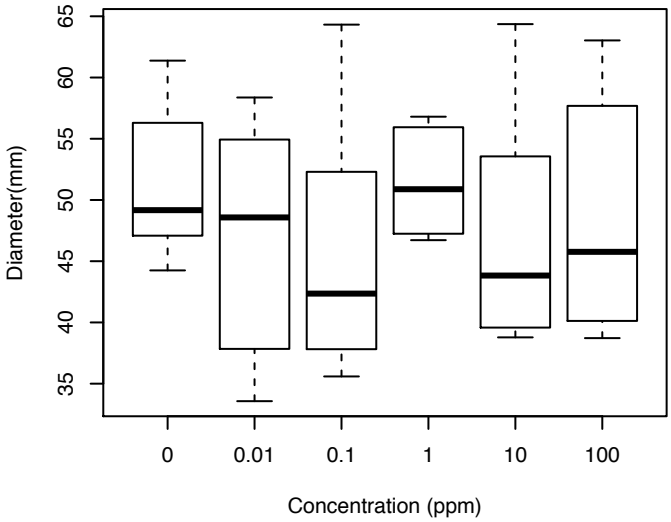


Phytophthora capsici



Alternaria alternata



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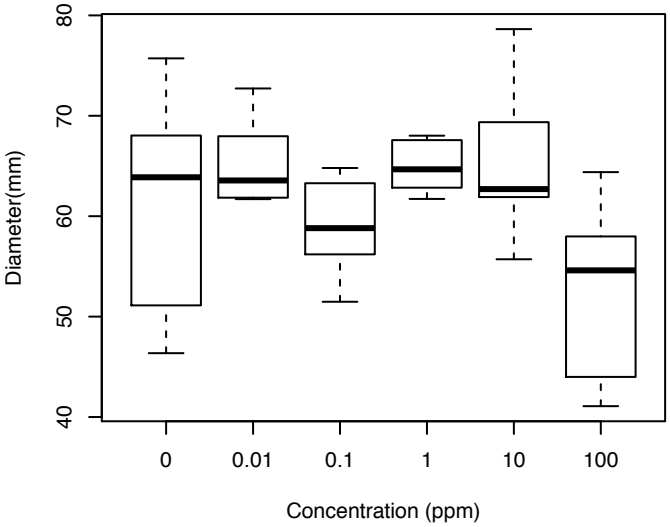

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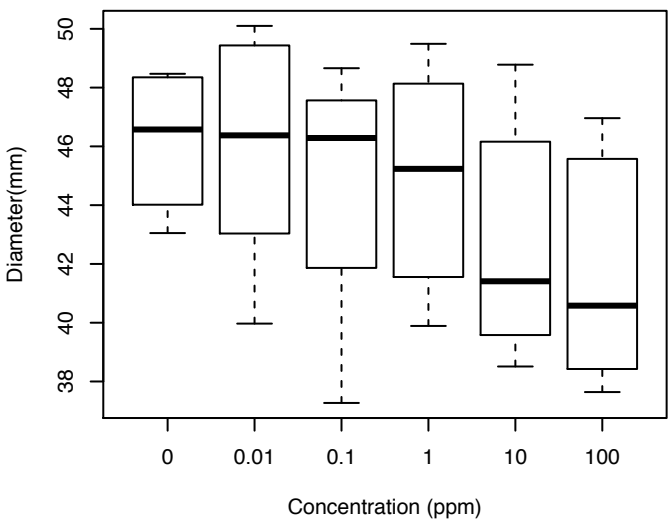
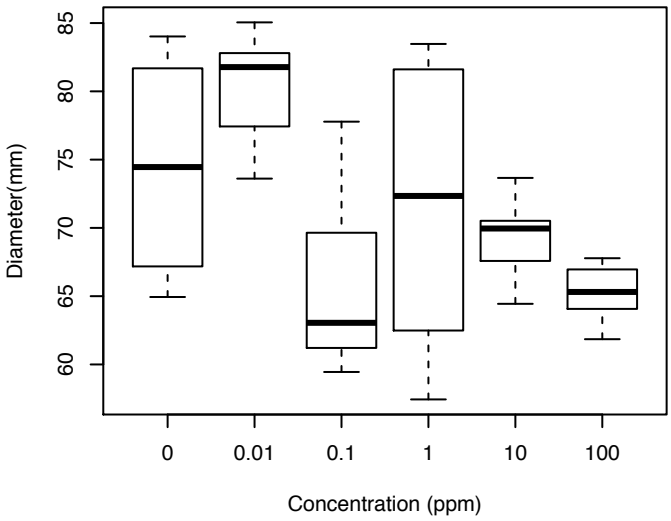
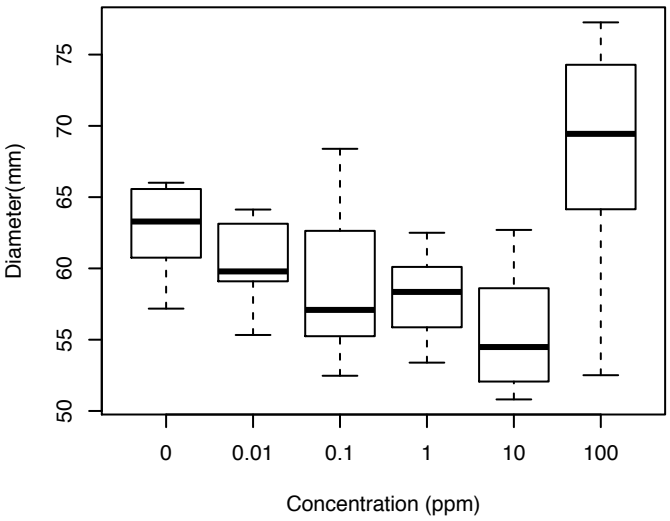


L03

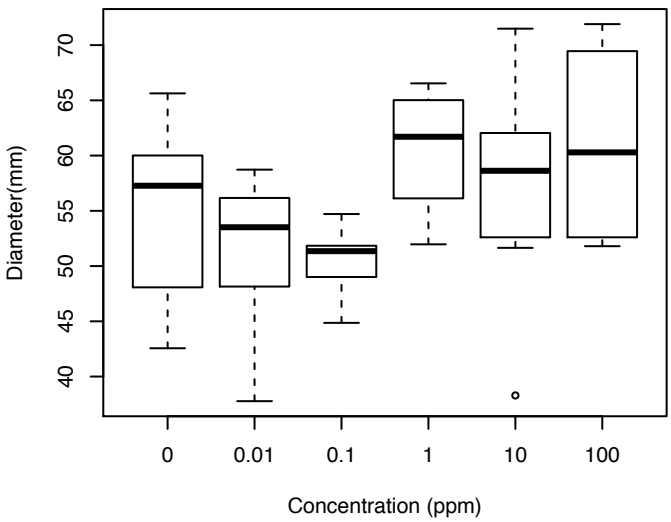
Phytophthora citrophthora



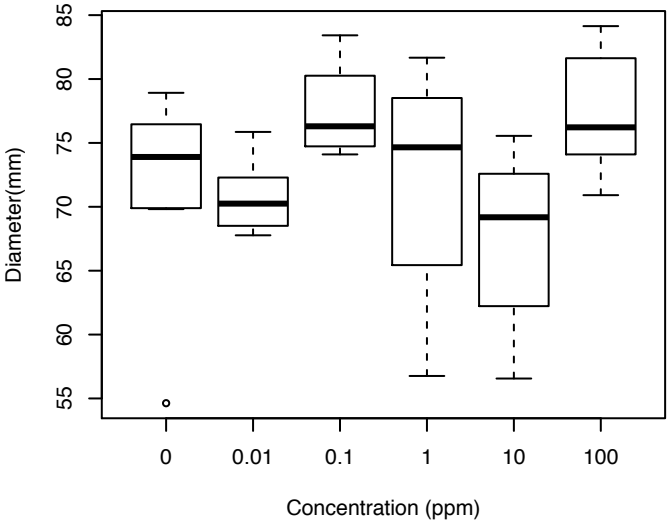
Phytophthora capsici



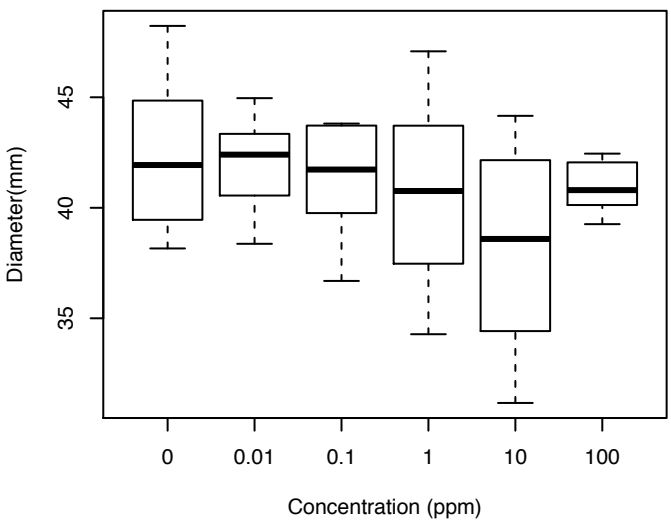
Alternaria alternata



Fusarium solani

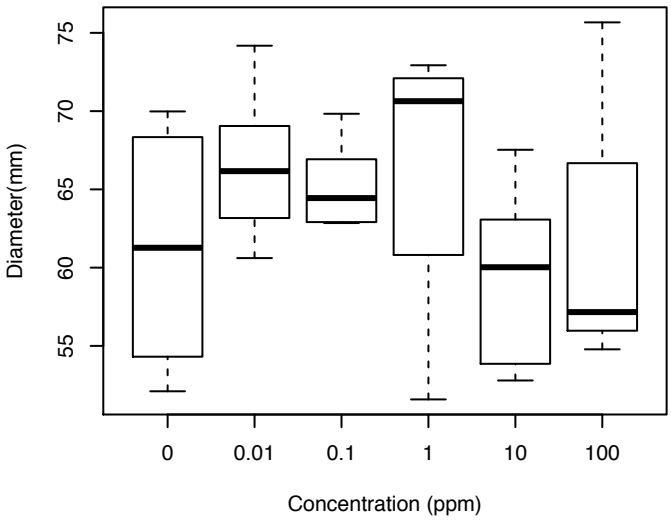


Verticillium dahliae

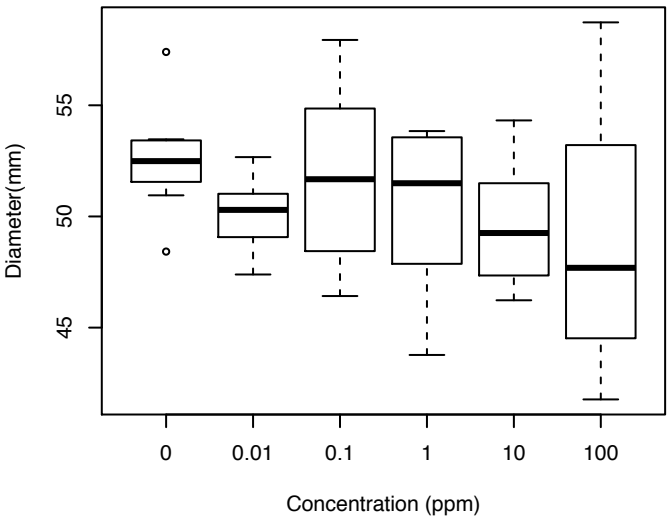


L04

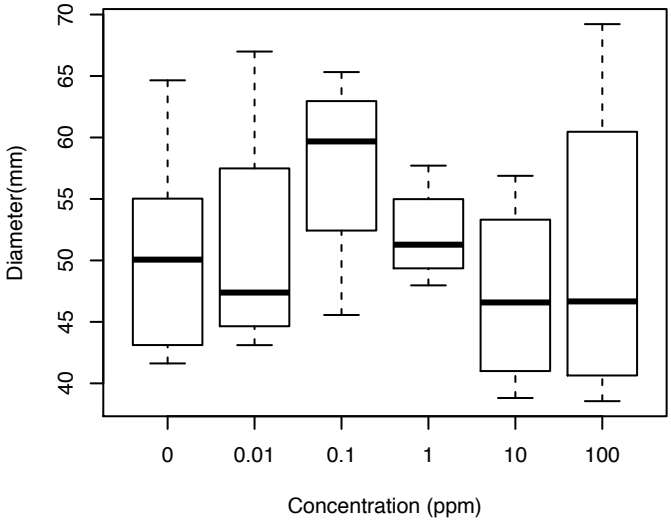
Phytophthora citrophthora



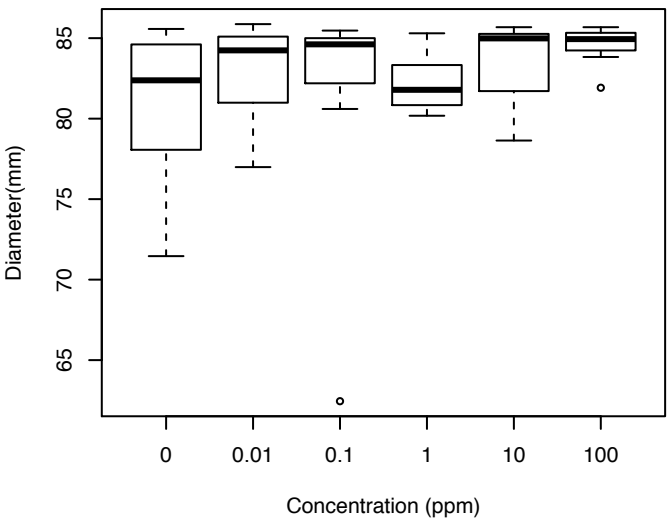
Phytophthora capsici



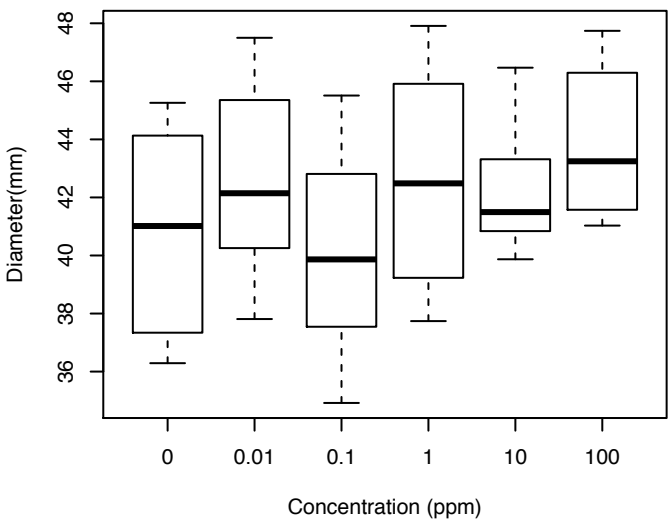
Alternaria alternata



Fusarium solani

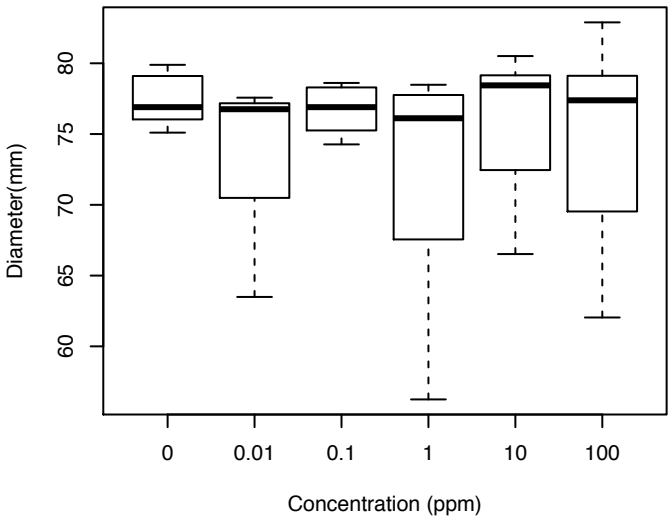


Verticillium dahliae

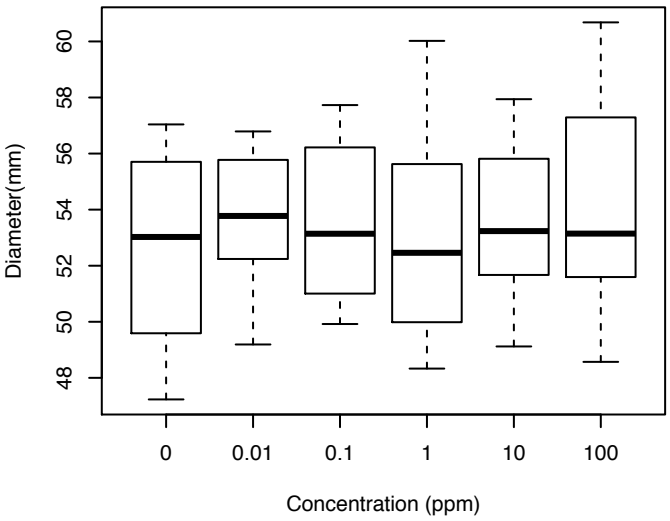


L05

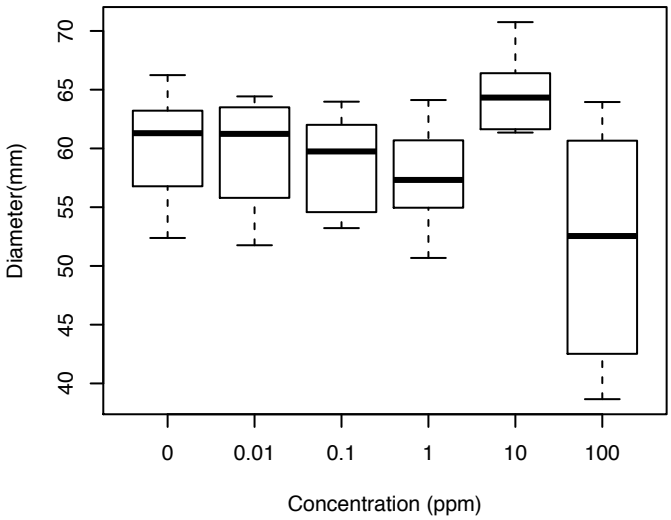
Phytophthora citrophthora



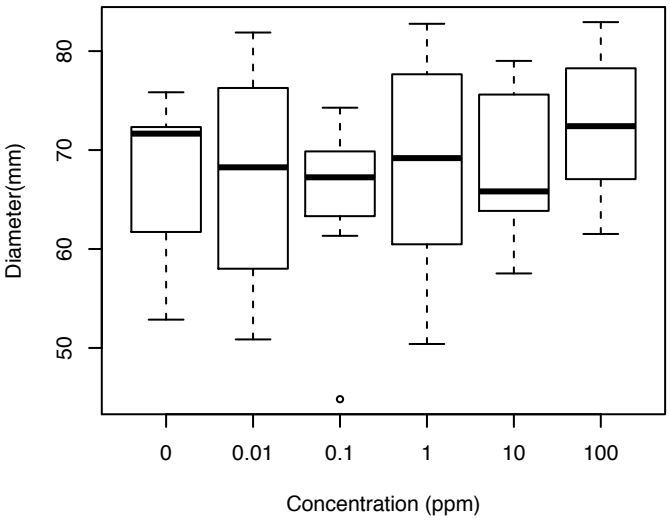
Phytophthora capsici



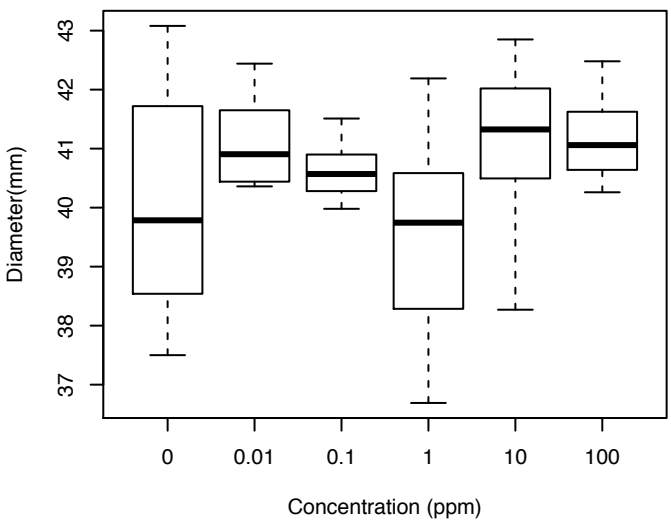
Alternaria alternata



Fusarium solani

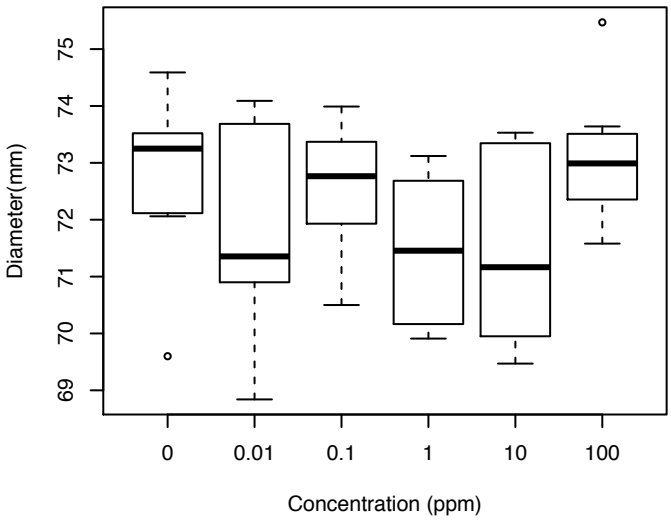


Verticillium dahliae

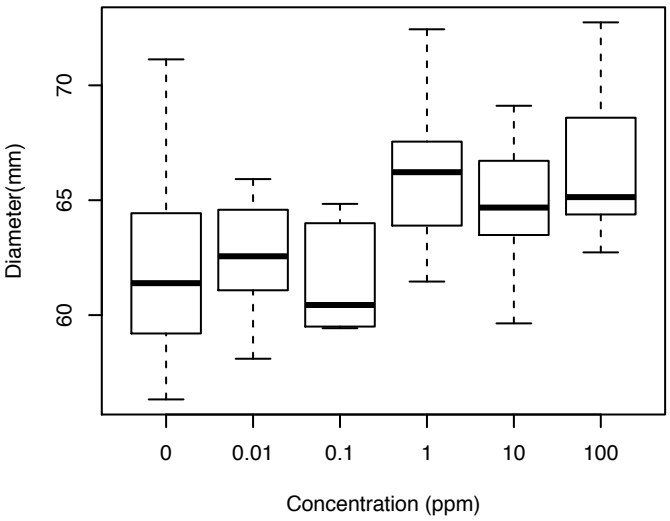


L06

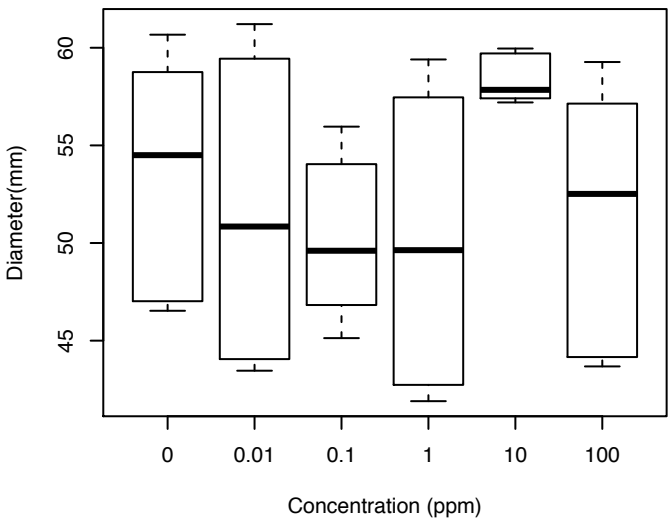
Phytophthora citrophthora



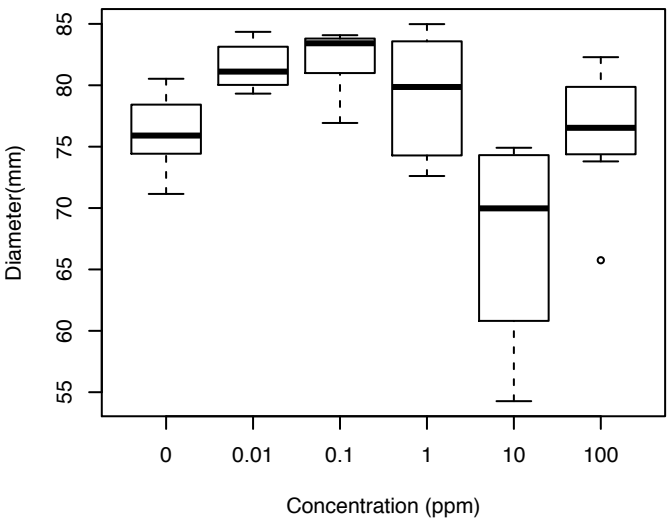
Phytophthora capsici



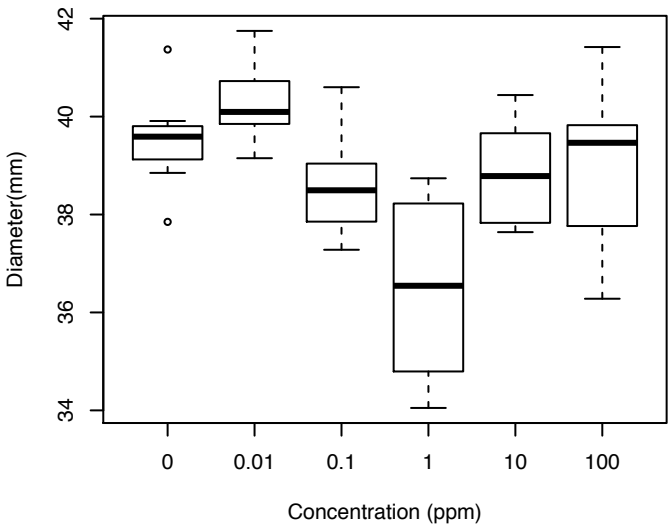
Alternaria alternata



Fusarium solani

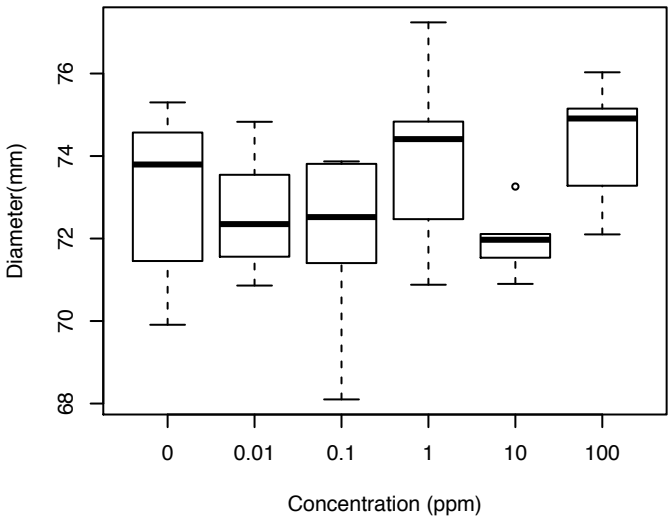


Verticillium dahliae

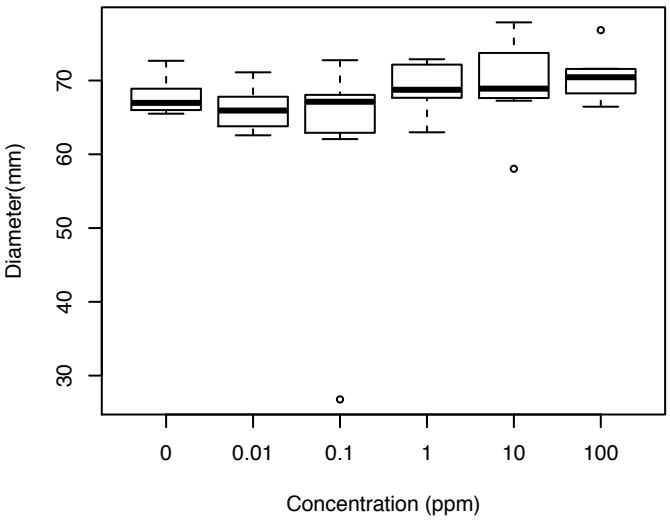


L07

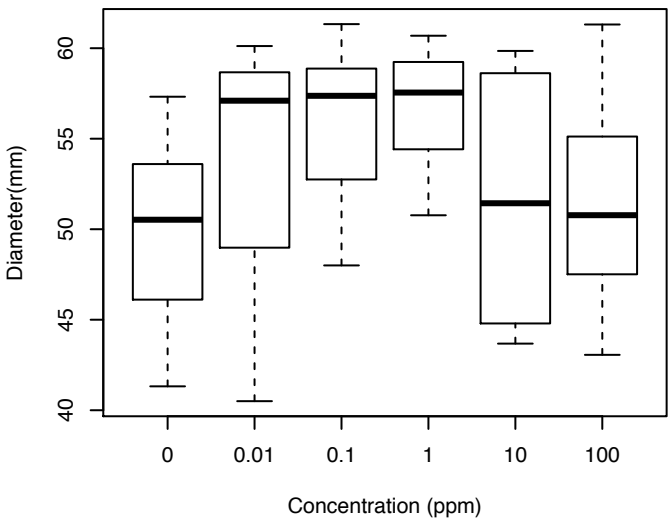
Phytophthora citrophthora



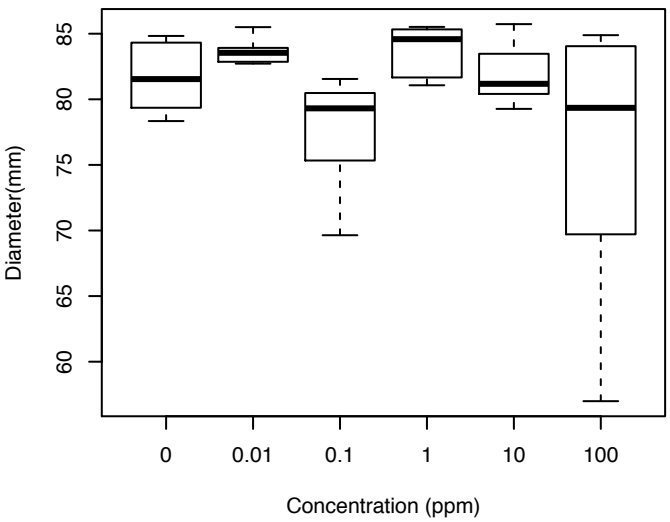
Phytophthora capsici



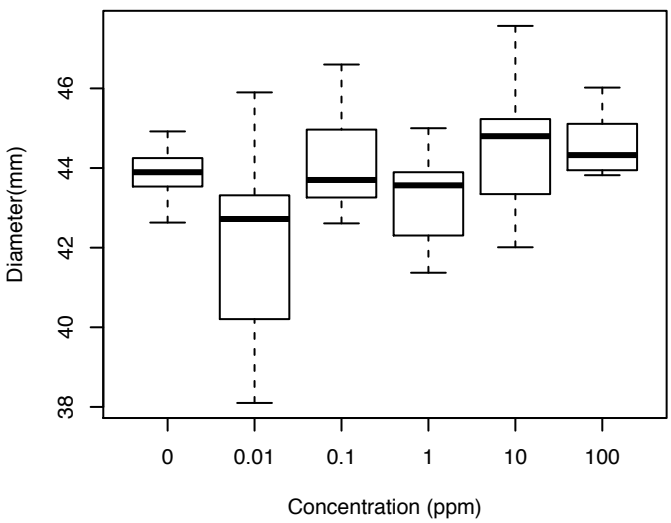
Alternaria alternata



Fusarium solani

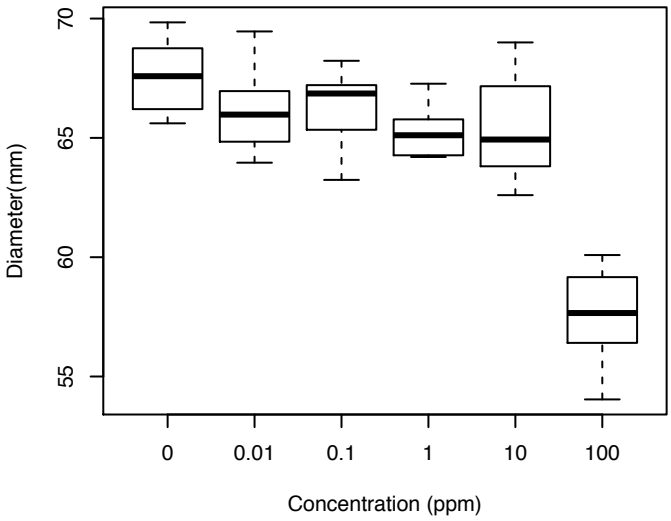


Verticillium dahliae

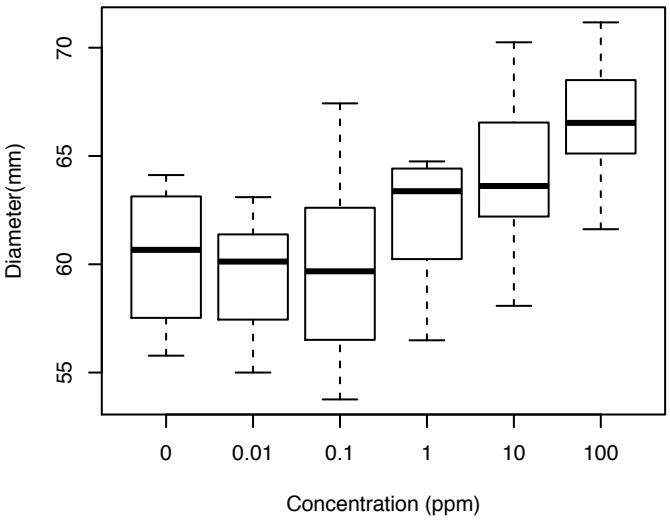


L08

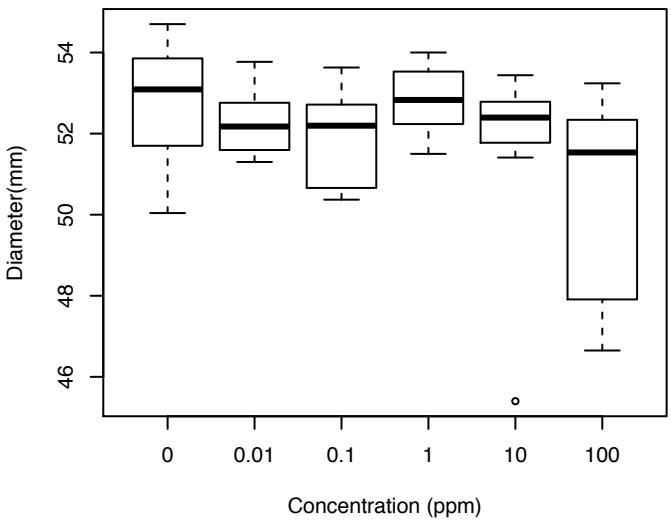
Phytophthora citrophthora



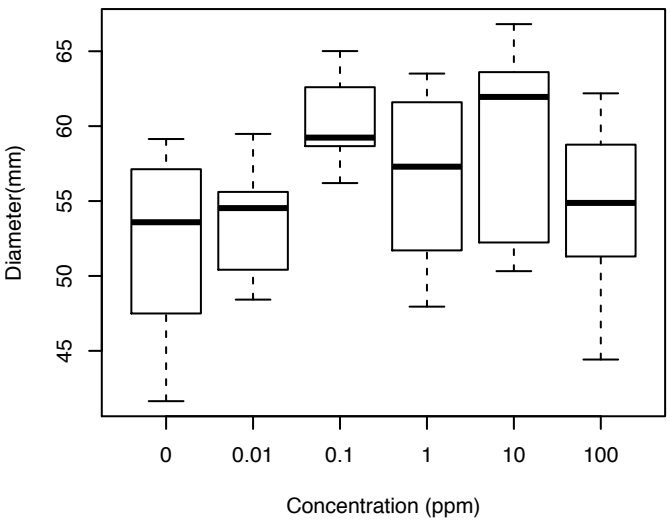
Phytophthora capsici



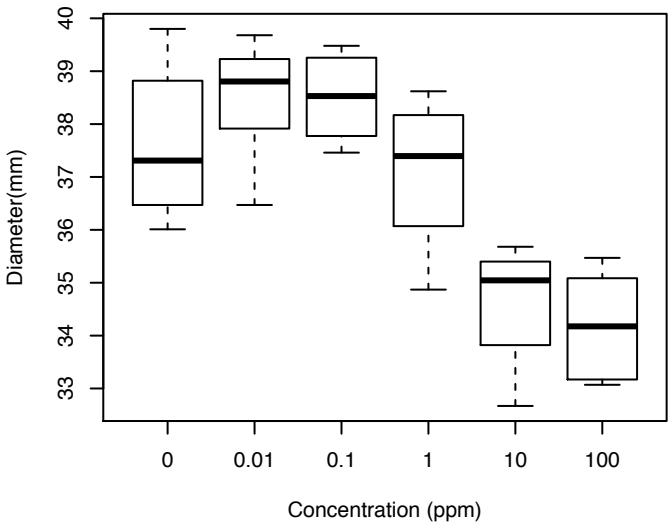
Alternaria alternata



Fusarium solani

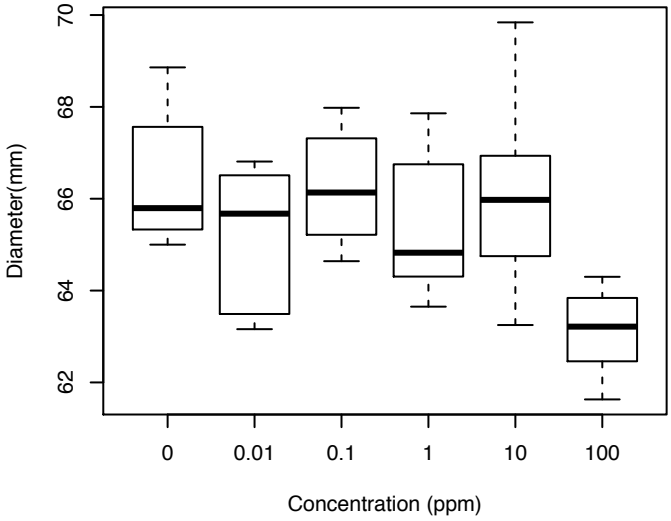


Verticillium dahliae

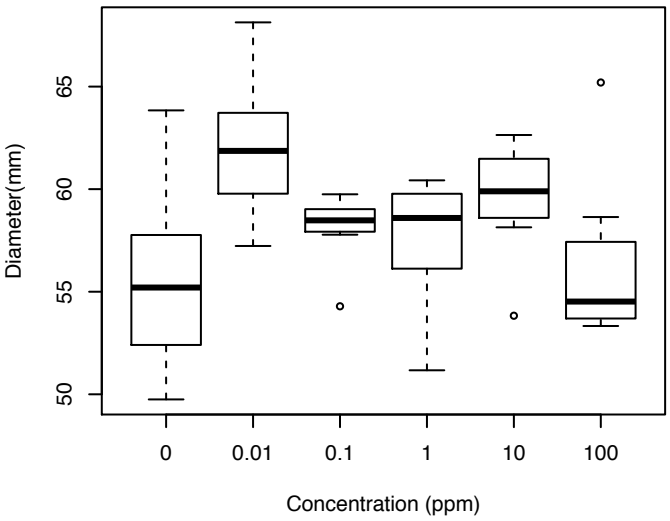


L09

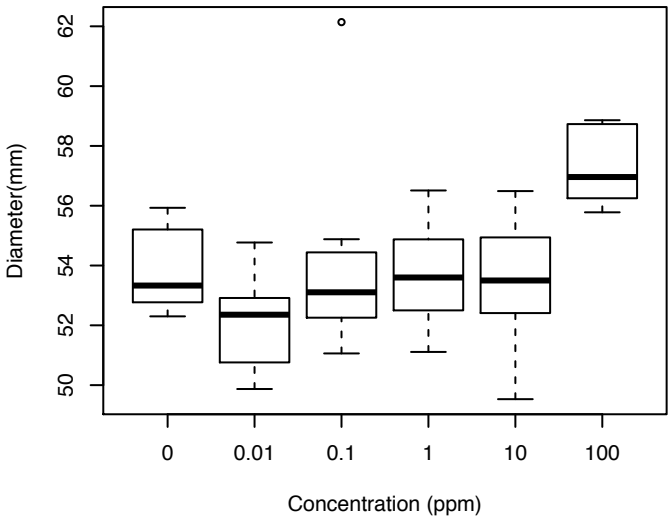
Phytophthora citrophthora



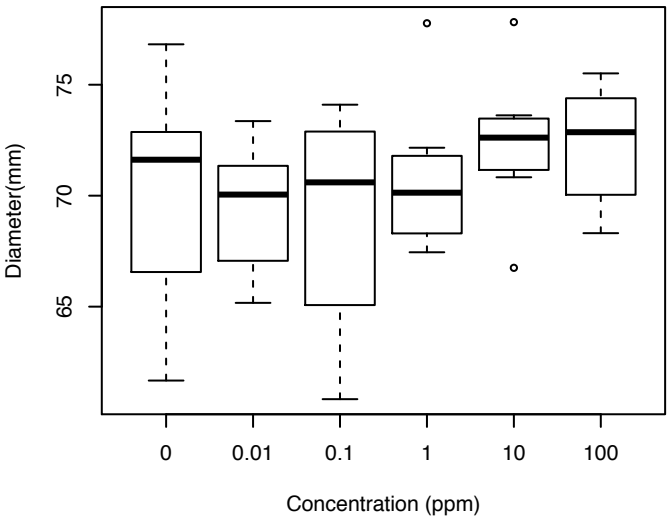
Phytophthora capsici



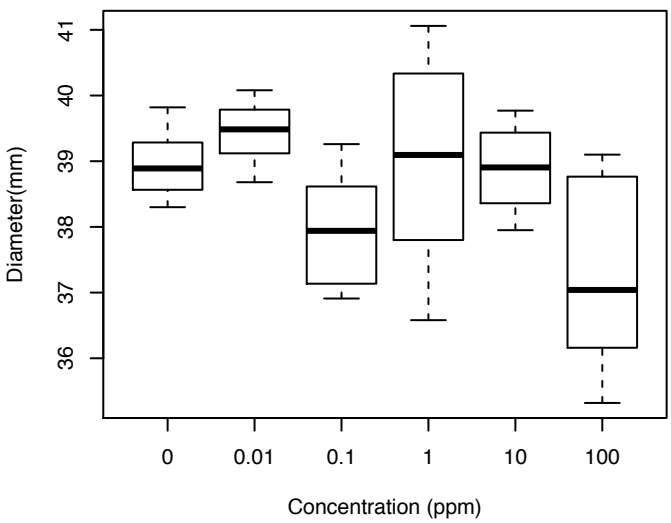
Alternaria alternata



Fusarium solani

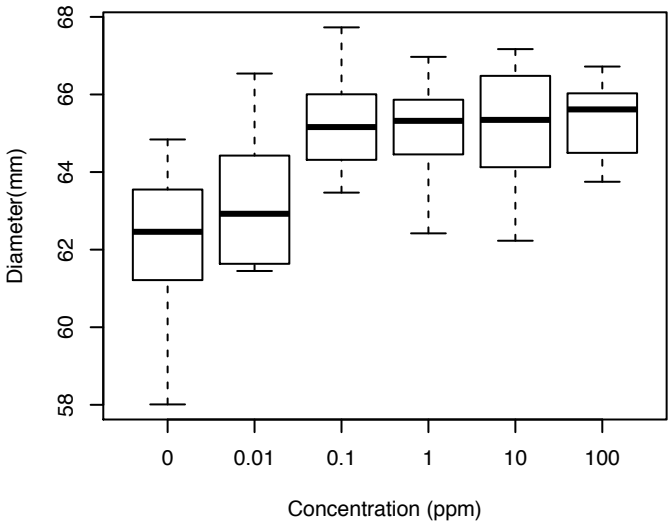


Verticillium dahliae

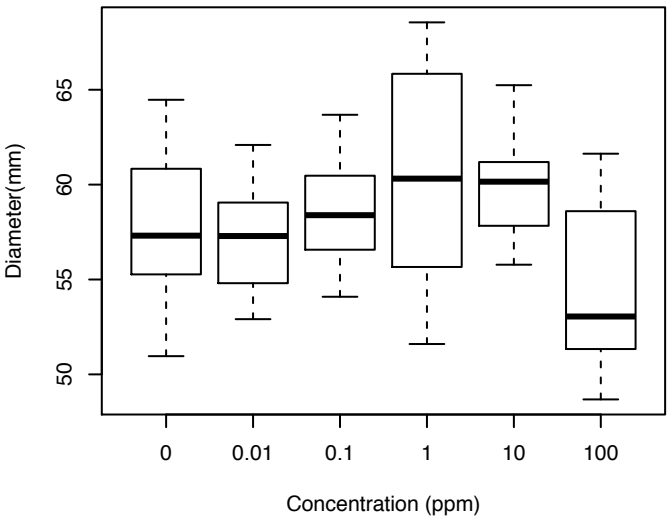


L10

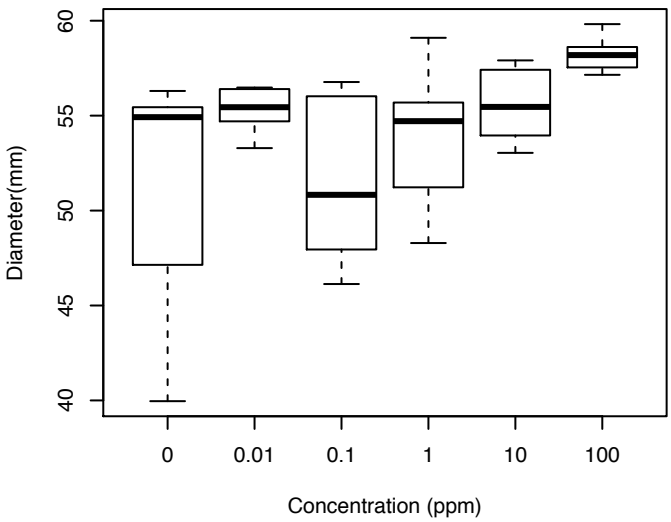
Phytophthora citrophthora



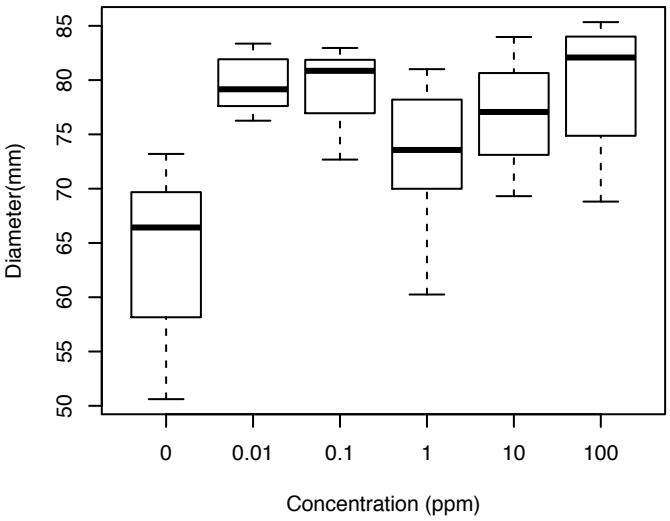
Phytophthora capsici



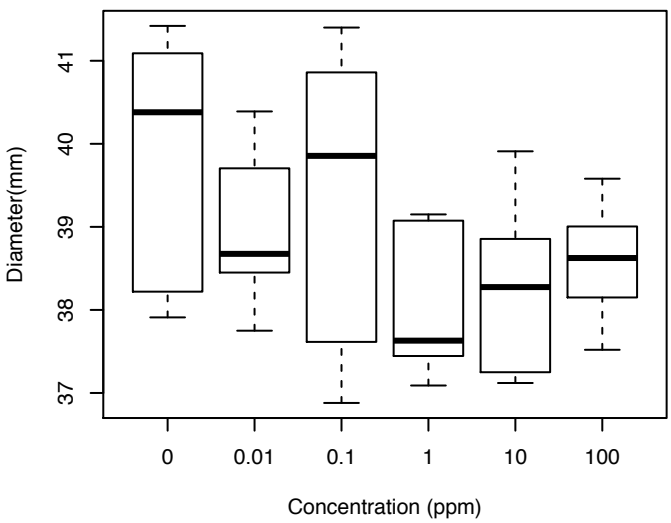
Alternaria alternata



Fusarium solani

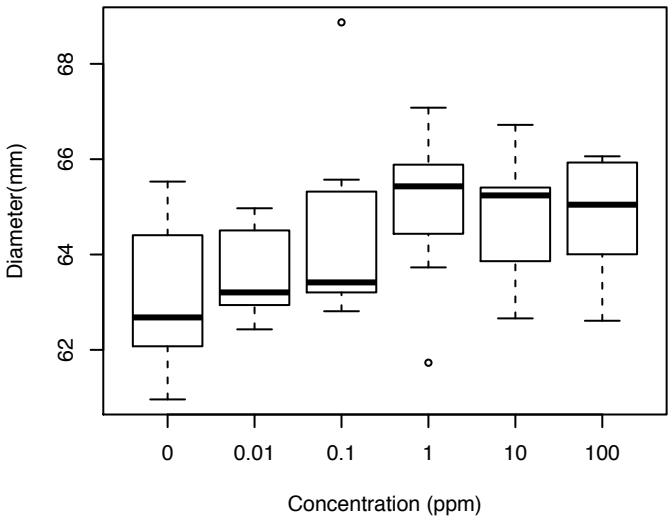


Verticillium dahliae

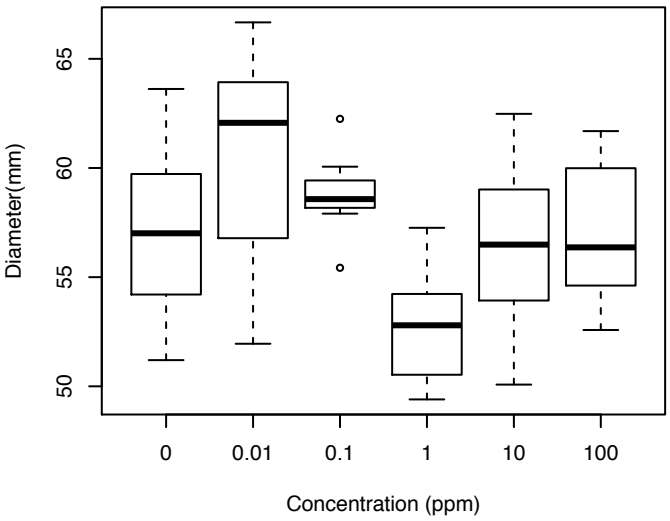


L11

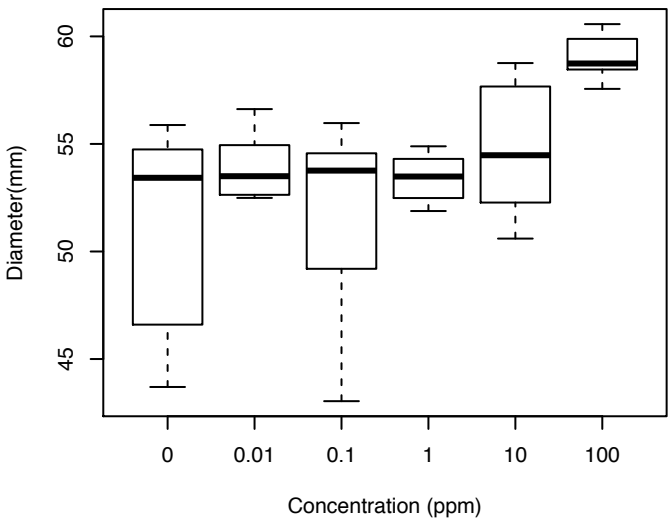
Phytophthora citrophthora



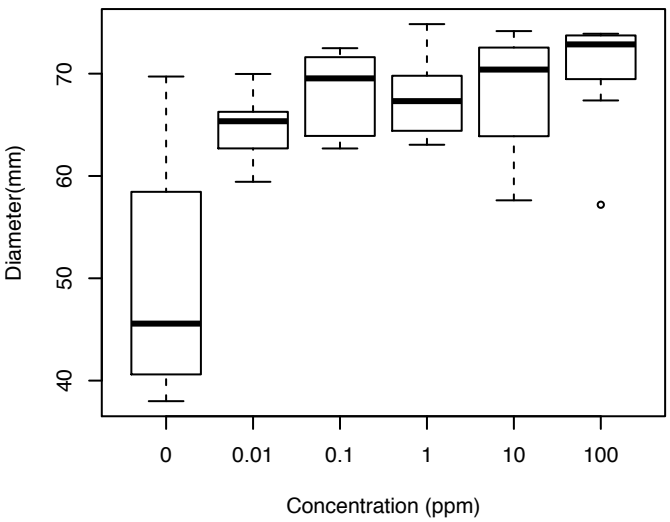
Phytophthora capsici



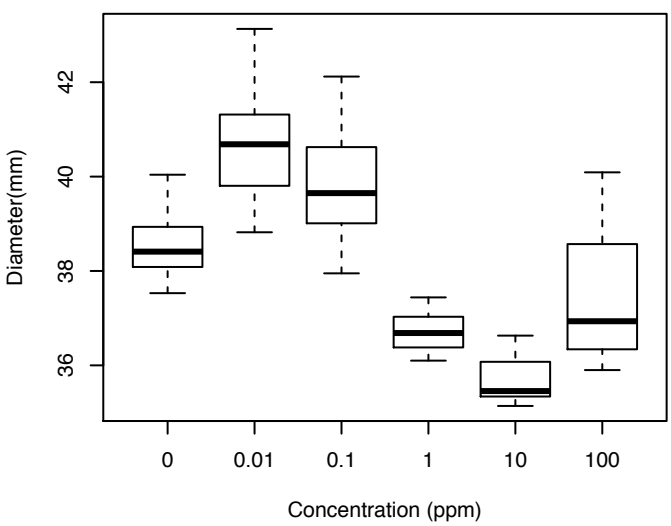
Alternaria alternata



Fusarium solani

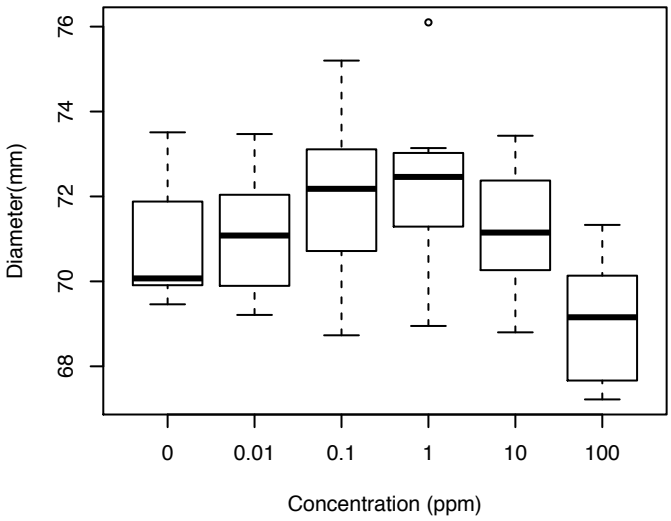


Verticillium dahliae

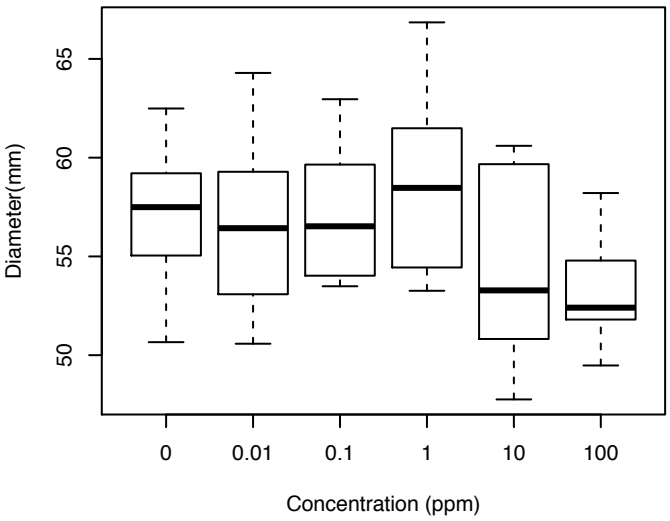


L12

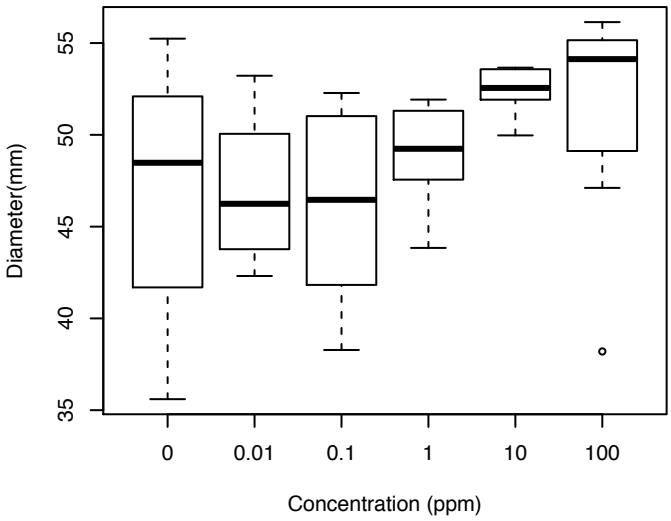
Phytophthora citrophthora



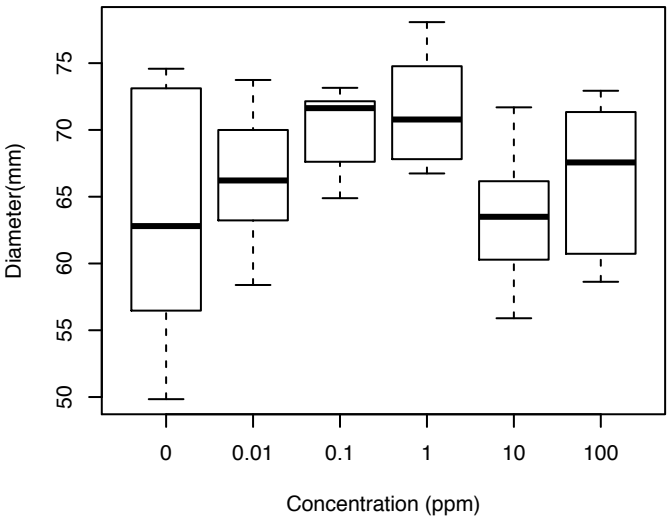
Phytophthora capsici



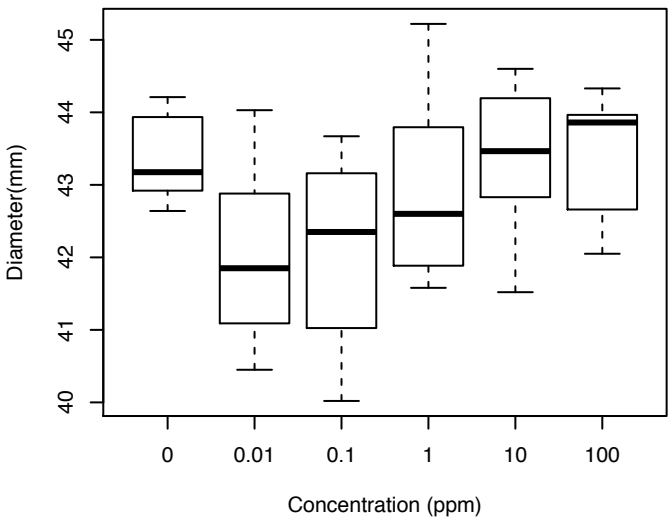
Alternaria alternata



Fusarium solani

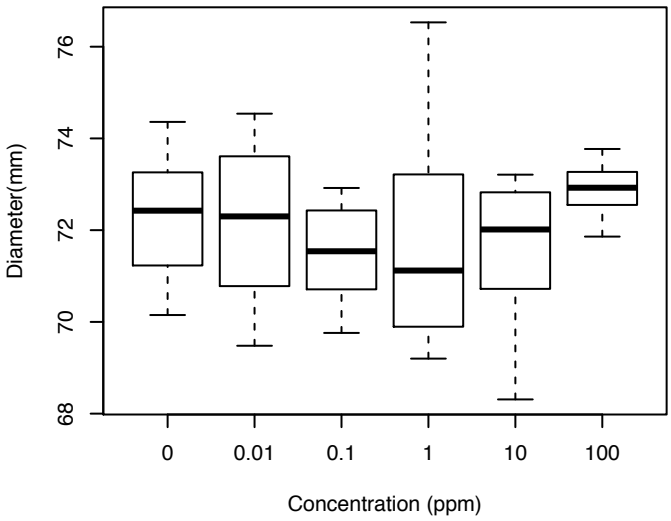


Verticillium dahliae

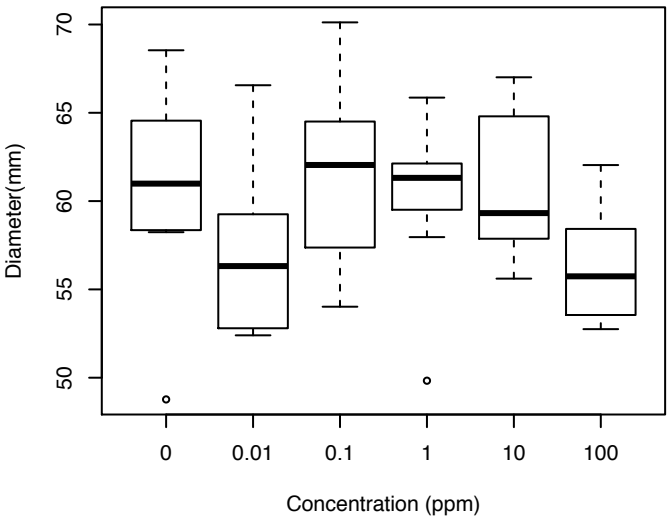


L13

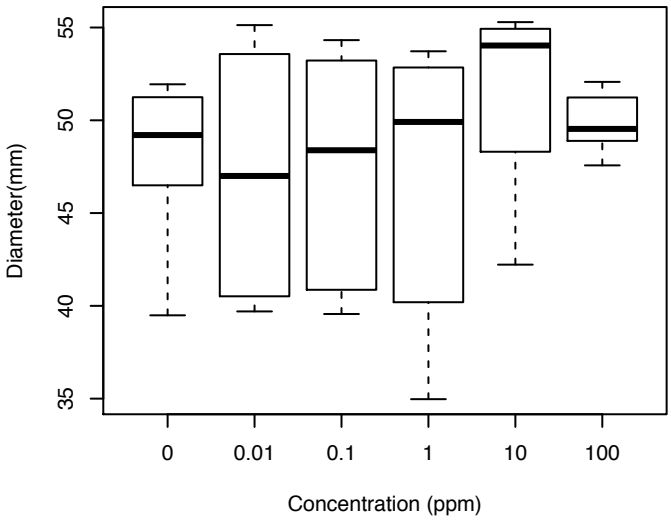
Phytophthora citrophthora



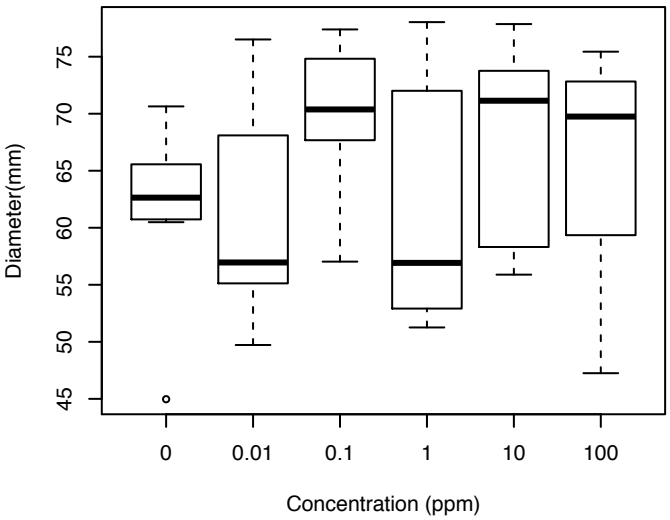
Phytophthora capsici



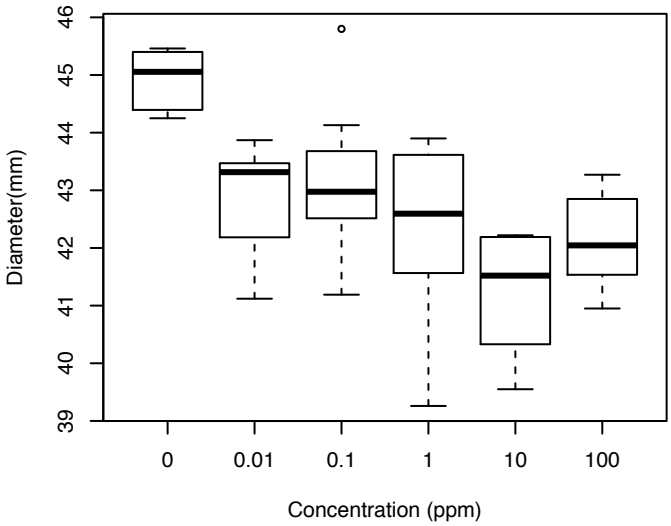
Alternaria alternata



Fusarium solani

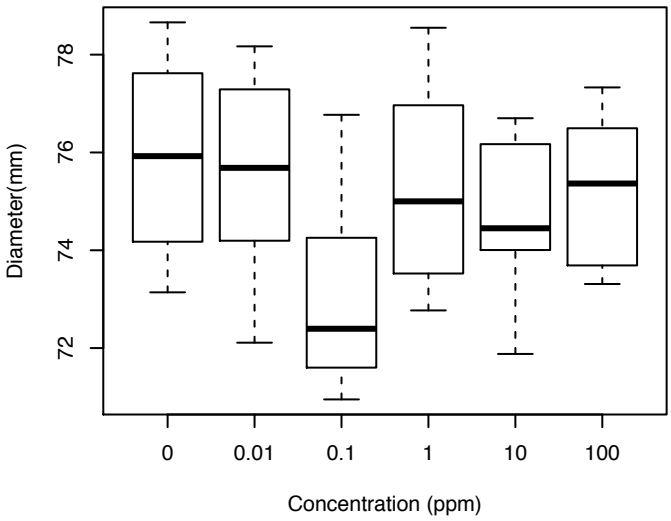


Verticillium dahliae

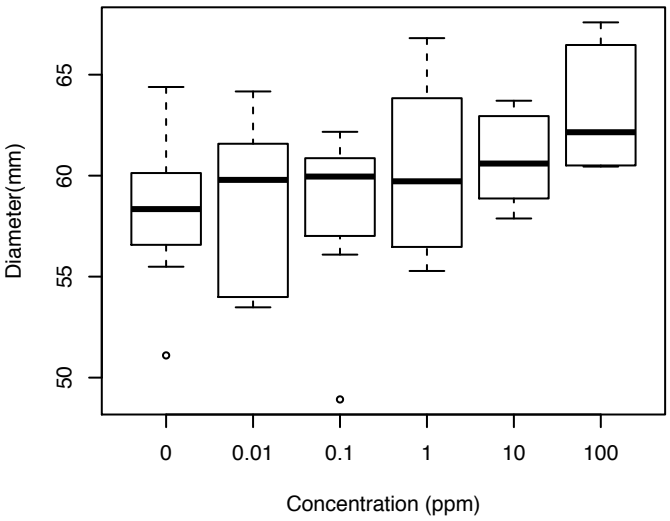


A

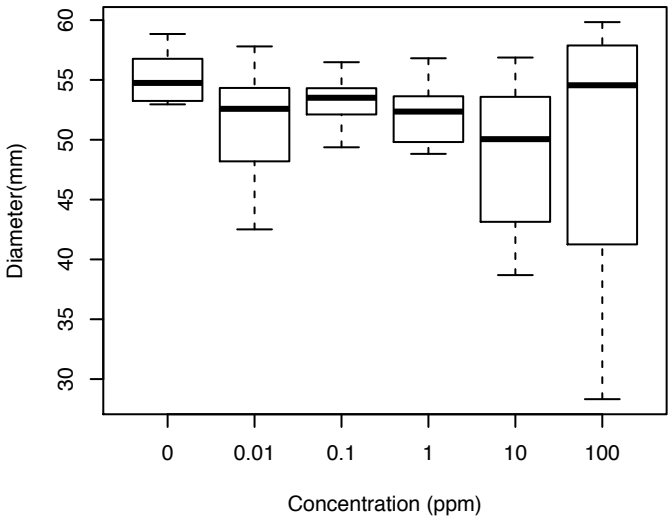
Phytophthora citrophthora



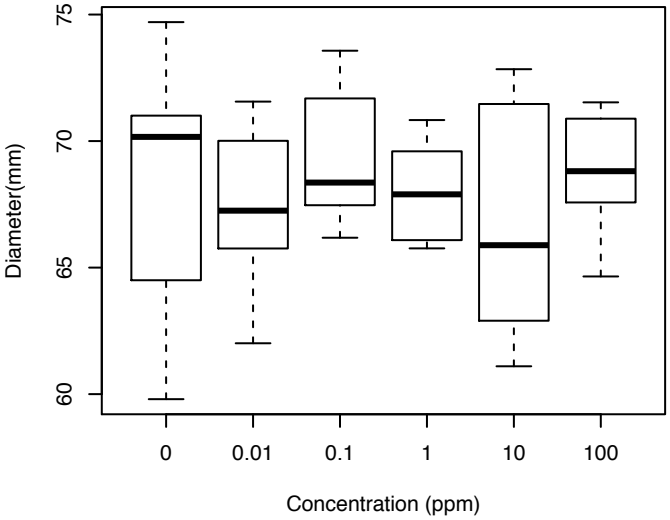
Phytophthora capsici



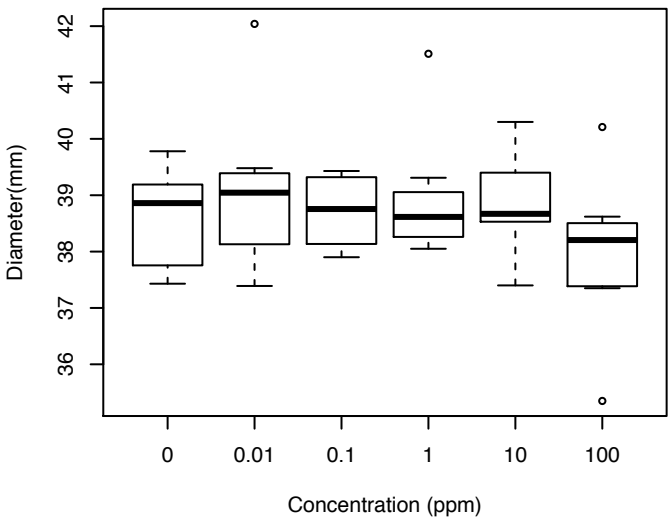
Alternaria alternata



Fusarium solani

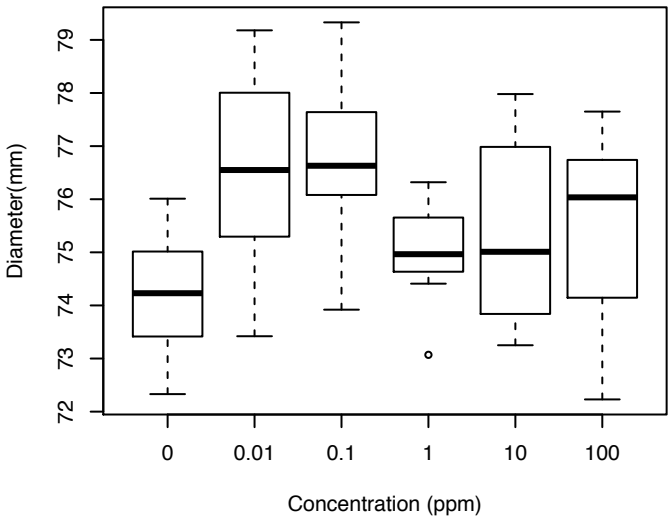


Verticillium dahliae

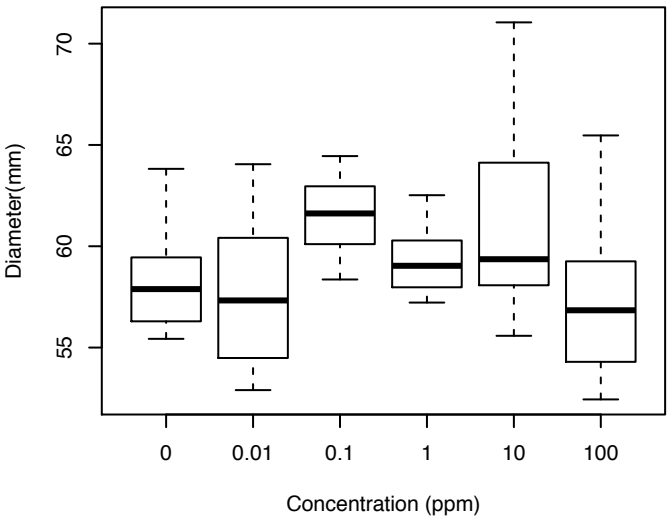


B

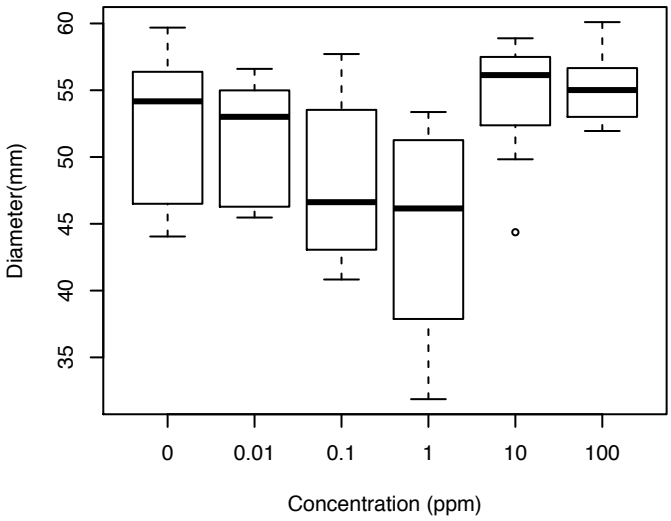
Phytophthora citrophthora



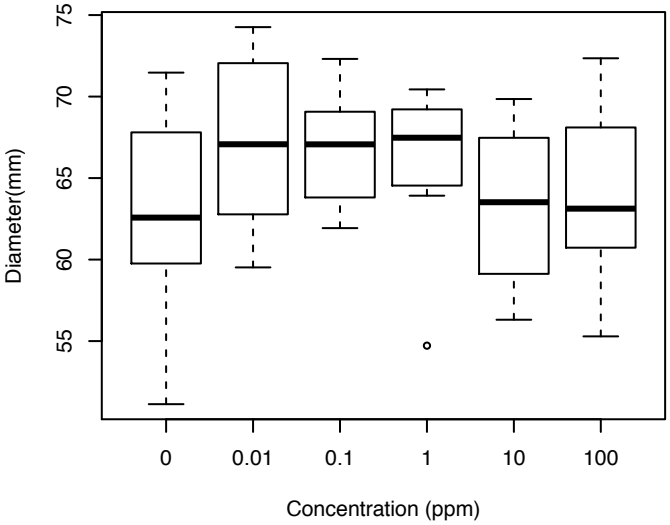
Phytophthora capsici



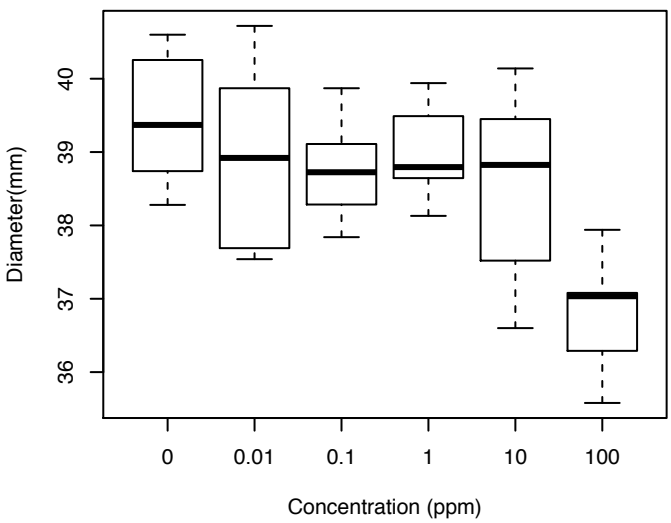
Alternaria alternata



Fusarium solani

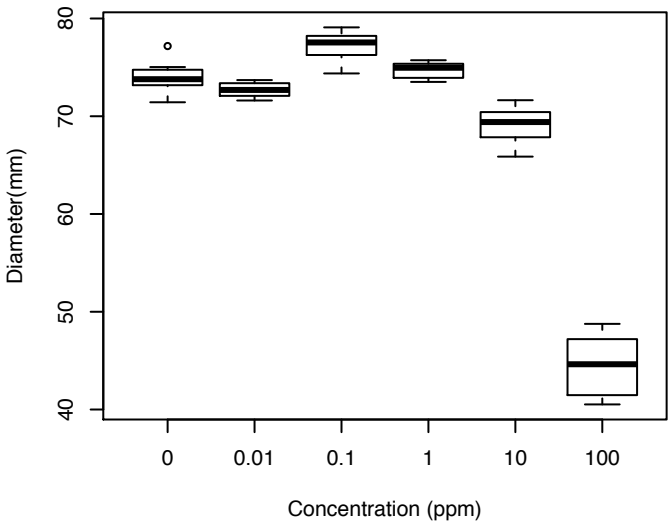


Verticillium dahliae

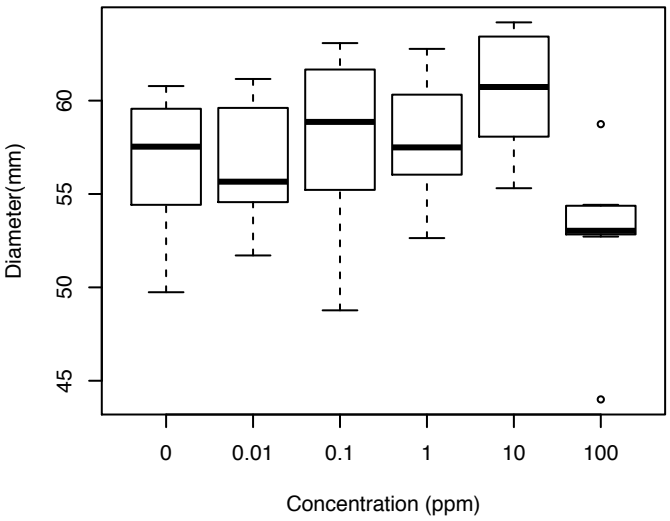


Fosetyl–Al

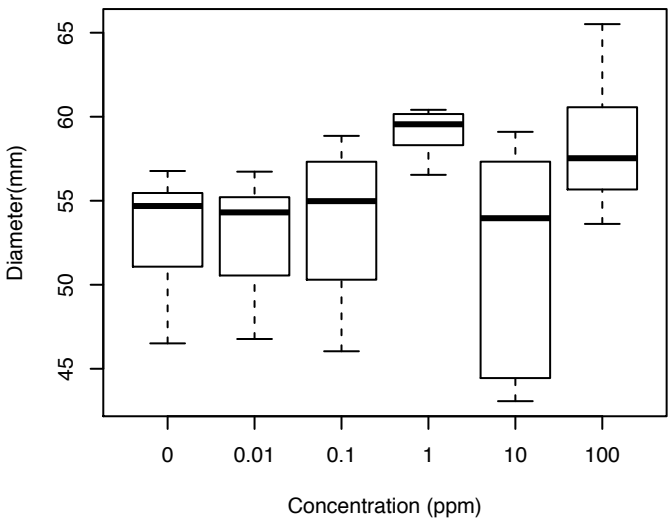
Phytophthora citrophthora



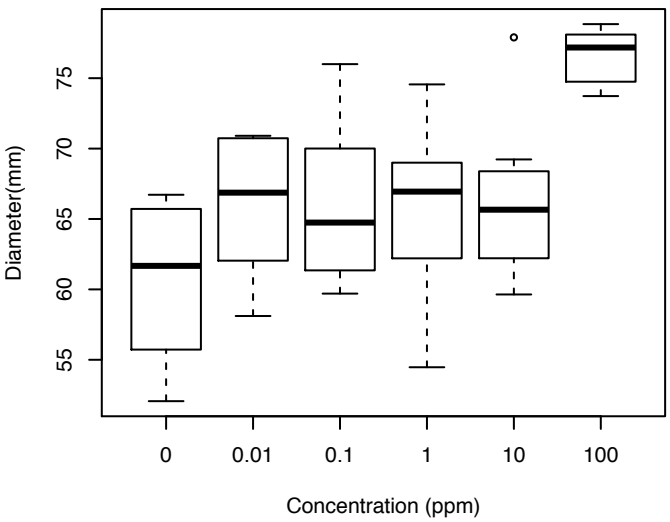
Phytophthora capsici



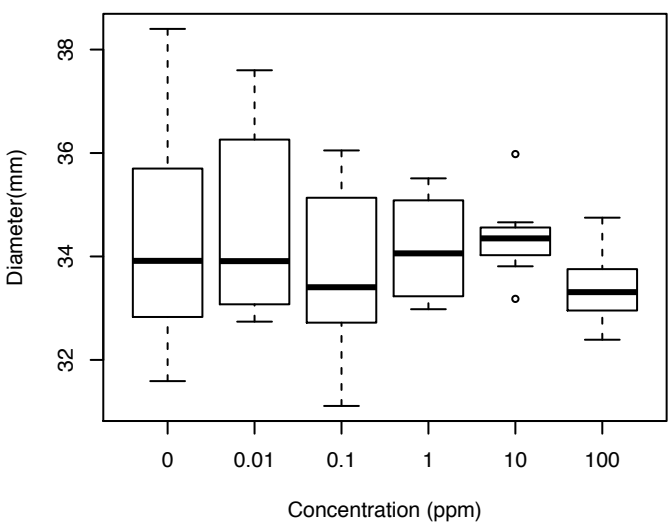
Alternaria alternata



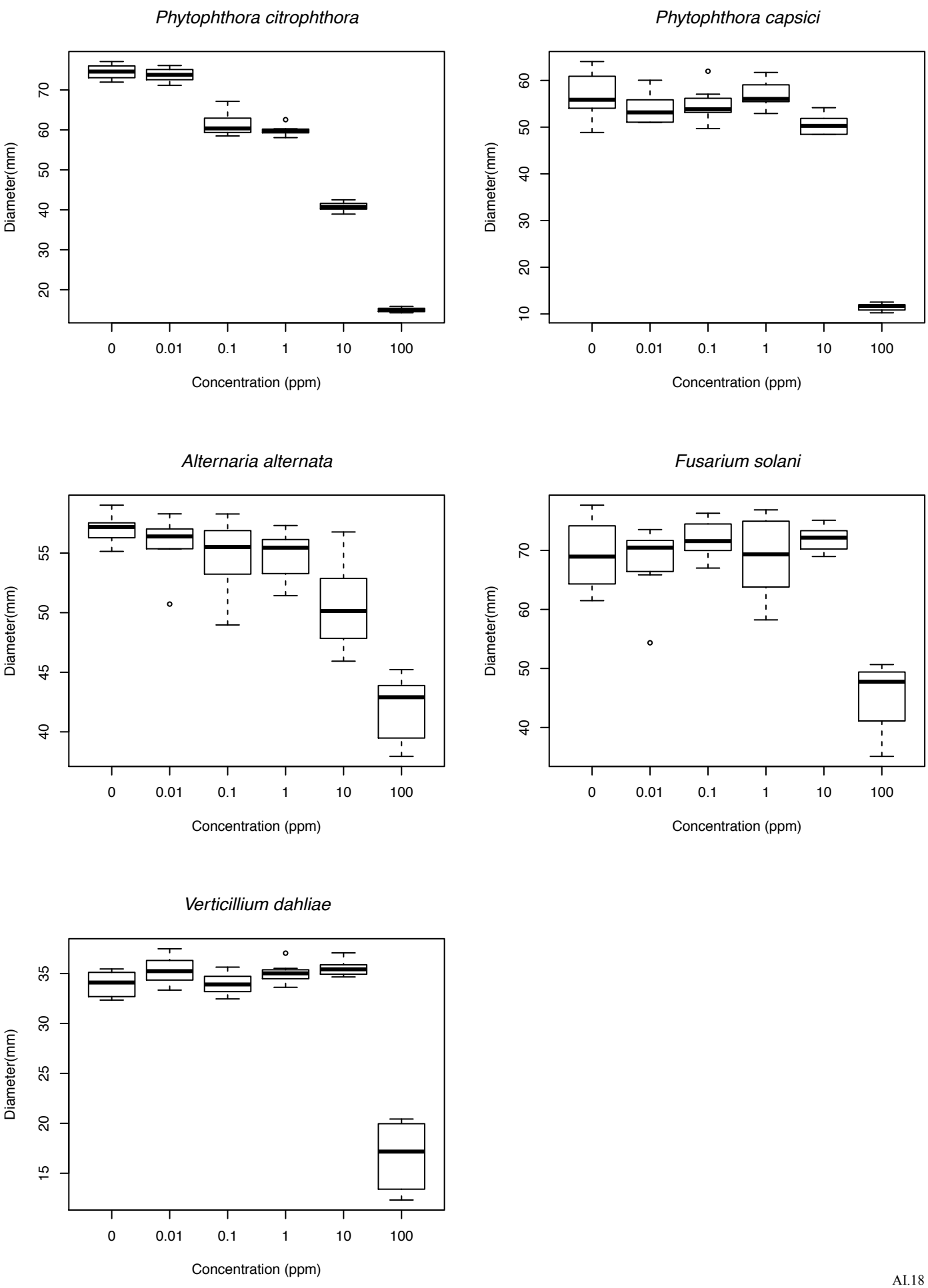
Fusarium solani



Verticillium dahliae

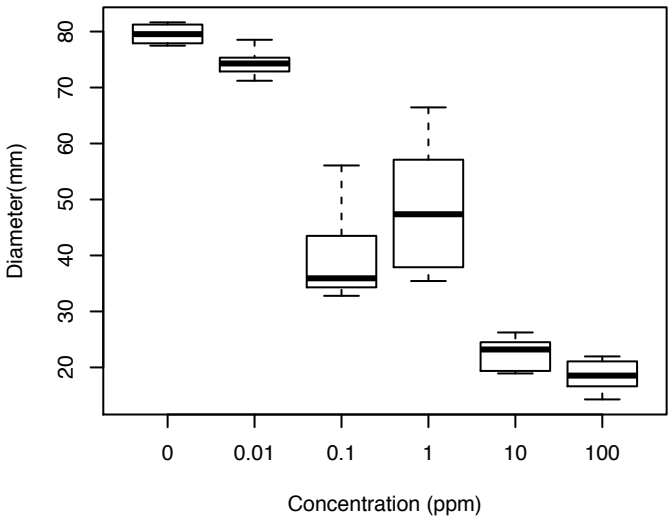


C

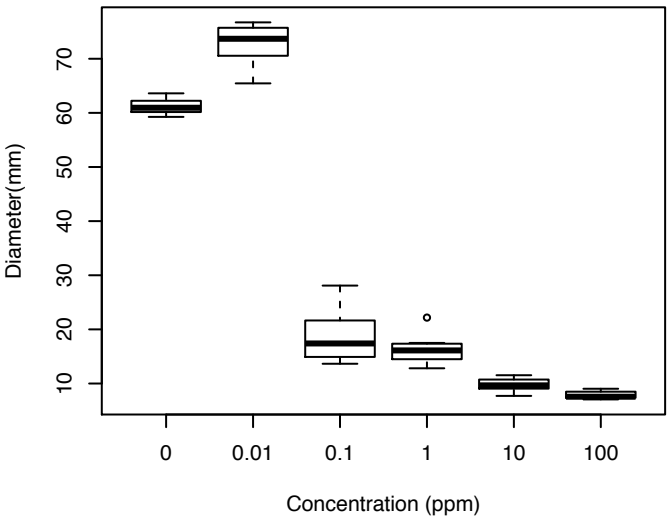

Phytophthora citrophthora
Diameter(mm)
20
30
40
50
60
70
0
0.01
0.1
1
10
100
Concentration (ppm)
Phytophthora capsici
Diameter(mm)
10
20
30
40
50
60
0
0.01
0.1
1
10
100
Concentration (ppm)
Alternaria alternata
Diameter(mm)
40
45
50
55
0
0.01
0.1
1
10
100
Concentration (ppm)
Fusarium solani
Diameter(mm)
40
50
60
70
0
0.01
0.1
1
10
100
Concentration (ppm)
Verticillium dahliae
Diameter(mm)
15
20
25
30
35
0
0.01
0.1
1
10
100
Concentration (ppm)

Mefenoxam

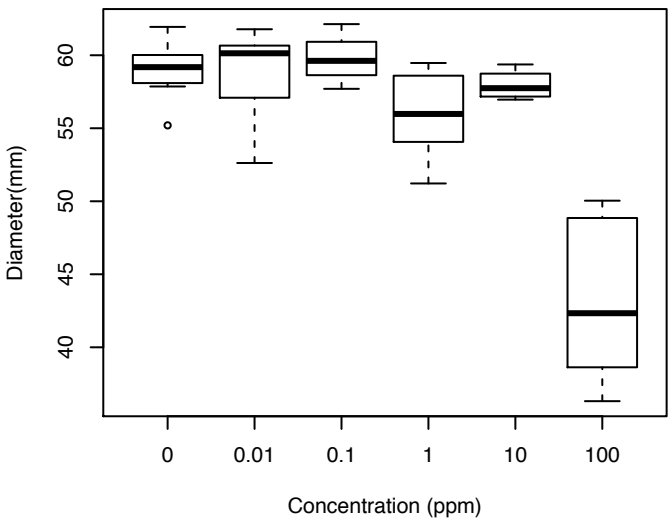
Phytophthora citrophthora



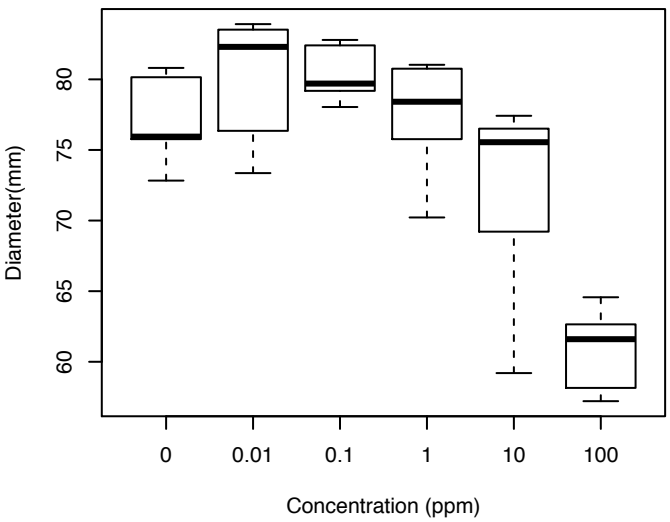
Phytophthora capsici



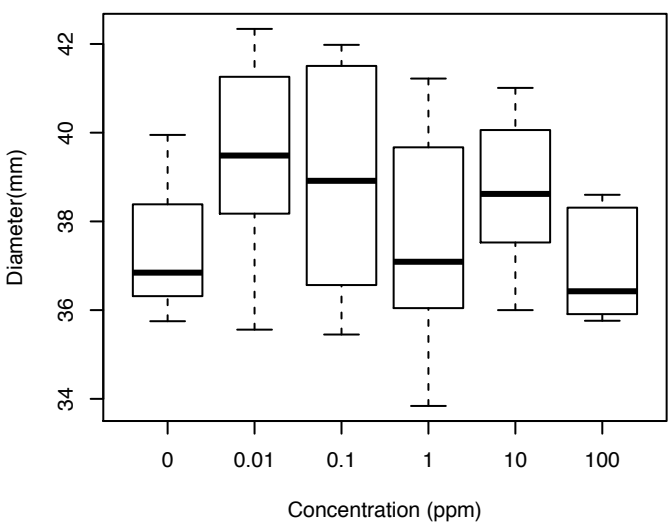
Alternaria alternata



Fusarium solani

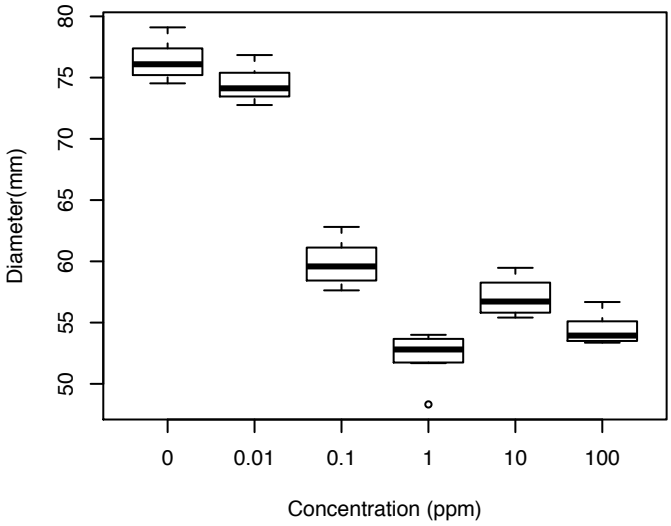


Verticillium dahliae

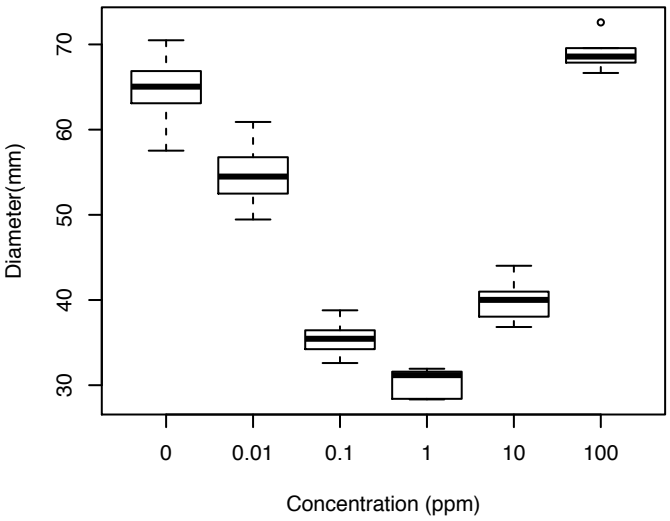


Pyraclostrobin

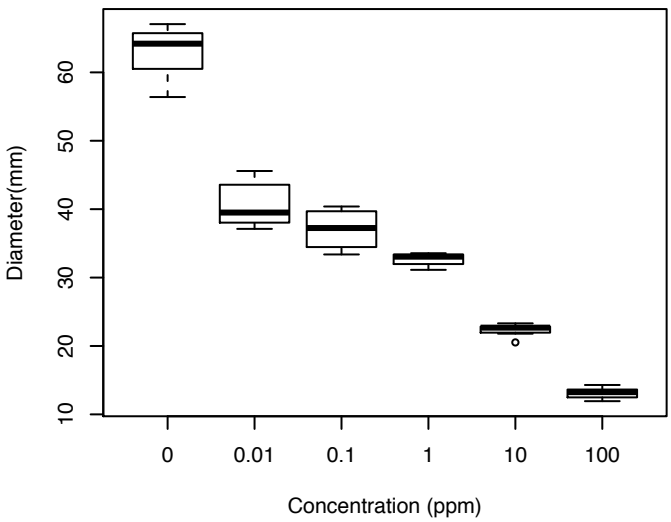
Phytophthora citrophthora



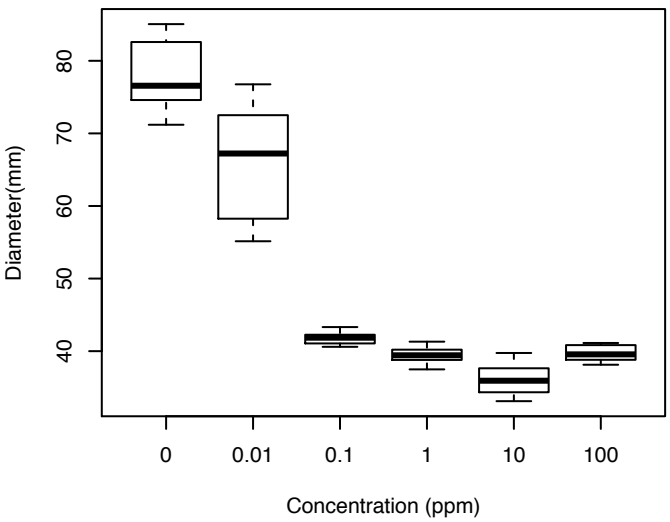
Phytophthora capsici



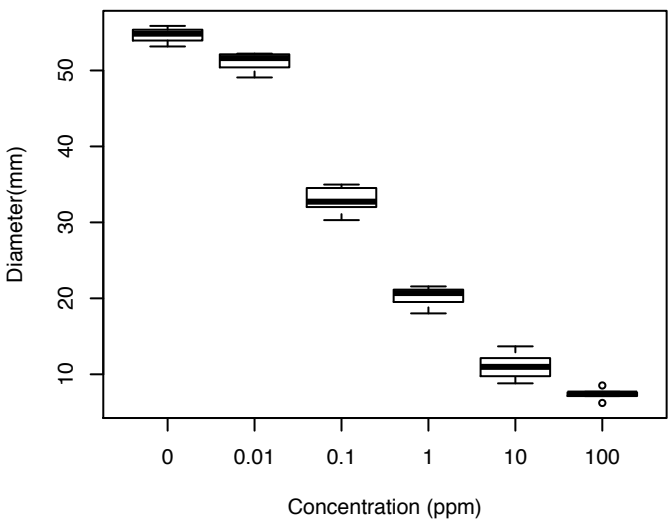
Alternaria alternata



Fusarium solani



Verticillium dahliae



Annex II

Statistical analysis: All data, whether ordinal or ratio, produced in the *in vitro* experiments and greenhouse trials was statistically analysed in R with the use of suitable statistical tests and methods. A detailed presentation of the analysis, R commands and outputs is presented below.

1. *In vitro* experiments

Data (Diameter)

In total, 95 product-pathogen combinations were tested. These were comprised of the five pathogens of the experiment, being tested separately against each of the 19 products of the study. The five pathogens are the target oomycetes *Phytophthora capsici* Leonian and *P. citrophthora* (R.E. Sm. and E.H. Sm.) Leonian, the foliar fungal pathogen *Alternaria alternata* (Fr.) Keissl., as well as the soil-borne fungi *Fusarium solani* (Mart.) Sacc. and *Verticillium dahliae* Kleb. In the data table, Trt stands for product treatment, Conc for product concentration and D for diameter (mm).

```
invitro <- read.csv("invitro.csv")
invitro$groupident <- as.character(paste(invitro$Trt, invitro$Pathogen,
sep="_"))

head(invitro)
```

```
##   Trt                   Pathogen Conc     D                     groupident
## 1 L01 Phytophthora citrophthora    0 68.01 L01_Phytophthora citrophthora
## 2 L01 Phytophthora citrophthora    0 72.74 L01_Phytophthora citrophthora
## 3 L01 Phytophthora citrophthora    0 58.08 L01_Phytophthora citrophthora
## 4 L01 Phytophthora citrophthora    0 57.80 L01_Phytophthora citrophthora
## 5 L01 Phytophthora citrophthora    0 71.67 L01_Phytophthora citrophthora
## 6 L01 Phytophthora citrophthora    0 69.03 L01_Phytophthora citrophthora
```

GLM D~Conc

The regressions conducted with the generalized lineal model, aimed to detect whether product concentration as an independent variable had a significant effect on colony growth (diameter). The regressions were done using the glm function of the multcomp package. The deviance residuals of models based on growth reduction proportion remained within the recommended range of -2.00 to 2.00 (see min-max values on code output below). The goodness of fit can also be assessed by observing the ratio of the residual deviance and degrees of freedom (df) of each model; well fitted models have a deviance/df ratio approximating a 1:1 ratio. The coefficient of 'Conc' (b_2 coefficient), its sign and P-value will be discussed below. Note: GLM summaries take up the next 46 pages.

```
setglm <- list()
Sumsetglm <- list()
for(i in 1:95){
  setglm[[i]] <- glm(D~Conc,
data=invitro[invitro$groupident==unique(invitro$groupident)
                                              [[i]],], family=Gamma)
  names(setglm)[i] <- unique(invitro$groupident)[i]
  Sumsetglm[[i]]<-summary(setglm[[i]])
  names(Sumsetglm)[i] <- unique(invitro$groupident)[i]
}

print(Sumsetglm)

## $`L01_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.230243  -0.076866  -0.000571   0.099530   0.138369
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.362e-02  2.422e-04   56.21   <2e-16 ***
## Conc        4.142e-06  5.920e-06    0.70    0.488
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01146253)
##
##     Null deviance: 0.52526  on 45  degrees of freedom
## Residual deviance: 0.51958  on 44  degrees of freedom
## AIC: 324.61
##
## Number of Fisher Scoring iterations: 4
```

```
##
##
## $`L01_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.190383  -0.041564   0.001035   0.038714   0.188695
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.633e-02  1.909e-04  85.525  < 2e-16 ***
## Conc        1.556e-05  5.011e-06   3.105  0.00325 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.005204836)
##
##     Null deviance: 0.28989  on 47  degrees of freedom
## Residual deviance: 0.23765  on 46  degrees of freedom
## AIC: 280.65
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L01_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.22858  -0.11132  -0.01493   0.10637   0.25652
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.102e-02  4.417e-04  47.587   <2e-16 ***
## Conc        -9.436e-06  1.038e-05  -0.909    0.368
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01691045)
##
##     Null deviance: 0.79354  on 47  degrees of freedom
```

```
## Residual deviance: 0.77983  on 46  degrees of freedom
## AIC: 315.42
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L01_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.42190  -0.06615  -0.00165   0.07829   0.25069
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.601e-02  3.481e-04  45.991   <2e-16 ***
## Conc        -1.995e-05  7.638e-06  -2.612   0.0121 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01816621)
##
##     Null deviance: 1.0181  on 47  degrees of freedom
## Residual deviance: 0.9007  on 46  degrees of freedom
## AIC: 349.91
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L01_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.19004  -0.06421   0.00146   0.08519   0.14511
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.349e-02  3.441e-04  68.262   <2e-16 ***
## Conc        7.861e-06  8.614e-06   0.913    0.366
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for Gamma family taken to be 0.008191286)
##
##     Null deviance: 0.38923  on 47  degrees of freedom
## Residual deviance: 0.38231  on 46  degrees of freedom
## AIC: 269.45
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L02_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.21800  -0.07696   0.01043   0.07909   0.10459
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.295e-02  1.880e-04  68.873   <2e-16 ***
## Conc        3.532e-06  4.682e-06   0.754    0.454
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.008048595)
##
##     Null deviance: 0.38973  on 47  degrees of freedom
## Residual deviance: 0.38509  on 46  degrees of freedom
## AIC: 327.11
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L02_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.225092  -0.046483  -0.000013   0.062460   0.173171
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)  1.690e-02  2.619e-04  64.535   <2e-16 ***
## Conc        -1.454e-05  5.942e-06  -2.447   0.0183 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.009211057)
##
##     Null deviance: 0.48720  on 47  degrees of freedom
## Residual deviance: 0.43405  on 46  degrees of freedom
## AIC: 309.3
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L02_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.34661  -0.14900  -0.02466   0.13749   0.29700
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.062e-02  6.060e-04  34.029   <2e-16 ***
## Conc        -3.035e-08  1.477e-05  -0.002    0.998
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.03300911)
##
##     Null deviance: 1.5269  on 47  degrees of freedom
## Residual deviance: 1.5269  on 46  degrees of freedom
## AIC: 348.07
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L02_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
```

```
## -0.296392  -0.030208   0.006301   0.066467   0.246267
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.579e-02  3.027e-04   52.18  < 2e-16 ***
## Conc        3.195e-05  8.588e-06    3.72  0.00054 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01392325)
##
##     Null deviance: 0.86975  on 47  degrees of freedom
## Residual deviance: 0.66023  on 46  degrees of freedom
## AIC: 330.85
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L02_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.182771  -0.073146   0.009963   0.073159   0.125553
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.222e-02  3.086e-04  71.998   <2e-16 ***
## Conc        1.862e-05  8.031e-06   2.318   0.0249 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.007347978)
##
##     Null deviance: 0.38766  on 47  degrees of freedom
## Residual deviance: 0.34675  on 46  degrees of freedom
## AIC: 269.29
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L03_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
```

```
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.223300  -0.085124  -0.000066   0.108201   0.163782
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.379e-02  2.416e-04  57.089   <2e-16 ***
## Conc        1.587e-05  6.436e-06   2.465   0.0175 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01167205)
##
##     Null deviance: 0.62090  on 47  degrees of freedom
## Residual deviance: 0.54643  on 46  degrees of freedom
## AIC: 336.24
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L03_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.244387  -0.060899   0.003091   0.059103   0.150469
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.694e-02  2.319e-04  73.036  < 2e-16 ***
## Conc        -2.175e-05  5.071e-06  -4.289 9.11e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.007204546)
##
##     Null deviance: 0.46569  on 47  degrees of freedom
## Residual deviance: 0.34030  on 46  degrees of freedom
## AIC: 298.32
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L03_Alternaria alternata`
```

```
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.34904  -0.07804  -0.00193   0.10865   0.26817
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.828e-02  4.110e-04  44.472   <2e-16 ***
## Conc        -1.958e-05  9.157e-06  -2.138   0.0378 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01941353)
##
##     Null deviance: 1.01742  on 47  degrees of freedom
## Residual deviance: 0.93267  on 46  degrees of freedom
## AIC: 338.48
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L03_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.262437  -0.040358   0.009975   0.048798   0.152588
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.391e-02  2.091e-04  66.521   <2e-16 ***
## Conc        -9.063e-06  4.830e-06  -1.876    0.067 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.008661586)
##
##     Null deviance: 0.45494  on 47  degrees of freedom
## Residual deviance: 0.42529  on 46  degrees of freedom
## AIC: 326.6
##
```

```
## Number of Fisher Scoring iterations: 4
##
##
## $`L03_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.260152  -0.033850   0.006834   0.046999   0.168580
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.443e-02  3.556e-04  68.701   <2e-16 ***
## Conc        1.501e-06  8.525e-06   0.176    0.861
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.007673386)
##
##     Null deviance: 0.35523  on 45  degrees of freedom
## Residual deviance: 0.35499  on 44  degrees of freedom
## AIC: 253.88
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L04_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.205807  -0.073529   0.003065   0.078862   0.226042
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.566e-02  2.783e-04  56.261   <2e-16 ***
## Conc        7.732e-06  7.054e-06   1.096    0.279
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01205068)
##
```

```
##     Null deviance: 0.57540  on 47  degrees of freedom
## Residual deviance: 0.56062  on 46  degrees of freedom
## AIC: 326.34
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L04_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.151569  -0.051650   0.001248   0.035942   0.191178
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.962e-02  2.339e-04  83.876   <2e-16 ***
## Conc        8.760e-06  5.906e-06   1.483    0.145
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.005422885)
##
##     Null deviance: 0.25845  on 47  degrees of freedom
## Residual deviance: 0.24629  on 46  degrees of freedom
## AIC: 265.57
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L04_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.27230  -0.13350  -0.02283   0.10151   0.34436
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.930e-02  5.266e-04  36.650   <2e-16 ***
## Conc        7.069e-06  1.321e-05   0.535    0.595
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.02841208)
##
##     Null deviance: 1.2792  on 47  degrees of freedom
## Residual deviance: 1.2709  on 46  degrees of freedom
## AIC: 345.18
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L04_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.26186  -0.01601   0.01216   0.03302   0.04502
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.218e-02  9.844e-05 123.710   <2e-16 ***
## Conc        -3.703e-06  2.340e-06  -1.582     0.12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.00250069)
##
##     Null deviance: 0.13398  on 47  degrees of freedom
## Residual deviance: 0.12780  on 46  degrees of freedom
## AIC: 281.27
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L04_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.17038  -0.05421  -0.01847   0.06782   0.14380
##
## Coefficients:
```

```
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.403e-02  3.089e-04  77.794   <2e-16 ***
## Conc        -1.264e-05  7.211e-06  -1.753   0.0863 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.006329709)
##
##     Null deviance: 0.31058  on 47  degrees of freedom
## Residual deviance: 0.29157  on 46  degrees of freedom
## AIC: 255.88
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L05_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.276747   0.000992   0.025222   0.042147   0.106277
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.330e-02  1.692e-04  78.626   <2e-16 ***
## Conc        9.223e-07  4.146e-06   0.222    0.825
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.006181044)
##
##     Null deviance: 0.31480  on 47  degrees of freedom
## Residual deviance: 0.31449  on 46  degrees of freedom
## AIC: 315.21
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L05_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
```

```
##       Min         1Q     Median         3Q        Max
## -0.118022  -0.042438  -0.005011   0.043844   0.121502
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.877e-02  1.872e-04   100.3   <2e-16 ***
## Conc        -3.151e-06  4.500e-06    -0.7    0.487
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.003802436)
##
##     Null deviance: 0.17640  on 47  degrees of freedom
## Residual deviance: 0.17455  on 46  degrees of freedom
## AIC: 254.41
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L05_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.28695  -0.09664   0.01733   0.06331   0.20897
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.660e-02  2.917e-04  56.892  < 2e-16 ***
## Conc        2.539e-05  7.992e-06   3.177  0.00266 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01173452)
##
##     Null deviance: 0.68541  on 47  degrees of freedom
## Residual deviance: 0.55918  on 46  degrees of freedom
## AIC: 318.94
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L05_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
```

```
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.37939  -0.09126   0.01573   0.08522   0.21509
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.488e-02  3.120e-04  47.705   <2e-16 ***
## Conc        -1.103e-05  7.151e-06  -1.542     0.13
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01684818)
##
##     Null deviance: 0.86203  on 47  degrees of freedom
## Residual deviance: 0.82321  on 46  degrees of freedom
## AIC: 351.67
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L05_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.096197  -0.014795   0.000469   0.023166   0.063645
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.472e-02  1.446e-04 170.947   <2e-16 ***
## Conc        -4.625e-06  3.399e-06  -1.361     0.18
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001240708)
##
##     Null deviance: 0.057844  on 45  degrees of freedom
## Residual deviance: 0.055565  on 44  degrees of freedom
## AIC: 168.17
##
## Number of Fisher Scoring iterations: 3
##
##
```

```
## $`L06_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.044756  -0.016215   0.001777   0.016932   0.035338
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.389e-02  4.670e-05  297.37   <2e-16 ***
## Conc        -1.925e-06  1.125e-06   -1.71   0.0939 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.000432504)
##
##     Null deviance: 0.021233  on 47  degrees of freedom
## Residual deviance: 0.019975  on 46  degrees of freedom
## AIC: 179.37
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L06_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.115185  -0.034059   0.000082   0.038375   0.136646
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.579e-02  1.412e-04 111.783   <2e-16 ***
## Conc        -7.707e-06  3.307e-06  -2.331   0.0242 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.00306518)
##
##     Null deviance: 0.15553  on 47  degrees of freedom
## Residual deviance: 0.13923  on 46  degrees of freedom
## AIC: 260.81
```

```
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L06_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.21539  -0.13393   0.04117   0.10854   0.15971
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.909e-02  3.968e-04  48.108   <2e-16 ***
## Conc        1.031e-06  1.074e-05   0.096    0.924
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.015819)
##
##     Null deviance: 0.68557  on 43  degrees of freedom
## Residual deviance: 0.68542  on 42  degrees of freedom
## AIC: 295.47
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L06_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.33908  -0.03806   0.01967   0.06202   0.08819
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.282e-02  1.726e-04  74.277   <2e-16 ***
## Conc        4.354e-06  4.236e-06   1.028     0.31
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.006632637)
```

```
##
##     Null deviance: 0.33116  on 45  degrees of freedom
## Residual deviance: 0.32406  on 44  degrees of freedom
## AIC: 308.56
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L06_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.12643  -0.02288   0.01007   0.02603   0.07572
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.581e-02  1.924e-04 134.136   <2e-16 ***
## Conc        -1.449e-06  4.576e-06  -0.317    0.753
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.002036495)
##
##     Null deviance: 0.092455  on 45  degrees of freedom
## Residual deviance: 0.092251  on 44  degrees of freedom
## AIC: 187.25
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L07_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.065071  -0.016428  -0.003258   0.015381   0.060575
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.375e-02  5.169e-05 266.020   <2e-16 ***
## Conc        -2.847e-06  1.239e-06  -2.299   0.0261 *
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0005405875)
##
##     Null deviance: 0.027728  on 47  degrees of freedom
## Residual deviance: 0.024897  on 46  degrees of freedom
## AIC: 191.01
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L07_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.79349  -0.01959   0.01158   0.02889   0.15224
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.498e-02  2.542e-04  58.925   <2e-16 ***
## Conc        -8.431e-06  5.916e-06  -1.425    0.161
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01103443)
##
##     Null deviance: 0.79620  on 47  degrees of freedom
## Residual deviance: 0.77433  on 46  degrees of freedom
## AIC: 347.81
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L07_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.26904  -0.08189   0.04501   0.08456   0.18467
##
```

```
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.863e-02  3.554e-04  52.419   <2e-16 ***
## Conc        8.806e-06  8.993e-06   0.979    0.333
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0138831)
##
##     Null deviance: 0.69117  on 47  degrees of freedom
## Residual deviance: 0.67759  on 46  degrees of freedom
## AIC: 318.7
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L07_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.275915  -0.022574   0.007945   0.036123   0.111299
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.223e-02  1.302e-04  93.933  < 2e-16 ***
## Conc        9.083e-06  3.292e-06   2.759  0.00841 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.004091974)
##
##     Null deviance: 0.22625  on 45  degrees of freedom
## Residual deviance: 0.19412  on 44  degrees of freedom
## AIC: 288.72
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L07_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
```

```
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.130228  -0.018222   0.002747   0.017348   0.087582
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.298e-02  1.416e-04 162.267   <2e-16 ***
## Conc        -5.856e-06  3.380e-06  -1.732   0.0899 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001453195)
##
##     Null deviance: 0.072759  on 47  degrees of freedom
## Residual deviance: 0.068445  on 46  degrees of freedom
## AIC: 190.32
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L08_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.062655  -0.017427  -0.003035   0.015966   0.054832
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.507e-02  6.923e-05  217.71  < 2e-16 ***
## Conc        2.297e-05  1.896e-06   12.12 6.44e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0008013217)
##
##     Null deviance: 0.162167  on 47  degrees of freedom
## Residual deviance: 0.036772  on 46  degrees of freedom
## AIC: 198
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L08_Phytophthora capsici`
##
## Call:
```

```
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.124121  -0.037807  -0.002206   0.036315   0.135013
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.639e-02  1.542e-04 106.266  < 2e-16 ***
## Conc        -1.441e-05  3.494e-06  -4.126 0.000153 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.003397351)
##
##     Null deviance: 0.21252  on 47  degrees of freedom
## Residual deviance: 0.15684  on 46  degrees of freedom
## AIC: 263.65
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L08_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.134972  -0.013920   0.003008   0.021160   0.055636
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.911e-02  1.036e-04 184.525  < 2e-16 ***
## Conc        7.352e-06  2.603e-06   2.825  0.00698 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001120754)
##
##     Null deviance: 0.062487  on 47  degrees of freedom
## Residual deviance: 0.053398  on 46  degrees of freedom
## AIC: 194.96
##
## Number of Fisher Scoring iterations: 3
##
```

```
##
## $`L08_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.287488  -0.071109   0.003855   0.063184   0.178663
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.776e-02  3.018e-04  58.826   <2e-16 ***
## Conc        4.719e-06  7.514e-06   0.628    0.533
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01103324)
##
##     Null deviance: 0.53009  on 47  degrees of freedom
## Residual deviance: 0.52568  on 46  degrees of freedom
## AIC: 311.61
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L08_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.122533  -0.026932   0.008801   0.032687   0.062800
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.674e-02  1.924e-04 138.996  < 2e-16 ***
## Conc        2.734e-05  5.076e-06   5.386 2.39e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001970042)
##
##     Null deviance: 0.15211  on 47  degrees of freedom
## Residual deviance: 0.09245  on 46  degrees of freedom
```

```
## AIC: 187.98
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L09_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.042324  -0.014787  -0.001609   0.012188   0.062908
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.517e-02  5.682e-05 267.006  < 2e-16 ***
## Conc        6.612e-06  1.434e-06   4.612 3.19e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0005351622)
##
##     Null deviance: 0.036071  on 47  degrees of freedom
## Residual deviance: 0.024474  on 46  degrees of freedom
## AIC: 179.61
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L09_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.159188  -0.042416  -0.002801   0.032671   0.154777
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.707e-02  1.812e-04  94.194   <2e-16 ***
## Conc        6.820e-06  4.559e-06   1.496    0.141
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for Gamma family taken to be 0.004300822)
##
##     Null deviance: 0.20764  on 47  degrees of freedom
## Residual deviance: 0.19784  on 46  degrees of freedom
## AIC: 268.54
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L09_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.08034  -0.01955  -0.00696   0.02457   0.15615
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.874e-02  1.178e-04 159.096  < 2e-16 ***
## Conc        -1.285e-05  2.713e-06  -4.737 2.12e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001514449)
##
##     Null deviance: 0.100452  on 47  degrees of freedom
## Residual deviance: 0.067463  on 46  degrees of freedom
## AIC: 209.99
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L09_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.140401  -0.029914   0.005863   0.032994   0.103378
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.424e-02  1.225e-04 116.262   <2e-16 ***
```

```
## Conc        -4.445e-06  2.910e-06  -1.528    0.133
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.002831452)
##
##     Null deviance: 0.13987  on 47  degrees of freedom
## Residual deviance: 0.13335  on 46  degrees of freedom
## AIC: 268.32
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L09_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.059962  -0.015304   0.001759   0.017869   0.055474
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.572e-02  1.189e-04  216.36  < 2e-16 ***
## Conc        1.081e-05  2.996e-06    3.61 0.000754 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0008150949)
##
##     Null deviance: 0.048545  on 47  degrees of freedom
## Residual deviance: 0.037732  on 46  degrees of freedom
## AIC: 149.73
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L10_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.098741  -0.017136   0.004007   0.019759   0.055000
```

```
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.559e-02  7.489e-05 208.188   <2e-16 ***
## Conc        -3.116e-06  1.796e-06  -1.735   0.0895 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0008826125)
##
##     Null deviance: 0.043822  on 47  degrees of freedom
## Residual deviance: 0.041188  on 46  degrees of freedom
## AIC: 203.08
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L10_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.14055  -0.04667  -0.01943   0.05111   0.15738
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.699e-02  2.002e-04  84.862   <2e-16 ***
## Conc        1.288e-05  5.179e-06   2.486   0.0166 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.005290753)
##
##     Null deviance: 0.27482  on 47  degrees of freedom
## Residual deviance: 0.24104  on 46  degrees of freedom
## AIC: 277.8
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L10_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
```

```
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.27675  -0.01335   0.02105   0.04311   0.10208
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.872e-02  2.227e-04  84.054  < 2e-16 ***
## Conc        -1.594e-05  5.058e-06  -3.151  0.00286 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.005429482)
##
##     Null deviance: 0.32913  on 47  degrees of freedom
## Residual deviance: 0.27717  on 46  degrees of freedom
## AIC: 278.04
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L10_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.36272  -0.05391   0.02866   0.06809   0.11587
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.343e-02  2.218e-04  60.556   <2e-16 ***
## Conc        -8.827e-06  5.120e-06  -1.724   0.0914 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01045203)
##
##     Null deviance: 0.56690  on 47  degrees of freedom
## Residual deviance: 0.53671  on 46  degrees of freedom
## AIC: 341.07
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L10_Verticillium dahliae`
##
```

```
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.05228  -0.02578  -0.00134   0.01941   0.06402
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.572e-02  1.410e-04 182.405   <2e-16 ***
## Conc        2.434e-06  3.390e-06   0.718    0.477
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001088242)
##
##     Null deviance: 0.048097  on 45  degrees of freedom
## Residual deviance: 0.047534  on 44  degrees of freedom
## AIC: 156.85
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L11_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.050810  -0.015631  -0.001658   0.016731   0.071592
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.558e-02  6.196e-05 251.543   <2e-16 ***
## Conc        -1.750e-06  1.496e-06  -1.169    0.248
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0006043651)
##
##     Null deviance: 0.028478  on 47  degrees of freedom
## Residual deviance: 0.027656  on 46  degrees of freedom
## AIC: 183.86
##
## Number of Fisher Scoring iterations: 3
```

```
##
##
## $`L11_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.141905  -0.055610   0.007691   0.042408   0.158504
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.750e-02  2.108e-04  83.051   <2e-16 ***
## Conc        6.577e-07  5.152e-06   0.128    0.899
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.005540634)
##
##     Null deviance: 0.25531  on 47  degrees of freedom
## Residual deviance: 0.25522  on 46  degrees of freedom
## AIC: 278.92
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L11_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.198531  -0.012005   0.009918   0.026628   0.096895
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.892e-02  1.869e-04 101.237  < 2e-16 ***
## Conc        -2.025e-05  4.165e-06  -4.862 1.39e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.003746324)
##
##     Null deviance: 0.26943  on 47  degrees of freedom
```

```
## Residual deviance: 0.18485  on 46  degrees of freedom
## AIC: 258.08
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L11_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.47228  -0.01667   0.03679   0.08935   0.16904
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.577e-02  3.659e-04  43.087   <2e-16 ***
## Conc        -1.653e-05  8.169e-06  -2.023   0.0489 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.02067956)
##
##     Null deviance: 1.2181  on 47  degrees of freedom
## Residual deviance: 1.1371  on 46  degrees of freedom
## AIC: 361.97
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L11_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.083771  -0.043288  -0.001424   0.038186   0.119047
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.606e-02  2.192e-04 118.869   <2e-16 ***
## Conc        8.336e-06  5.480e-06   1.521    0.135
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## (Dispersion parameter for Gamma family taken to be 0.002701481)
##
##     Null deviance: 0.12967  on 47  degrees of freedom
## Residual deviance: 0.12334  on 46  degrees of freedom
## AIC: 205.44
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L12_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.03991  -0.02027   0.00006   0.01399   0.06265
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.398e-02  5.371e-05 260.214  < 2e-16 ***
## Conc        5.042e-06  1.347e-06   3.743 0.000504 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0005636432)
##
##     Null deviance: 0.033811  on 47  degrees of freedom
## Residual deviance: 0.025793  on 46  degrees of freedom
## AIC: 190.14
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L12_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.163231  -0.049520  -0.006483   0.053530   0.166419
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept) 1.758e-02  2.041e-04  86.108   <2e-16 ***
## Conc        1.282e-05  5.268e-06   2.434   0.0189 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.005139402)
##
##     Null deviance: 0.26772  on 47  degrees of freedom
## Residual deviance: 0.23632  on 46  degrees of freedom
## AIC: 273.66
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L12_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.28979  -0.07081   0.03512   0.07164   0.14078
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.077e-02  3.461e-04  60.012   <2e-16 ***
## Conc        -1.466e-05  7.958e-06  -1.842   0.0719 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01064466)
##
##     Null deviance: 0.56793  on 47  degrees of freedom
## Residual deviance: 0.53288  on 46  degrees of freedom
## AIC: 298.96
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L12_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
```

```
## -0.283132  -0.061345   0.009035   0.067882   0.155738
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.491e-02  2.245e-04  66.405   <2e-16 ***
## Conc        2.349e-06  5.541e-06   0.424    0.674
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.008662242)
##
##     Null deviance: 0.41887  on 47  degrees of freedom
## Residual deviance: 0.41730  on 46  degrees of freedom
## AIC: 317.6
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L12_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.064783  -0.019314   0.006071   0.018073   0.057052
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.340e-02  1.033e-04 226.524   <2e-16 ***
## Conc        -4.040e-06  2.483e-06  -1.627    0.111
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0007454255)
##
##     Null deviance: 0.036497  on 47  degrees of freedom
## Residual deviance: 0.034538  on 46  degrees of freedom
## AIC: 155.59
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L13_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
```

```
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.051467  -0.014212   0.001572   0.011138   0.063619
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.392e-02  5.001e-05 278.287   <2e-16 ***
## Conc        -1.912e-06  1.205e-06  -1.586     0.12
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0004938365)
##
##     Null deviance: 0.023886  on 47  degrees of freedom
## Residual deviance: 0.022651  on 46  degrees of freedom
## AIC: 185.18
##
## Number of Fisher Scoring iterations: 3
##
##
## $`L13_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.201696  -0.040084   0.004017   0.055104   0.158528
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.664e-02  2.178e-04  76.422   <2e-16 ***
## Conc        1.091e-05  5.589e-06   1.952   0.0571 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.00652671)
##
##     Null deviance: 0.33121  on 47  degrees of freedom
## Residual deviance: 0.30564  on 46  degrees of freedom
## AIC: 291.32
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L13_Alternaria alternata`
```

```
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.30287  -0.07705   0.02768   0.09350   0.13984
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.080e-02  3.897e-04  53.361   <2e-16 ***
## Conc        -8.656e-06  9.180e-06  -0.943    0.351
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01344731)
##
##     Null deviance: 0.66870  on 47  degrees of freedom
## Residual deviance: 0.65696  on 46  degrees of freedom
## AIC: 308.25
##
## Number of Fisher Scoring iterations: 4
##
##
## $`L13_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.33659  -0.12053   0.03642   0.10367   0.20073
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.557e-02  3.619e-04  43.016   <2e-16 ***
## Conc        -4.404e-06  8.620e-06  -0.511    0.612
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.02068159)
##
##     Null deviance: 1.0107  on 47  degrees of freedom
## Residual deviance: 1.0053  on 46  degrees of freedom
## AIC: 355.93
##
```

```
## Number of Fisher Scoring iterations: 4
##
##
## $`L13_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.090299  -0.020321   0.001189   0.023877   0.062827
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.323e-02  1.346e-04 172.612   <2e-16 ***
## Conc        5.755e-06  3.280e-06   1.755   0.0863 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001228538)
##
##     Null deviance: 0.058412  on 45  degrees of freedom
## Residual deviance: 0.054590  on 44  degrees of freedom
## AIC: 172.31
##
## Number of Fisher Scoring iterations: 3
##
##
## $`A_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.053728  -0.022237  -0.003564   0.023413   0.049352
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.335e-02  5.872e-05 227.362   <2e-16 ***
## Conc        -5.270e-07  1.427e-06  -0.369    0.713
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0007395259)
##
```

```
##     Null deviance: 0.034147  on 47  degrees of freedom
## Residual deviance: 0.034046  on 46  degrees of freedom
## AIC: 208.55
##
## Number of Fisher Scoring iterations: 3
##
##
## $`A_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.184730  -0.038523  -0.004258   0.037961   0.122937
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.690e-02  1.733e-04  97.487  < 2e-16 ***
## Conc        -1.127e-05  3.916e-06  -2.878  0.00616 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.003822775)
##
##     Null deviance: 0.20275  on 45  degrees of freedom
## Residual deviance: 0.17197  on 44  degrees of freedom
## AIC: 255.95
##
## Number of Fisher Scoring iterations: 4
##
##
## $`A_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.50438  -0.03234   0.02086   0.07218   0.20406
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.914e-02  3.962e-04  48.314   <2e-16 ***
## Conc        1.217e-05  1.015e-05   1.198    0.237
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0163312)
##
##     Null deviance: 0.91517  on 47  degrees of freedom
## Residual deviance: 0.89108  on 46  degrees of freedom
## AIC: 328.78
##
## Number of Fisher Scoring iterations: 4
##
##
## $`A_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.125353  -0.025866   0.002154   0.037424   0.095957
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.471e-02  1.190e-04 123.665   <2e-16 ***
## Conc        -1.605e-06  2.874e-06  -0.559    0.579
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.002500501)
##
##     Null deviance: 0.11763  on 47  degrees of freedom
## Residual deviance: 0.11686  on 46  degrees of freedom
## AIC: 258.48
##
## Number of Fisher Scoring iterations: 3
##
##
## $`A_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.070894  -0.015208  -0.001544   0.010942   0.079862
##
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.574e-02  1.127e-04 228.437   <2e-16 ***
## Conc        5.928e-06  2.797e-06   2.119   0.0395 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0007317586)
##
##     Null deviance: 0.036642  on 47  degrees of freedom
## Residual deviance: 0.033323  on 46  degrees of freedom
## AIC: 144.04
##
## Number of Fisher Scoring iterations: 3
##
##
## $`B_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.043577  -0.017646   0.001067   0.014641   0.048879
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.323e-02  5.009e-05 264.146   <2e-16 ***
## Conc        2.372e-07  1.223e-06   0.194    0.847
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0005477688)
##
##     Null deviance: 0.025178  on 47  degrees of freedom
## Residual deviance: 0.025157  on 46  degrees of freedom
## AIC: 194.8
##
## Number of Fisher Scoring iterations: 3
##
##
## $`B_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
```

```
##       Min         1Q     Median         3Q        Max
## -0.117188  -0.036197  -0.007627   0.033081   0.184607
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.677e-02  1.681e-04  99.776   <2e-16 ***
## Conc        6.123e-06  4.218e-06   1.452    0.153
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.00383359)
##
##     Null deviance: 0.18005  on 47  degrees of freedom
## Residual deviance: 0.17185  on 46  degrees of freedom
## AIC: 263.52
##
## Number of Fisher Scoring iterations: 4
##
##
## $`B_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.41864  -0.07528   0.01146   0.09243   0.18397
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.003e-02  4.041e-04  49.566   <2e-16 ***
## Conc        -2.014e-05  9.054e-06  -2.225    0.031 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01562443)
##
##     Null deviance: 0.86784  on 47  degrees of freedom
## Residual deviance: 0.79378  on 46  degrees of freedom
## AIC: 321.95
##
## Number of Fisher Scoring iterations: 4
##
##
## $`B_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
```

```
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.234822  -0.048646  -0.001153   0.065475   0.131646
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.532e-02  1.997e-04  76.685   <2e-16 ***
## Conc        3.637e-06  4.961e-06   0.733    0.467
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.006493277)
##
##     Null deviance: 0.31219  on 47  degrees of freedom
## Residual deviance: 0.30867  on 46  degrees of freedom
## AIC: 300.46
##
## Number of Fisher Scoring iterations: 4
##
##
## $`B_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.056765  -0.015885   0.001586   0.017185   0.043656
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.565e-02  1.031e-04 248.747  < 2e-16 ***
## Conc        1.551e-05  2.579e-06   6.014 3.22e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0005838636)
##
##     Null deviance: 0.047455  on 45  degrees of freedom
## Residual deviance: 0.025801  on 44  degrees of freedom
## AIC: 128.15
##
## Number of Fisher Scoring iterations: 3
##
##
```

```
## $`Fosetyl-al_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.090449  -0.023407  -0.002225   0.022483   0.094754
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.340e-02  8.438e-05   158.8   <2e-16 ***
## Conc        9.113e-05  3.198e-06    28.5   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.0014753)
##
##     Null deviance: 1.607538  on 47  degrees of freedom
## Residual deviance: 0.067773  on 46  degrees of freedom
## AIC: 231.67
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Fosetyl-al_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.184136  -0.039699   0.000298   0.044763   0.112982
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.725e-02  1.924e-04   89.65  < 2e-16 ***
## Conc        1.544e-05  5.029e-06    3.07  0.00359 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.004737874)
##
##     Null deviance: 0.27070  on 47  degrees of freedom
## Residual deviance: 0.22434  on 46  degrees of freedom
## AIC: 272.69
```

```
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Fosetyl-al_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.22629  -0.06228   0.01335   0.05722   0.12243
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.848e-02  2.639e-04  70.024   <2e-16 ***
## Conc        -1.269e-05  6.077e-06  -2.088   0.0424 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.007817817)
##
##     Null deviance: 0.41269  on 47  degrees of freedom
## Residual deviance: 0.37961  on 46  degrees of freedom
## AIC: 294
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Fosetyl-al_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.209394  -0.044600   0.006966   0.042623   0.175299
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.546e-02  2.057e-04  75.165  < 2e-16 ***
## Conc        -2.415e-05  4.389e-06  -5.503  1.6e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.006810378)
```

```
##
##     Null deviance: 0.51115  on 47  degrees of freedom
## Residual deviance: 0.31837  on 46  degrees of freedom
## AIC: 304.45
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Fosetyl-al_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.094806  -0.029673  -0.001572   0.019792   0.116389
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.919e-02  2.023e-04 144.280   <2e-16 ***
## Conc        7.337e-06  5.031e-06   1.458    0.152
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.001834217)
##
##     Null deviance: 0.087067  on 47  degrees of freedom
## Residual deviance: 0.083125  on 46  degrees of freedom
## AIC: 175.75
##
## Number of Fisher Scoring iterations: 3
##
##
## $`C_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.21131  -0.09456   0.01067   0.09906   0.15433
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.508e-02  2.857e-04   52.76   <2e-16 ***
## Conc        5.558e-04  2.686e-05   20.70   <2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01226335)
##
##     Null deviance: 11.60054  on 47  degrees of freedom
## Residual deviance:  0.57493  on 46  degrees of freedom
## AIC: 301.66
##
## Number of Fisher Scoring iterations: 4
##
##
## $`C_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.17741  -0.07611  -0.02674   0.06397   0.25766
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.724e-02  3.287e-04   52.43   <2e-16 ***
## Conc        6.402e-04  3.106e-05   20.61   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01241157)
##
##     Null deviance: 11.64627  on 47  degrees of freedom
## Residual deviance:  0.54821  on 46  degrees of freedom
## AIC: 286.41
##
## Number of Fisher Scoring iterations: 4
##
##
## $`C_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.14578  -0.04165   0.02251   0.03588   0.08254
##
```

```
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.817e-02  1.636e-04  111.06  < 2e-16 ***
## Conc        5.821e-05  5.027e-06   11.58 3.13e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.003058609)
##
##     Null deviance: 0.61195  on 47  degrees of freedom
## Residual deviance: 0.14521  on 46  degrees of freedom
## AIC: 243.43
##
## Number of Fisher Scoring iterations: 4
##
##
## $`C_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.25395  -0.04603   0.02180   0.06537   0.11504
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.413e-02  2.099e-04   67.34  < 2e-16 ***
## Conc        7.721e-05  7.395e-06   10.44 1.01e-13 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.008247752)
##
##     Null deviance: 1.51848  on 47  degrees of freedom
## Residual deviance: 0.41095  on 46  degrees of freedom
## AIC: 314.34
##
## Number of Fisher Scoring iterations: 4
##
##
## $`C_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
```

```
## Deviance Residuals:
##       Min         1Q     Median         3Q        Max
## -0.309619  -0.043446  -0.005819   0.054887   0.184848
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.819e-02  4.509e-04   62.53   <2e-16 ***
## Conc        3.037e-04  2.063e-05   14.72   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.009382106)
##
##     Null deviance: 3.36612  on 47  degrees of freedom
## Residual deviance: 0.45087  on 46  degrees of freedom
## AIC: 246.85
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Mefenoxam_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##     Min       1Q   Median       3Q      Max
## -0.7554  -0.4061   0.0216   0.3053   0.4068
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0179289  0.0010927  16.407  < 2e-16 ***
## Conc        0.0004355  0.0000781   5.576 1.24e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.1307401)
##
##     Null deviance: 14.4754  on 47  degrees of freedom
## Residual deviance:  7.0247  on 46  degrees of freedom
## AIC: 406.54
##
## Number of Fisher Scoring iterations: 5
##
##
## $`Mefenoxam_Phytophthora capsici`
##
## Call:
```

```
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.99642  -0.76924  -0.07998   0.46838   0.75138
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0254063  0.0026904   9.443 2.44e-12 ***
## Conc        0.0013927  0.0003341   4.168 0.000134 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.3700078)
##
##     Null deviance: 35.398  on 47  degrees of freedom
## Residual deviance: 20.135  on 46  degrees of freedom
## AIC: 398.46
##
## Number of Fisher Scoring iterations: 5
##
##
## $`Mefenoxam_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.17211  -0.01776   0.01088   0.02794   0.14705
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.703e-02  1.738e-04   98.01  < 2e-16 ***
## Conc        6.039e-05  5.458e-06   11.06 1.48e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.003922159)
##
##     Null deviance: 0.73684  on 47  degrees of freedom
## Residual deviance: 0.18357  on 46  degrees of freedom
## AIC: 260.39
##
## Number of Fisher Scoring iterations: 4
##
```

```
##
## $`Mefenoxam_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.23879  -0.02844   0.01372   0.03520   0.07224
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.280e-02  1.175e-04  108.94  < 2e-16 ***
## Conc        3.738e-05  3.544e-06   10.55 7.25e-14 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.003182429)
##
##     Null deviance: 0.55505  on 47  degrees of freedom
## Residual deviance: 0.15643  on 46  degrees of freedom
## AIC: 281.02
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Mefenoxam_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.12412  -0.04586  -0.01024   0.04281   0.09854
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.602e-02  2.357e-04 110.401   <2e-16 ***
## Conc        1.042e-05  6.701e-06   1.555    0.127
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.00312844)
##
##     Null deviance: 0.14513  on 45  degrees of freedom
## Residual deviance: 0.13742  on 44  degrees of freedom
```

```
## AIC: 204.16
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Pyraclostrobin_Phytophthora citrophthora`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.27291  -0.10960  -0.01544   0.14232   0.21219
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.552e-02  3.499e-04  44.349  < 2e-16 ***
## Conc        3.119e-05  9.919e-06   3.145  0.00291 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.01927295)
##
##     Null deviance: 1.09607  on 47  degrees of freedom
## Residual deviance: 0.88897  on 46  degrees of freedom
## AIC: 346.64
##
## Number of Fisher Scoring iterations: 4
##
##
## $`Pyraclostrobin_Phytophthora capsici`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.42947  -0.22481  -0.03705   0.20001   0.48928
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.230e-02  9.835e-04  22.677  < 2e-16 ***
## Conc        -7.618e-05  1.756e-05  -4.339 7.76e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for Gamma family taken to be 0.07542776)
##
##     Null deviance: 4.6068  on 47  degrees of freedom
## Residual deviance: 3.3740  on 46  degrees of freedom
## AIC: 384.36
##
## Number of Fisher Scoring iterations: 5
##
##
## $`Pyraclostrobin_Alternaria alternata`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.44343  -0.19458  -0.05635   0.10634   0.52933
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 2.426e-02  1.160e-03  20.921  < 2e-16 ***
## Conc        5.933e-04  8.324e-05   7.128 5.85e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.08037597)
##
##     Null deviance: 10.8970  on 47  degrees of freedom
## Residual deviance:  3.3946  on 46  degrees of freedom
## AIC: 345.53
##
## Number of Fisher Scoring iterations: 5
##
##
## $`Pyraclostrobin_Fusarium solani`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.40344  -0.26715  -0.09687   0.20845   0.51269
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.886e-02  9.154e-04  20.600   <2e-16 ***
```

```
## Conc        7.410e-05  2.945e-05   2.516   0.0154 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.08864704)
##
##     Null deviance: 4.5192  on 47  degrees of freedom
## Residual deviance: 3.8636  on 46  degrees of freedom
## AIC: 393.27
##
## Number of Fisher Scoring iterations: 5
##
##
## $`Pyraclostrobin_Verticillium dahliae`
##
## Call:
## glm(formula = D ~ Conc, family = Gamma, data = invitro[invitro$groupident
==
##     unique(invitro$groupident)[[i]], ])
##
## Deviance Residuals:
##      Min        1Q    Median        3Q       Max
## -0.87093  -0.48828  -0.00329   0.34679   0.43178
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.0267770  0.0018733  14.294  < 2e-16 ***
## Conc        0.0014239  0.0002276   6.256  1.2e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.1619306)
##
##     Null deviance: 23.9471  on 47  degrees of freedom
## Residual deviance:  9.0386  on 46  degrees of freedom
## AIC: 364.84
##
## Number of Fisher Scoring iterations: 5
```

P-values and b_2 coefficient values

Interpreting the b_2 coefficient values reveals the effect of an increasing product concentration on colony growth (diameter). Negative glm b_2 coefficient signs suggest an increase in growth with increasing product concentration and vice versa. When P-value < 0.05, there is an effect of concentration on colony growth that is significant at the $\alpha = 0.05$ level.

```
pvalue<-c()
b2<-c()
for(i in 1:95){
  b2[i]<-Sumsetglm[[i]]$coefficients[2,1]
  pvalue[i]<-Sumsetglm[[i]]$coefficients[2,4]
  names(pvalue)[i] <- unique(invitro$groupident)[i]
  names(b2)[i] <- unique(invitro$groupident)[i]

}

(Val<-data.frame(b2,pvalue))
```

```
##                                                 b2       pvalue
## L01_Phytophthora citrophthora            4.141548e-06 4.878983e-01
## L01_Phytophthora capsici                 1.555869e-05 3.253907e-03
## L01_Alternaria alternata                -9.435620e-06 3.678788e-01
## L01_Fusarium solani                     -1.994807e-05 1.212697e-02
## L01_Verticillium dahliae                 7.861270e-06 3.661969e-01
## L02_Phytophthora citrophthora            3.531931e-06 4.544478e-01
## L02_Phytophthora capsici                -1.453967e-05 1.828676e-02
## L02_Alternaria alternata                -3.035176e-08 9.983689e-01
## L02_Fusarium solani                      3.195169e-05 5.399906e-04
## L02_Verticillium dahliae                 1.861877e-05 2.493398e-02
## L03_Phytophthora citrophthora            1.586700e-05 1.747367e-02
## L03_Phytophthora capsici                -2.175026e-05 9.113884e-05
## L03_Alternaria alternata                -1.957965e-05 3.784803e-02
## L03_Fusarium solani                     -9.062532e-06 6.699119e-02
## L03_Verticillium dahliae                 1.500662e-06 8.610818e-01
## L04_Phytophthora citrophthora            7.731964e-06 2.787192e-01
## L04_Phytophthora capsici                 8.760305e-06 1.447956e-01
## L04_Alternaria alternata                 7.069204e-06 5.952618e-01
## L04_Fusarium solani                     -3.703034e-06 1.204568e-01
## L04_Verticillium dahliae                -1.263866e-05 8.631096e-02
## L05_Phytophthora citrophthora            9.222500e-07 8.249410e-01
## L05_Phytophthora capsici                -3.150779e-06 4.873333e-01
## L05_Alternaria alternata                 2.538824e-05 2.660458e-03
## L05_Fusarium solani                     -1.103022e-05 1.298239e-01
## L05_Verticillium dahliae                -4.625429e-06 1.804911e-01
## L06_Phytophthora citrophthora           -1.924804e-06 9.394103e-02
## L06_Phytophthora capsici                -7.706956e-06 2.420570e-02
## L06_Alternaria alternata                 1.030926e-06 9.239754e-01
```

```
## L06_Fusarium solani                          4.353760e-06 3.096602e-01
## L06_Verticillium dahliae                    -1.448949e-06 7.530207e-01
## L07_Phytophthora citrophthora               -2.847420e-06 2.611556e-02
## L07_Phytophthora capsici                    -8.430749e-06 1.608636e-01
## L07_Alternaria alternata                     8.805854e-06 3.325953e-01
## L07_Fusarium solani                          9.082526e-06 8.409483e-03
## L07_Verticillium dahliae                    -5.855726e-06 8.989972e-02
## L08_Phytophthora citrophthora                2.297198e-05 6.436732e-16
## L08_Phytophthora capsici                    -1.441354e-05 1.534105e-04
## L08_Alternaria alternata                     7.351682e-06 6.976699e-03
## L08_Fusarium solani                          4.718996e-06 5.331150e-01
## L08_Verticillium dahliae                     2.733803e-05 2.385095e-06
## L09_Phytophthora citrophthora                6.612141e-06 3.188717e-05
## L09_Phytophthora capsici                     6.820391e-06 1.414585e-01
## L09_Alternaria alternata                    -1.284894e-05 2.115384e-05
## L09_Fusarium solani                         -4.445464e-06 1.334229e-01
## L09_Verticillium dahliae                     1.081395e-05 7.535203e-04
## L10_Phytophthora citrophthora               -3.115666e-06 8.946547e-02
## L10_Phytophthora capsici                     1.287770e-05 1.659717e-02
## L10_Alternaria alternata                    -1.593795e-05 2.860918e-03
## L10_Fusarium solani                         -8.826992e-06 9.143878e-02
## L10_Verticillium dahliae                     2.433950e-06 4.765490e-01
## L11_Phytophthora citrophthora               -1.749681e-06 2.483110e-01
## L11_Phytophthora capsici                     6.577324e-07 8.989751e-01
## L11_Alternaria alternata                    -2.025304e-05 1.392937e-05
## L11_Fusarium solani                         -1.652884e-05 4.887271e-02
## L11_Verticillium dahliae                     8.336313e-06 1.350750e-01
## L12_Phytophthora citrophthora                5.042056e-06 5.043795e-04
## L12_Phytophthora capsici                     1.282075e-05 1.888685e-02
## L12_Alternaria alternata                    -1.466145e-05 7.187835e-02
## L12_Fusarium solani                          2.349092e-06 6.735529e-01
## L12_Verticillium dahliae                    -4.040240e-06 1.105444e-01
## L13_Phytophthora citrophthora               -1.912166e-06 1.195196e-01
## L13_Phytophthora capsici                     1.090746e-05 5.706966e-02
## L13_Alternaria alternata                    -8.656200e-06 3.506458e-01
## L13_Fusarium solani                         -4.404494e-06 6.118023e-01
## L13_Verticillium dahliae                     5.755012e-06 8.626005e-02
## A_Phytophthora citrophthora                 -5.270388e-07 7.134934e-01
## A_Phytophthora capsici                      -1.126860e-05 6.158653e-03
## A_Alternaria alternata                       1.216681e-05 2.369187e-01
## A_Fusarium solani                           -1.605382e-06 5.791733e-01
## A_Verticillium dahliae                       5.927944e-06 3.948274e-02
## B_Phytophthora citrophthora                  2.372019e-07 8.470222e-01
## B_Phytophthora capsici                       6.122779e-06 1.534107e-01
## B_Alternaria alternata                      -2.014416e-05 3.103452e-02
## B_Fusarium solani                            3.636954e-06 4.672547e-01
## B_Verticillium dahliae                       1.550920e-05 3.218459e-07
## Fosetyl-al_Phytophthora citrophthora         9.112731e-05 7.123420e-31
## Fosetyl-al_Phytophthora capsici              1.543795e-05 3.589827e-03
## Fosetyl-al_Alternaria alternata             -1.268776e-05 4.239092e-02
```

```
## Fosetyl-al_Fusarium solani                -2.414945e-05 1.600101e-06
## Fosetyl-al_Verticillium dahliae            7.336686e-06 1.515583e-01
## C_Phytophthora citrophthora                5.558409e-04 6.072357e-25
## C_Phytophthora capsici                     6.402474e-04 7.152471e-25
## C_Alternaria alternata                     5.821545e-05 3.125764e-15
## C_Fusarium solani                          7.721370e-05 1.014148e-13
## C_Verticillium dahliae                     3.036674e-04 5.038197e-19
## Mefenoxam_Phytophthora citrophthora        4.355025e-04 1.244773e-06
## Mefenoxam_Phytophthora capsici             1.392672e-03 1.339562e-04
## Mefenoxam_Alternaria alternata             6.038611e-05 1.481234e-14
## Mefenoxam_Fusarium solani                  3.738001e-05 7.252514e-14
## Mefenoxam_Verticillium dahliae             1.042081e-05 1.270775e-01
## Pyraclostrobin_Phytophthora citrophthora  3.119222e-05 2.912354e-03
## Pyraclostrobin_Phytophthora capsici       -7.618128e-05 7.762528e-05
## Pyraclostrobin_Alternaria alternata        5.933276e-04 5.853982e-09
## Pyraclostrobin_Fusarium solani             7.409510e-05 1.543356e-02
## Pyraclostrobin_Verticillium dahliae        1.423868e-03 1.196024e-07
```

Data (Growth reduction)

Out of the 95 combinations examined, product concentration had an effect on colony growth in 47 combinations at a significance level of $\alpha = 0.05$ and from these, maximum growth reduction exceeded the level of 50% in 9 combinations. For 8 of these data sets (excluding the *P. capsici* - pyraclostrobin combination), three-parameter logistic regressions were conducted, using growth reduction as the dependent variable. The regressions were done using the nplr function of the nplr package. They had a fixed lower asymptote of zero, conveying that the dose-response curve is asymptotic to the x axis. The $\log_{10}$ of product concentration was the independent variable. Growth reduction is calculated in comparison to the control treatment (0 ppm). In the data table, below, GR stands for growth reduction proportion and has values ranging from -1 to 1. Negative values represent growth increase in comparison to growth in 0 ppm of a given product.

```
invitro_gr <- read.csv("invitro_gr.csv", header=T, sep = ';')
invitro_gr$groupident <- as.character(paste(invitro_gr$Trt,
invitro_gr$Pathogen, sep="_"))
head(invitro_gr)
```

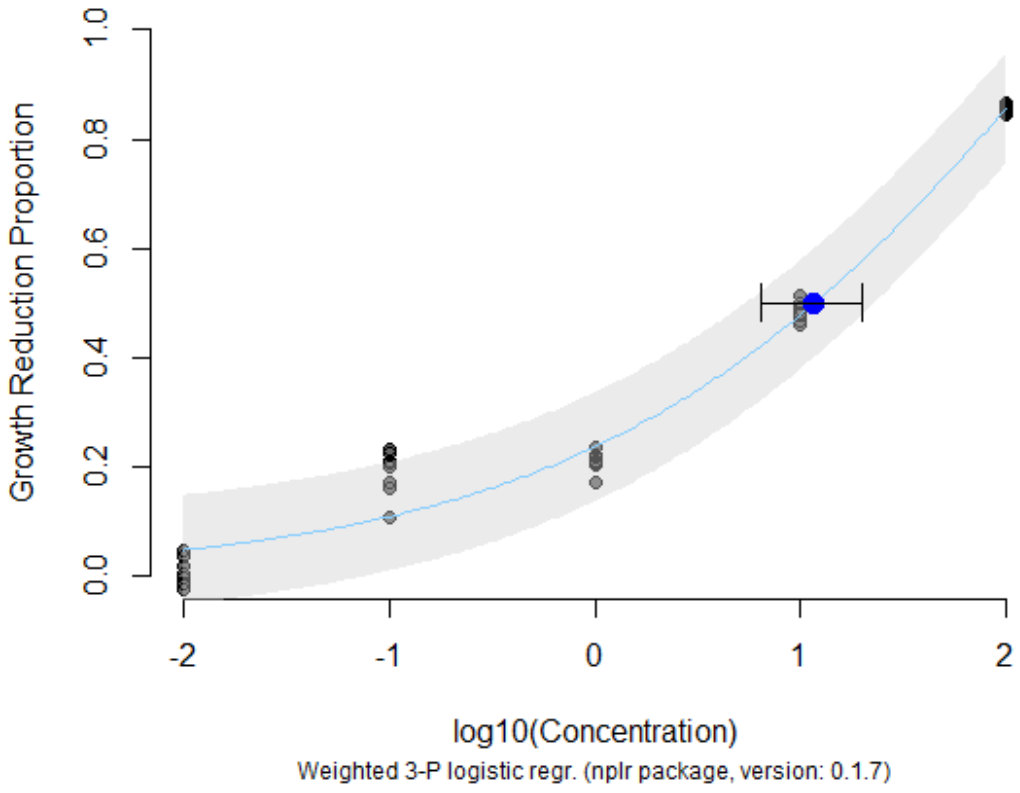
```
##   Trt                  Pathogen Conc     D Days           GR
## 1   C Phytophthora citrophthora 0.01 71.90    7  0.038032928
## 2   C Phytophthora citrophthora 0.01 74.23    7  0.004529441
## 3   C Phytophthora citrophthora 0.01 76.11    7 -0.022503415
## 4   C Phytophthora citrophthora 0.01 74.72    7 -0.002516356
## 5   C Phytophthora citrophthora 0.01 75.50    7 -0.013732116
## 6   C Phytophthora citrophthora 0.01 73.33    7  0.017470702
##                     groupident
## 1 C_Phytophthora citrophthora
## 2 C_Phytophthora citrophthora
## 3 C_Phytophthora citrophthora
## 4 C_Phytophthora citrophthora
## 5 C_Phytophthora citrophthora
## 6 C_Phytophthora citrophthora
```

Dose-response curves and EC_{50} values

The graphs below present the proportion of growth reduction of different pathogens achieved by increasing concentrations of different products. The grey dots designate the data points, the blue dot on each graph the EC_{50} value (error bars: 95% confidence interval along the x axis). Grey area surrounding the regression line is the 95% confidence interval.

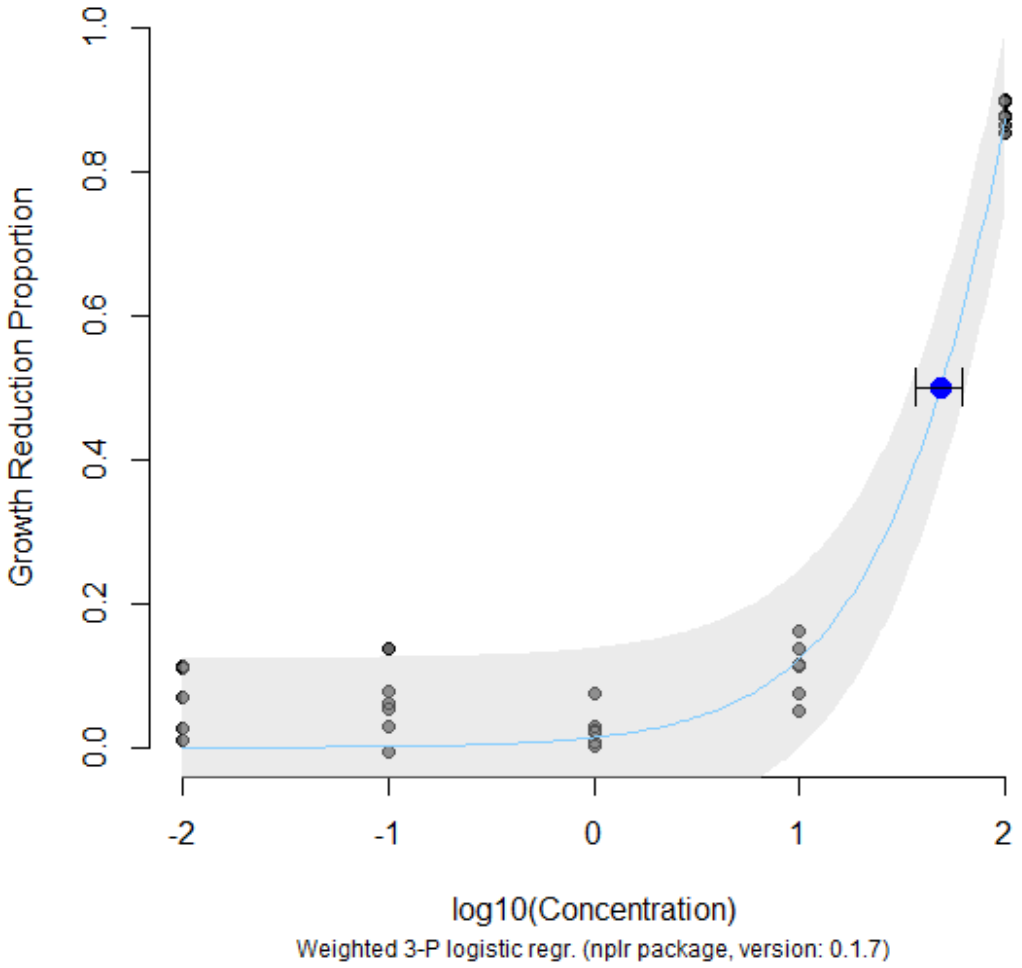
C - Phytophthora citrophthora

```
d<-invitro_gr[which(invitro_gr$groupident== 'C_Phytophthora citrophthora'),]
np3<-nplr(x=d$Conc, y=d$GR, npars=3)#npars specifies the number of parameters
for the model
(m<-getEstimates(np3, 0.5))# this estimation gives the absolute EC50 value
and the CI95%

##     y    x.025        x    x.975
## 1 0.5 6.360368 11.60783 20.01825

par(font.main = 3)
par(font.sub = 1)
plot(np3, pcol="grey40", lcol="skyblue1", showGOF = FALSE, ylim=c(0,1),
xlim=c(-2,2),
     xlab='log10(Concentration)', ylab='Growth Reduction Proportion')
points(log10(m[[3]]), 0.5, col=4, cex=1.5, pch=19)
x<-log10(m[3])
y<-0.5
errorBar(x, y, lower=log10(m[[2]]), upper=log10(m[[4]]), incr = FALSE,
draw.lower = TRUE,
         draw.upper = TRUE, bar.ends = TRUE, gap = TRUE, add = TRUE,
         horizontal = TRUE, gap.size = 0.01, bar.ends.size = 0.5, col = 1)
```



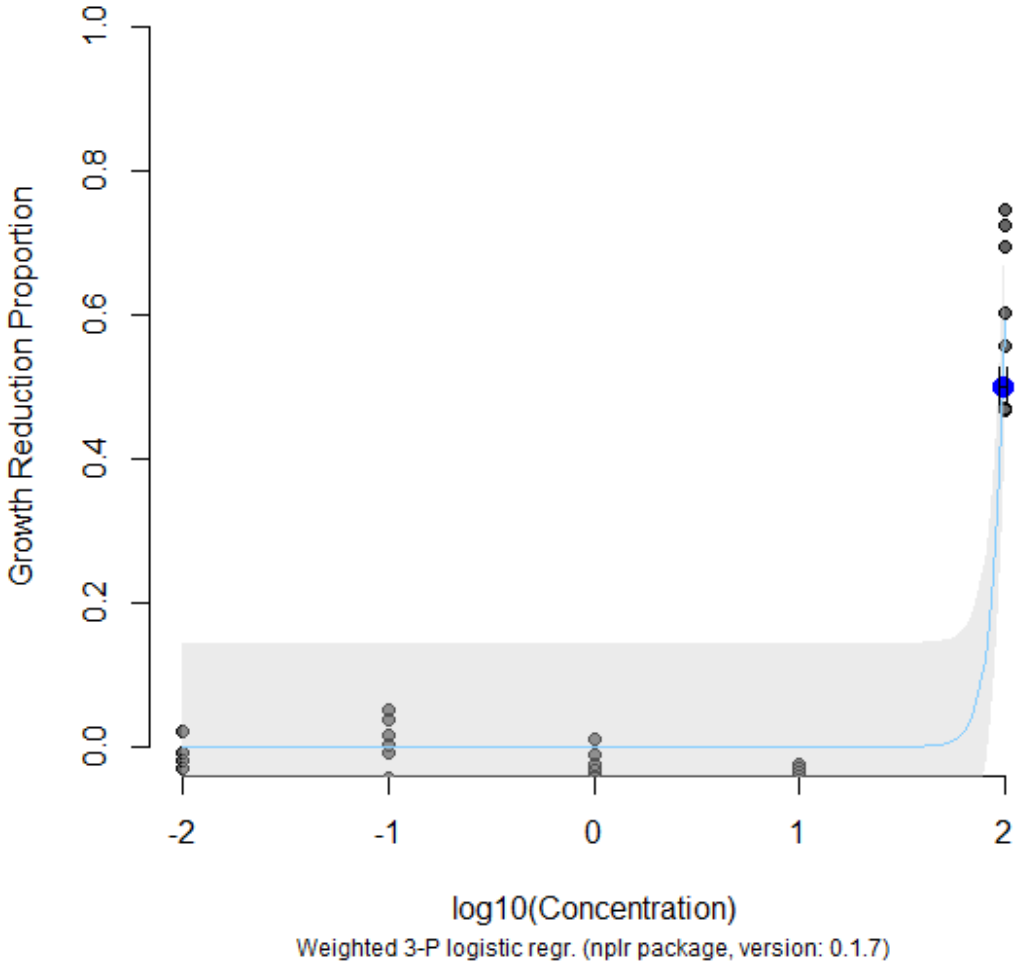
C - Phytophthora capsici

```
##     y   x.025        x    x.975
## 1 0.5 36.6343 48.41478 61.33888
```



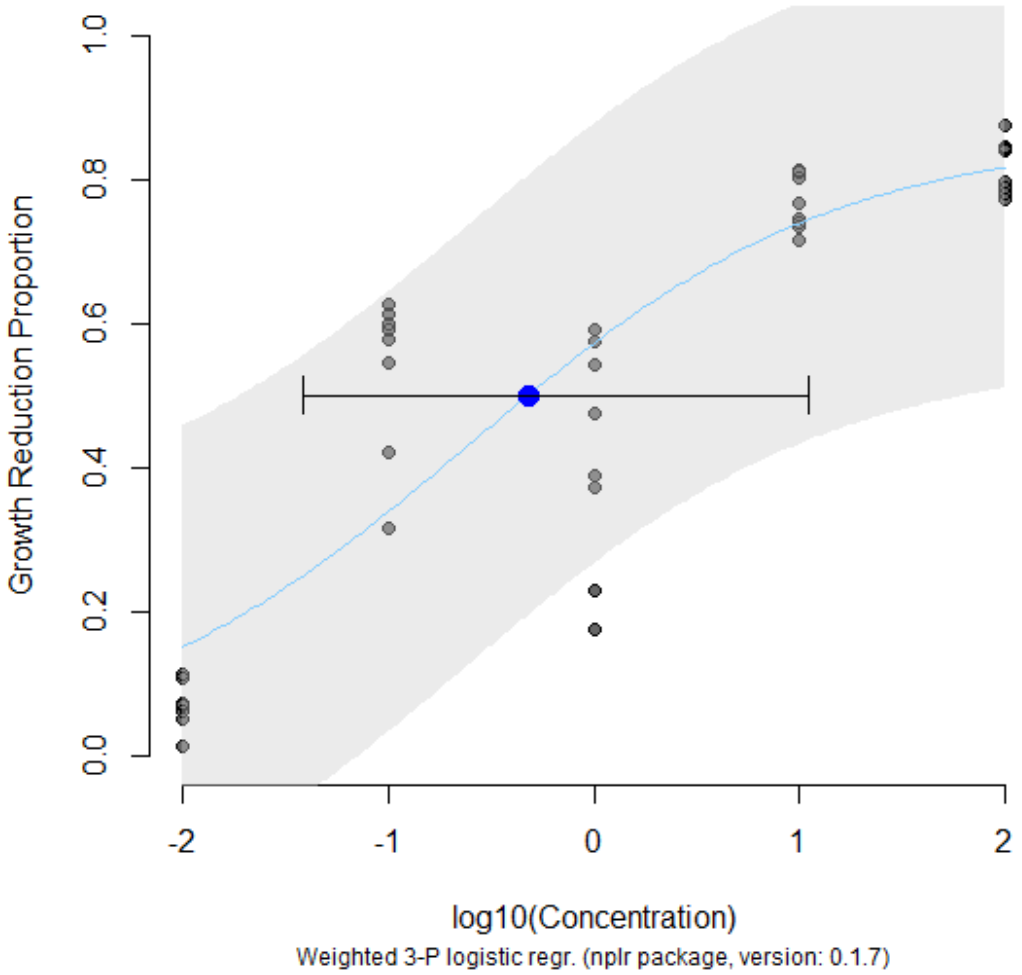
C - Verticillium dahliae

```
##     y    x.025        x    x.975
## 1 0.5 93.12189 97.26152 100.8107
```



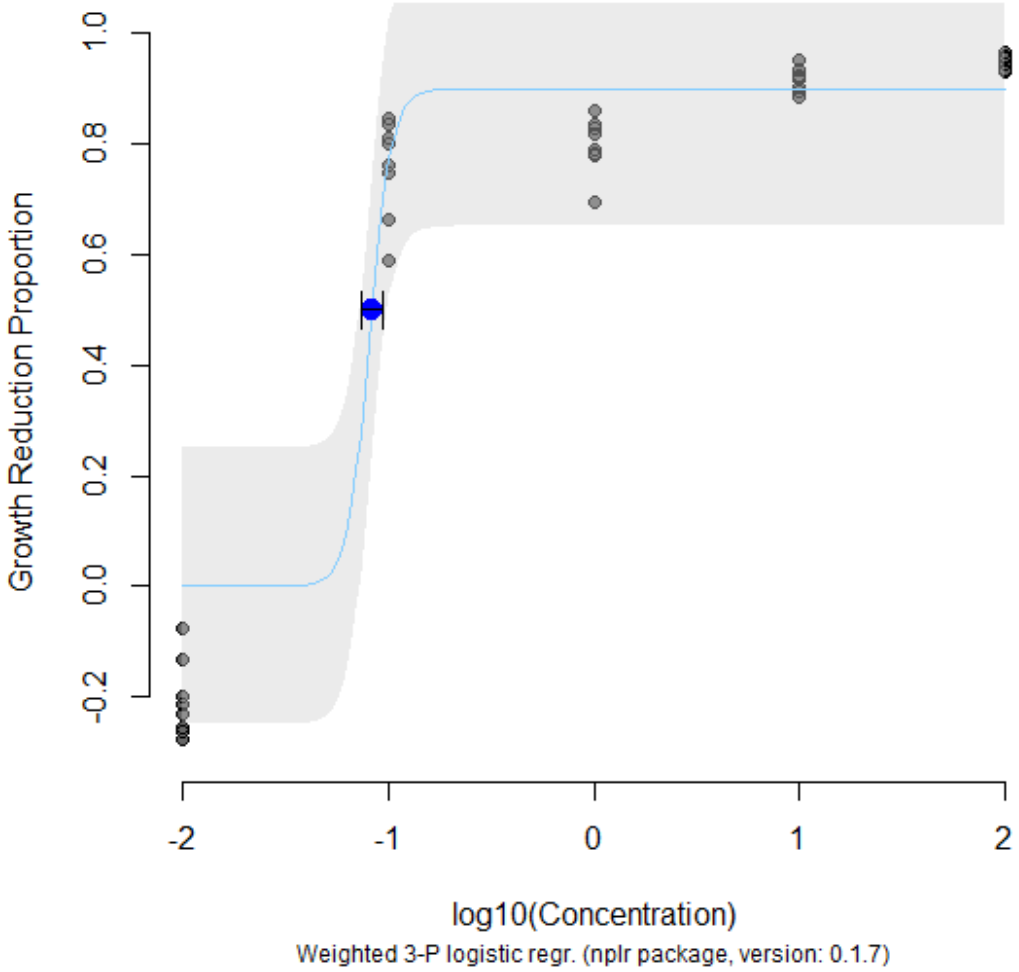
Mefenoxam - Phytophthora citrophthora

```
##     y      x.025         x    x.975
## 1 0.5 0.03839414 0.4750183 10.91764
```



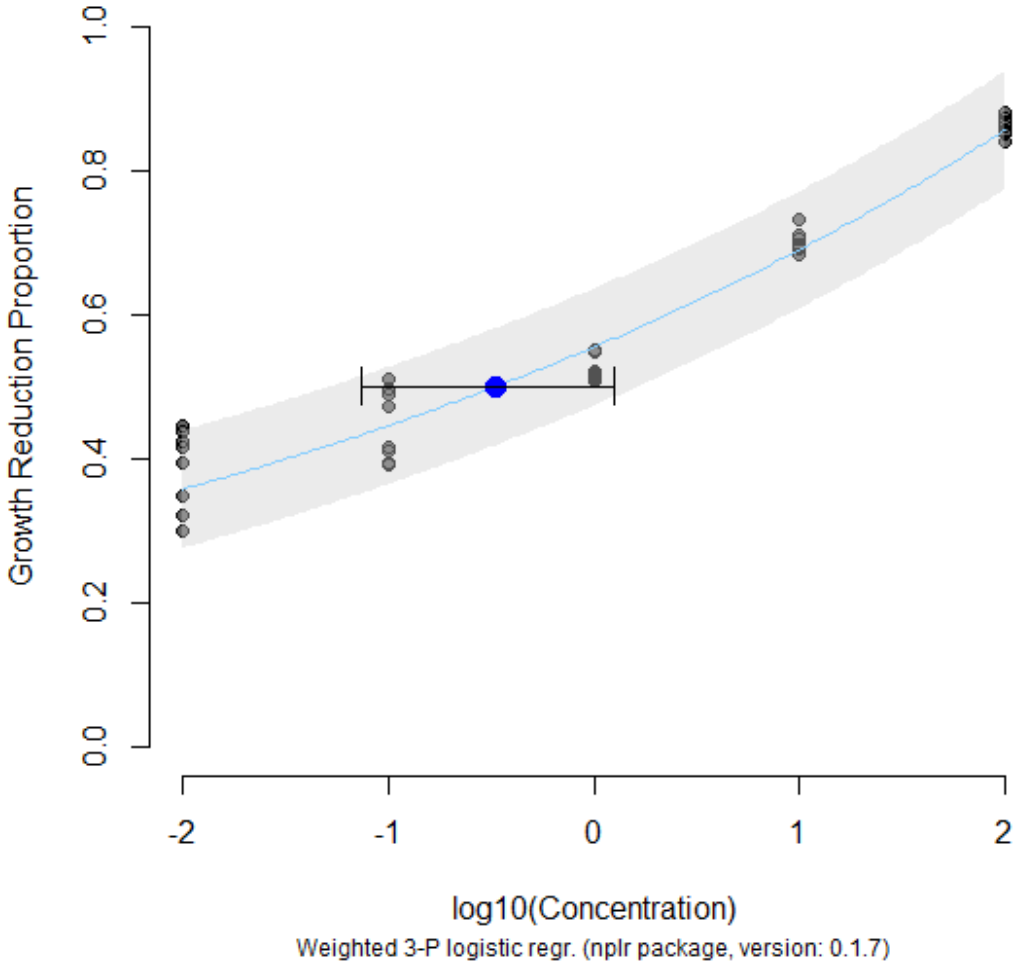
Mefenoxam - Phytophthora capsici

```
##     y      x.025          x      x.975
## 1 0.5 0.07392716 0.08308027 0.09484414
```



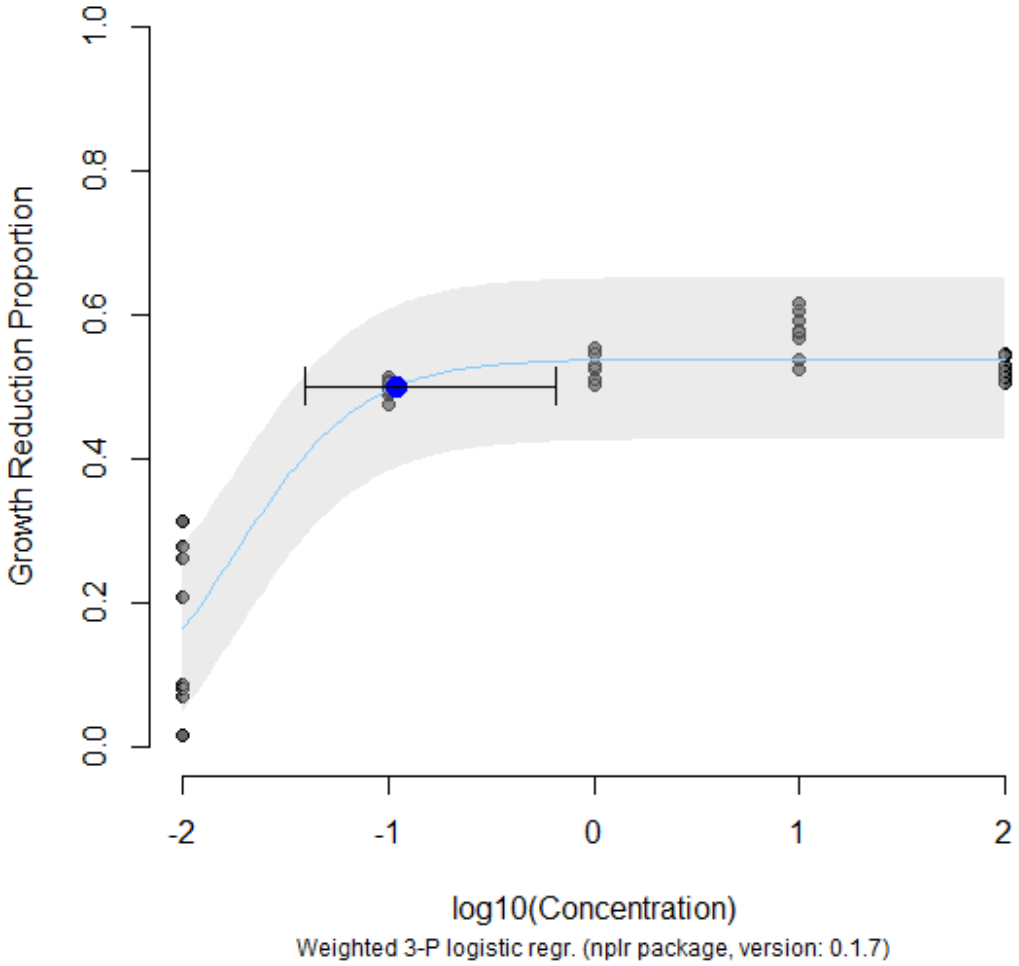
Pyraclostrobin - Alternaria alternata

```
##     y     x.025         x    x.975
## 1 0.5 0.0735849 0.3335437 1.262559
```



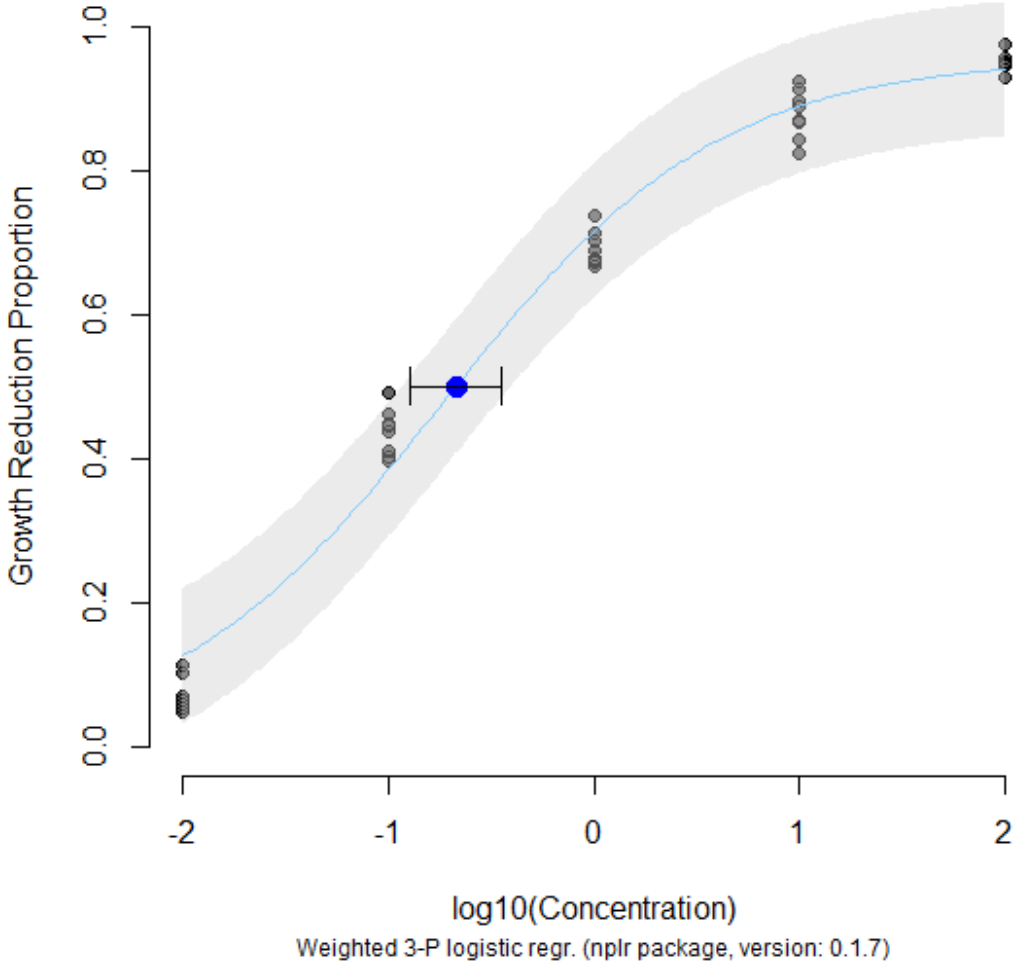
Pyraclostrobin - Fusarium solani

```
##     y      x.025         x     x.975
## 1 0.5 0.03922014 0.1096922 0.6506481
```



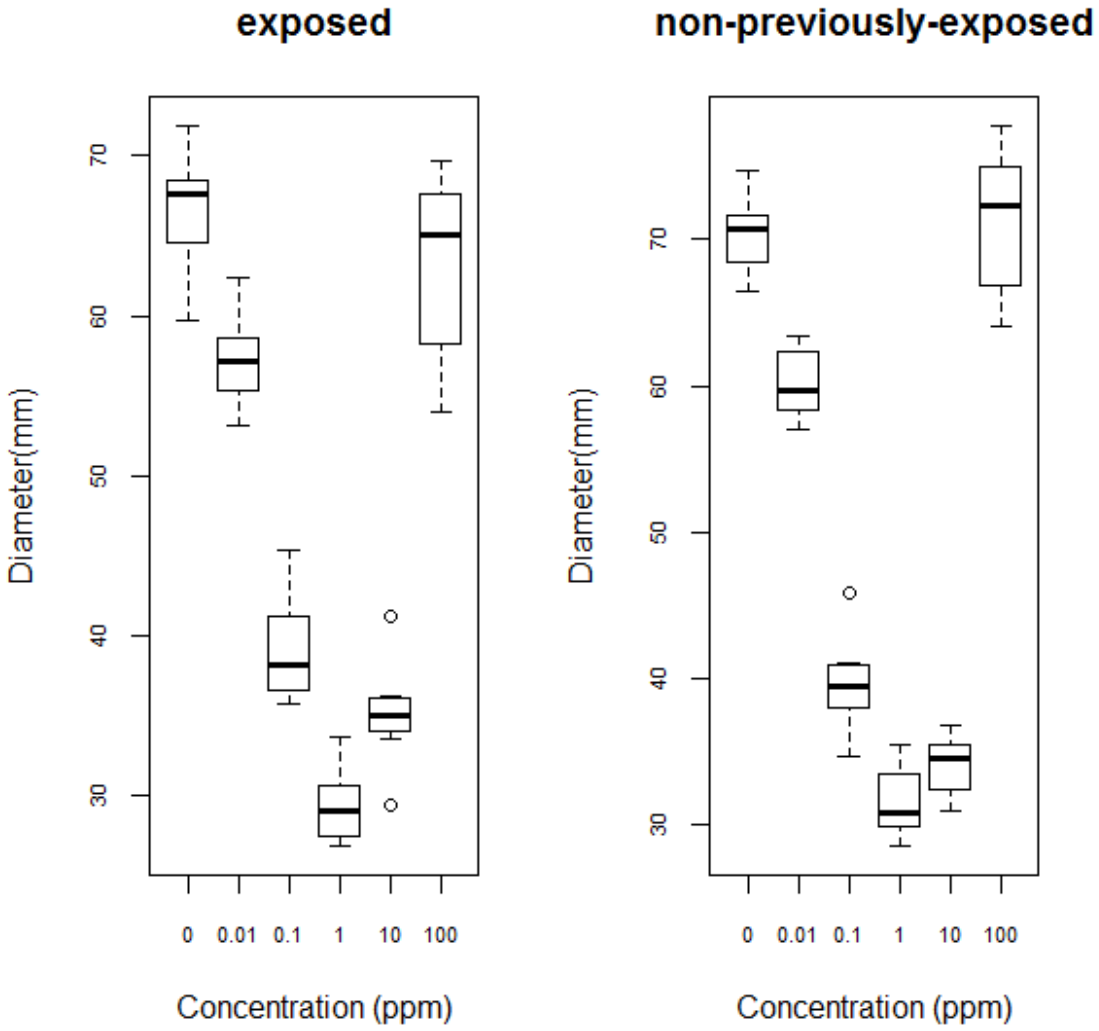
Pyraclostrobin - Verticillium dahliae

```
##     y     x.025         x     x.975
## 1 0.5 0.1272661 0.2123242 0.3575054
```



Data anomaly: Pyraclostrobin - *Phytophthora capsici*

The EC_{50} value of pyraclostrobin against *P. capsici* could not be calculated due to an anomaly of the data. The study was repeated and growth on pyraclostrobin was compared between that of the original *P. capsici* isolate (non-previously-exposed) and of a *P. capsici* isolate recovered after exposure to 100 ppm pyraclostrobin (exposed). Pyraclostrobin inhibited the growth of both isolates by more than 50% at concentrations of 1 ppm and 10 ppm. Lower concentration levels also had growth inhibiting effects, yet, to a lower extent. However, growing in 100 ppm pyraclostrobin did not have any substantial effect in the growth of either of the two isolates, in comparison to growth in the absence of pyraclostrobin (0 ppm).



Two-sample Kolmogorov-Smirnov tests

Since the data sets of both the non-previously-exposed and exposed *P. capsici* isolates do not follow a normal distribution, two-sample Kolmogorov-Smirnov tests were used to examine whether each isolate grows the same in 0 ppm and 100 ppm as well as whether the growth of the two isolates differs significantly when comparing them for each concentration. If p-value > 0.05, then the two distributions compared are not significantly different at the $\alpha = 0.05$ significance level.

There is no significant difference in growth for the non-previously-exposed *P. capsici* isolate in 0 ppm and 100 ppm.

```
NonExp_0ppm<-D_exposed$D[which(D_exposed$Pathogen==path[2] &
D_exposed$Conc==0)]
NonExp_100ppm<-D_exposed$D[which(D_exposed$Pathogen==path[2] &
D_exposed$Conc==100)]

NonExp_0ppm

## [1] 74.63 71.26 70.57 66.48 71.88 68.81 70.89 68.00

NonExp_100ppm

## [1] 65.42 64.05 68.31 73.24 71.52 73.05 76.81 77.75

ks.test(NonExp_0ppm,NonExp_100ppm)

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  NonExp_0ppm and NonExp_100ppm
## D = 0.375, p-value = 0.6601
## alternative hypothesis: two-sided
```

There is no significant difference in growth for the exposed *P. capsici* isolate in 0 ppm and 100 ppm.

```
Exposed_0ppm<-D_exposed$D[which(D_exposed$Pathogen==path[1] &
D_exposed$Conc==0)]
Exposed_100ppm<-D_exposed$D[which(D_exposed$Pathogen==path[1] &
D_exposed$Conc==100)]

Exposed_0ppm

## [1] 71.88 66.76 68.71 67.08 62.43 68.31 59.74 68.22

Exposed_100ppm

## [1] 63.76 58.47 53.96 57.97 69.67 67.03 68.23 66.28

ks.test(Exposed_0ppm,Exposed_100ppm)

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Exposed_0ppm and Exposed_100ppm
## D = 0.375, p-value = 0.6601
## alternative hypothesis: two-sided
```

The growth of the two isolates does not differ significantly when comparing them for each concentration ($\alpha = 0.05$ significance level).

```
##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Exposed_0ppm and NonExp_0ppm
## D = 0.625, p-value = 0.08787
## alternative hypothesis: two-sided

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Exposed_0.01ppm and NonExp_0.01ppm
## D = 0.625, p-value = 0.08702
## alternative hypothesis: two-sided

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Exposed_0.1ppm and NonExp_0.1ppm
## D = 0.375, p-value = 0.6601
## alternative hypothesis: two-sided

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Exposed_1ppm and NonExp_1ppm
## D = 0.625, p-value = 0.08702
## alternative hypothesis: two-sided

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Exposed_10ppm and NonExp_10ppm
## D = 0.25, p-value = 0.9801
## alternative hypothesis: two-sided

##
##  Two-sample Kolmogorov-Smirnov test
##
## data:  Exposed_100ppm and NonExp_100ppm
## D = 0.625, p-value = 0.08702
## alternative hypothesis: two-sided
```

2. Greenhouse trials

Data (plants per severity category)

In the data table, trt stands for product treatment, sev for disease severity and date for evaluation date (with T0 being the date of inoculation).

```
green<-read.table('green.csv',header=T, sep=";")
green[,"trt"]<-as.factor(green[,"trt"])
head(green)
```

```
##   date    trt sev0 sev1 sev2 sev3
## 1  T07  ARD-7   12   32    6    0
## 2  T07  BRD-7    6   41    3    0
## 3  T07  FRD-7    1   39   10    0
## 4  T07  CRD-7    0   26   24    0
## 5  T07 PCRD-7   16   33    1    0
## 6  T07 NCRD-7   50    0    0    0
```

Data (severity per plant)

In the data table, trt stands for product treatment, sev for disease severity and date for evaluation date (with T0 being the date of inoculation).

```
perdate<-read.table('perdate.csv',header=T, sep=",")
perdate[,"trt"]<-as.factor(perdate[,"trt"])
perdate[,"sev"]<-as.factor(perdate[,"sev"])
head(perdate)
```

```
##   date   trt plant sev
## 1  T07 ARD-7     1   1
## 2  T07 ARD-7     2   1
## 3  T07 ARD-7     3   1
## 4  T07 ARD-7     4   1
## 5  T07 ARD-7     5   1
## 6  T07 ARD-7     6   2
```

VGLM sev~trt

Since disease severity was evaluated along an ordinal scale, it was considered an order factor and was modelled through a proportional odds logistic regression model using the vglm function of the VGAM package which is a function used to fit vector generalized linear models. In the output summary, the expontiated coefficients correspond to the odds ratio values. The goodness of fit is assessed by observing the ratio of the residual deviance and degrees of freedom (df) of each model; well fitted models have a deviance/df ratio approximating a 1:1 ratio. Groups RD-07 and RD-14 were analysed seperately since they each had a different positive control treatment (i.e. reference treatment).

Data collected 7 days post-inoculation (7dpi) (07.1 corresponds to group RD-07 and 07.2 to group RD-14)

```
green07.1<-subset(green,date=="T07" & green$trt %in% c("ARD-7","BRD-7","FRD-
7","CRD-7",
                                                       "PCRD-7"))
green07.2<-subset(green,date=="T07" & green$trt %in% c("ARD-14","BRD-
14","FRD-14",
                                                       "CRD-14", "PCRD-14"))
green07.1<-within(green07.1,trt<-relevel(trt,ref="PCRD-7"))
green07.2<-within(green07.2,trt<-relevel(trt,ref="PCRD-14"))
fit07.1<-
vglm(cbind(sev0,sev1,sev2,sev3)~trt,family=cumulative(parallel=TRUE),
             data=green07.1)
fit07.2<-
vglm(cbind(sev0,sev1,sev2,sev3)~trt,family=cumulative(parallel=TRUE),
             data=green07.2)
```

```r
summary(fit07.1)
```

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green07.1)
##
##
## Pearson residuals:
##   logit(P[Y<=1]) logit(P[Y<=2])
## 1         1.1569        -2.0185
## 2        -0.3825         0.4979
## 3        -0.8785         0.4220
## 4        -0.8456         0.1830
## 5        -0.1028         0.3155
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -0.7310     0.2953  -2.476   0.0133 *
## (Intercept):2   3.5776     0.4312   8.298  < 2e-16 ***
## trtARD-7       -0.7535     0.4441  -1.697   0.0898 .
## trtBRD-7       -1.1097     0.4614  -2.405   0.0162 *
## trtCRD-7       -3.5267     0.5088  -6.931 4.18e-12 ***
## trtFRD-7       -2.3160     0.5036  -4.599 4.25e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  2
##
## Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])
##
## Residual deviance: 7.606 on 4 degrees of freedom
##
## Log-likelihood: -19.048 on 4 degrees of freedom
##
## Number of iterations: 5
##
## No Hauck-Donner effect found in any of the estimates
##
## Exponentiated coefficients:
##   trtARD-7   trtBRD-7   trtCRD-7   trtFRD-7
## 0.47072045 0.32966924 0.02940314 0.09866759
```

```r
summary(fit07.2)
```

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green07.2)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2])
## 7        -1.28023       0.412488
## 8        -0.04539       0.042318
## 9         1.13985      -0.851537
## 10        0.02567      -0.009644
## 11       -0.20726       0.906201
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1   0.3503     0.2858   1.226     0.22
## (Intercept):2   4.1239     0.4134   9.977  < 2e-16 ***
## trtARD-14      -3.7952     0.4875  -7.785 6.98e-15 ***
## trtBRD-14      -2.3244     0.4548  -5.111 3.21e-07 ***
## trtCRD-14      -3.5466     0.4850  -7.313 2.62e-13 ***
## trtFRD-14      -2.6028     0.4656  -5.591 2.26e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  2
##
## Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])
##
## Residual deviance: 6.8923 on 4 degrees of freedom
##
## Log-likelihood: -18.5977 on 4 degrees of freedom
##
## Number of iterations: 4
##
## No Hauck-Donner effect found in any of the estimates
##
## Exponentiated coefficients:
##  trtARD-14  trtBRD-14  trtCRD-14  trtFRD-14
## 0.02247832 0.09784451 0.02882388 0.07406281
```

Data collected 9 days post-inoculation (9dpi) (09.1 corresponds to group RD-07 and 09.2 to group RD-14)

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green09.1)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2])
## 13         2.7984       -0.75625
## 14        -1.0462        0.40033
## 15        -0.7112        0.14950
## 16        -0.3983        0.04267
## 17        -0.2592        0.47405
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -2.0843     0.4213  -4.947 7.53e-07 ***
## (Intercept):2   3.4234     0.5813   5.889 3.88e-09 ***
## trtARD-7       -2.1791     0.6501  -3.352 0.000803 ***
## trtBRD-7       -1.7514     0.6514  -2.689 0.007176 **
## trtCRD-7       -3.6702     0.6453  -5.687 1.29e-08 ***
## trtFRD-7       -2.5142     0.6470  -3.886 0.000102 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  2
##
## Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])
##
## Residual deviance: 8.8985 on 4 degrees of freedom
##
## Log-likelihood: -16.7267 on 4 degrees of freedom
##
## Number of iterations: 5
##
## No Hauck-Donner effect found in any of the estimates
##
## Exponentiated coefficients:
##   trtARD-7   trtBRD-7   trtCRD-7   trtFRD-7
## 0.11314652 0.17352234 0.02547245 0.08092661
```

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green09.2)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2])
## 19        -0.8659         0.1899
## 20         0.3509        -0.2088
## 21         3.2098        -3.2098
## 22        -1.1784         0.3535
## 23        -2.5307         2.7075
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1 -1.89000    0.35492  -5.325 1.01e-07 ***
## (Intercept):2  2.05533    0.36423   5.643 1.67e-08 ***
## trtARD-14     -2.32259    0.45913  -5.059 4.22e-07 ***
## trtBRD-14     -0.72898    0.46015  -1.584  0.11314
## trtCRD-14     -1.71558    0.45451  -3.775  0.00016 ***
## trtFRD-14     -0.08266    0.46096  -0.179  0.85768
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  2
##
## Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])
##
## Residual deviance: 43.7874 on 4 degrees of freedom
##
## Log-likelihood: -34.8611 on 4 degrees of freedom
##
## Number of iterations: 6
##
## No Hauck-Donner effect found in any of the estimates
##
## Exponentiated coefficients:
##  trtARD-14  trtBRD-14  trtCRD-14  trtFRD-14
## 0.09801941 0.48240096 0.17985856 0.92066138
```

Data collected 11 days post-inoculation (11dpi) (11.1 corresponds to group RD-07 and 11.2 to group RD-14)

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green11.1)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2])
## 25         1.0163       -0.27617
## 26        -0.7605        0.35032
## 27        -0.9282        0.22554
## 28        -0.4793        0.06579
## 29         0.4187       -0.67403
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -1.6535     0.3572  -4.629 3.67e-06 ***
## (Intercept):2   2.7825     0.4546   6.121 9.31e-10 ***
## trtARD-7       -2.2378     0.5269  -4.247 2.16e-05 ***
## trtBRD-7       -1.4999     0.5242  -2.862  0.00421 **
## trtCRD-7       -3.7333     0.5517  -6.766 1.32e-11 ***
## trtFRD-7       -2.4188     0.5272  -4.588 4.48e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  2
##
## Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])
##
## Residual deviance: 4.5072 on 4 degrees of freedom
##
## Log-likelihood: -16.3968 on 4 degrees of freedom
##
## Number of iterations: 4
##
## No Hauck-Donner effect found in any of the estimates
##
## Exponentiated coefficients:
##   trtARD-7   trtBRD-7   trtCRD-7   trtFRD-7
## 0.10669247 0.22314721 0.02391320 0.08903052
```

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green11.2)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2])
## 31        -0.5675        0.08643
## 32        -1.0330        0.28763
## 33         4.9083       -2.35196
## 34        -0.6692        0.11627
## 35        -2.4512        2.45117
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -2.2324     0.4104  -5.440 5.33e-08 ***
## (Intercept):2   2.2324     0.4104   5.440 5.33e-08 ***
## trtARD-14      -2.8177     0.5035  -5.596 2.19e-08 ***
## trtBRD-14      -1.6291     0.4941  -3.297 0.000976 ***
## trtCRD-14      -2.4893     0.4966  -5.012 5.38e-07 ***
## trtFRD-14      -0.8829     0.5006  -1.764 0.077754 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  2
##
## Names of linear predictors: logit(P[Y<=1]), logit(P[Y<=2])
##
## Residual deviance: 44.9799 on 4 degrees of freedom
##
## Log-likelihood: -32.942 on 4 degrees of freedom
##
## Number of iterations: 7
##
## No Hauck-Donner effect found in any of the estimates
##
## Exponentiated coefficients:
##  trtARD-14  trtBRD-14  trtCRD-14  trtFRD-14
## 0.05974334 0.19610412 0.08296804 0.41357928
```

Data collected 14 days post-inoculation (14dpi) (14.1 corresponds to group RD-07 and 14.2 to group RD-14)

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green14.1)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 37         2.7507       -0.56221         0.1946
## 38        -0.7025        0.05799         0.1812
## 39        -0.5350       -0.03751         0.2070
## 40        -0.1668        1.26424        -0.5169
## 41        -0.6342        0.03154         0.9654
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -3.2760     0.6135  -5.340 9.29e-08 ***
## (Intercept):2   1.5777     0.3631   4.345 1.39e-05 ***
## (Intercept):3   3.9968     0.4373   9.140  < 2e-16 ***
## trtARD-7       -1.6510     0.4529  -3.646 0.000267 ***
## trtBRD-7       -1.3485     0.4543  -2.968 0.002995 **
## trtCRD-7       -4.3289     0.5096  -8.495  < 2e-16 ***
## trtFRD-7       -1.8893     0.4534  -4.167 3.09e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 9.6854 on 8 degrees of freedom
##
## Log-likelihood: -23.8992 on 8 degrees of freedom
##
## Number of iterations: 5
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):1'
##
## Exponentiated coefficients:
##   trtARD-7   trtBRD-7   trtCRD-7   trtFRD-7
## 0.19185503 0.25963360 0.01318177 0.15118273
```

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green14.2)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 43        -0.2331        -0.1561         0.1697
## 44        -0.5116         0.1952        -0.2618
## 45         4.0514        -0.1425        -0.7615
## 46        -0.2721        -0.1931         0.2534
## 47        -1.2079         0.4118         0.8128
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -3.5626     0.7394  -4.818 1.45e-06 ***
## (Intercept):2   2.1507     0.4472   4.809 1.51e-06 ***
## (Intercept):3   4.2608     0.4910   8.678  < 2e-16 ***
## trtARD-14      -3.2583     0.5299  -6.149 7.78e-10 ***
## trtBRD-14      -1.6915     0.5271  -3.209 0.001332 **
## trtCRD-14      -2.9498     0.5257  -5.611 2.01e-08 ***
## trtFRD-14      -1.9608     0.5238  -3.743 0.000182 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 11.6921 on 8 degrees of freedom
##
## Log-likelihood: -24.2853 on 8 degrees of freedom
##
## Number of iterations: 6
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):1'
##
## Exponentiated coefficients:
##  trtARD-14  trtBRD-14  trtCRD-14  trtFRD-14
## 0.03845435 0.18424735 0.05235063 0.14074843
```

Data collected 16 days post-inoculation (16dpi) (16.1 corresponds to group RD-07 and 16.2 to group RD-14)

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green16.1)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 49         1.9391         0.7671       -1.20062
## 50        -0.8005         0.5828       -0.39745
## 51        -0.5784        -0.8290        0.73597
## 52        -0.2147         0.2657       -0.08977
## 53        -0.2881        -0.6542        1.48556
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -2.9778     0.5337  -5.579 2.42e-08 ***
## (Intercept):2   0.7278     0.2925   2.488 0.012847 *
## (Intercept):3   2.2528     0.3250   6.931 4.17e-12 ***
## trtARD-7       -1.5089     0.3945  -3.825 0.000131 ***
## trtBRD-7       -1.4104     0.3935  -3.585 0.000337 ***
## trtCRD-7       -4.0616     0.5182  -7.838 4.56e-15 ***
## trtFRD-7       -1.9807     0.4019  -4.928 8.31e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 11.2929 on 8 degrees of freedom
##
## Log-likelihood: -26.7461 on 8 degrees of freedom
##
## Number of iterations: 5
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):1'
##
## Exponentiated coefficients:
##   trtARD-7   trtBRD-7   trtCRD-7   trtFRD-7
## 0.22116143 0.24403499 0.01722072 0.13797017
```

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green16.2)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 55        -0.3787        -0.4280         0.2979
## 56         0.4877         0.2510        -0.4412
## 57         5.2110        -0.6104        -0.8603
## 58        -0.3689        -0.2522         0.1861
## 59        -2.2195         1.1081         1.3697
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -2.4164     0.4551  -5.310 1.10e-07 ***
## (Intercept):2   1.5890     0.3574   4.446 8.74e-06 ***
## (Intercept):3   3.1234     0.3906   7.997 1.28e-15 ***
## trtARD-14      -3.4064     0.4681  -7.276 3.43e-13 ***
## trtBRD-14      -1.9639     0.4427  -4.436 9.17e-06 ***
## trtCRD-14      -3.4715     0.4702  -7.384 1.54e-13 ***
## trtFRD-14      -1.8403     0.4421  -4.162 3.15e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 28.5182 on 8 degrees of freedom
##
## Log-likelihood: -34.3885 on 8 degrees of freedom
##
## Number of iterations: 6
##
## No Hauck-Donner effect found in any of the estimates
##
## Exponentiated coefficients:
##  trtARD-14  trtBRD-14  trtCRD-14  trtFRD-14
## 0.03316078 0.14030375 0.03107055 0.15877214
```

Data collected 18 days post-inoculation (18dpi) (18.1 corresponds to group RD-07 and 18.2 to group RD-14)

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green18.1)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 61      -0.008573         0.4936        -0.4498
## 62       0.216974         0.6309        -0.5748
## 63      -0.510302        -0.1146         0.1355
## 64      -0.133197        -0.8371         0.3455
## 65       0.038798        -0.7581         1.2047
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -2.4609     0.4451  -5.529 3.23e-08 ***
## (Intercept):2   0.6689     0.2875   2.326 0.020000 *
## (Intercept):3   1.9261     0.3164   6.088 1.15e-09 ***
## trtARD-7       -1.4359     0.3895  -3.686 0.000228 ***
## trtBRD-7       -1.6666     0.3936  -4.234 2.29e-05 ***
## trtCRD-7       -5.1162     0.7913  -6.466 1.01e-10 ***
## trtFRD-7       -2.7877     0.4333  -6.434 1.24e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 5.2573 on 8 degrees of freedom
##
## Log-likelihood: -22.8671 on 8 degrees of freedom
##
## Number of iterations: 4
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## 'trtCRD-7'
##
## Exponentiated coefficients:
##    trtARD-7    trtBRD-7    trtCRD-7    trtFRD-7
## 0.237904674 0.188890309 0.005998557 0.061561426
```

```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green18.2)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 67        -0.2456        -0.2331         0.1205
## 68        -0.7192         0.9100        -0.6600
## 69         5.7608        -1.0568        -0.3524
## 70        -0.2576        -0.4222         0.2073
## 71        -2.0407         0.5900         1.3664
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -2.5691     0.4876  -5.269 1.37e-07 ***
## (Intercept):2   1.1098     0.3172   3.498 0.000468 ***
## (Intercept):3   2.5890     0.3564   7.264 3.76e-13 ***
## trtARD-14      -4.1149     0.5091  -8.082 6.36e-16 ***
## trtBRD-14      -2.0540     0.4176  -4.918 8.74e-07 ***
## trtCRD-14      -3.9927     0.4986  -8.008 1.17e-15 ***
## trtFRD-14      -1.8435     0.4143  -4.450 8.59e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 28.2306 on 8 degrees of freedom
##
## Log-likelihood: -33.0582 on 8 degrees of freedom
##
## Number of iterations: 6
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):1'
##
## Exponentiated coefficients:
##  trtARD-14  trtBRD-14  trtCRD-14  trtFRD-14
## 0.01632778 0.12822700 0.01844979 0.15827031
```

Data collected 21 days post-inoculation (18dpi) (21.1 corresponds to group RD-07 and 21.2 to group RD-14)

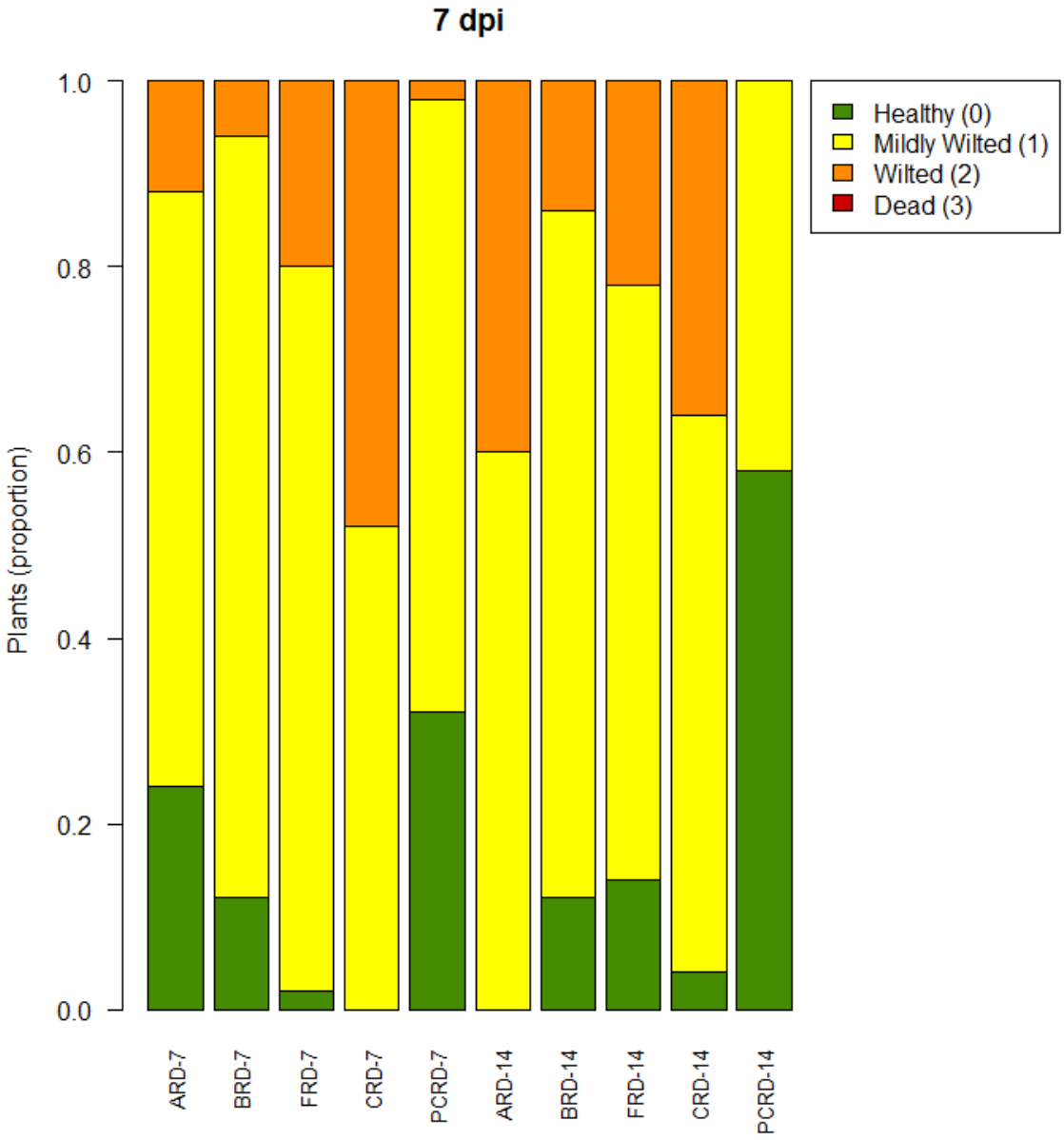
```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green21.1)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 73      4.551e-01      3.567e-01     -3.848e-01
## 74     -6.585e-01      1.063e+00     -5.922e-01
## 75     -3.851e-01     -6.038e-01      3.691e-01
## 76      3.059e-14      1.287e-13     -5.793e-14
## 77      1.151e-01     -7.423e-01      9.788e-01
##
## Coefficients:
##                Estimate Std. Error z value Pr(>|z|)
## (Intercept):1   -2.8159     0.5273  -5.340 9.28e-08 ***
## (Intercept):2    0.5011     0.2825   1.774   0.0761 .
## (Intercept):3    1.5153     0.3053   4.964 6.92e-07 ***
## trtARD-7        -1.5375     0.3920  -3.923 8.76e-05 ***
## trtBRD-7        -2.0201     0.4077  -4.955 7.22e-07 ***
## trtCRD-7       -22.7107  3434.7238      NA       NA
## trtFRD-7        -2.9309     0.4644  -6.312 2.76e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 5.0802 on 8 degrees of freedom
##
## Log-likelihood: -19.8975 on 8 degrees of freedom
##
## Number of iterations: 17
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):1', 'trtCRD-7'
##
## Exponentiated coefficients:
##     trtARD-7     trtBRD-7     trtCRD-7     trtFRD-7
## 2.149110e-01 1.326461e-01 1.370478e-10 5.334707e-02
```

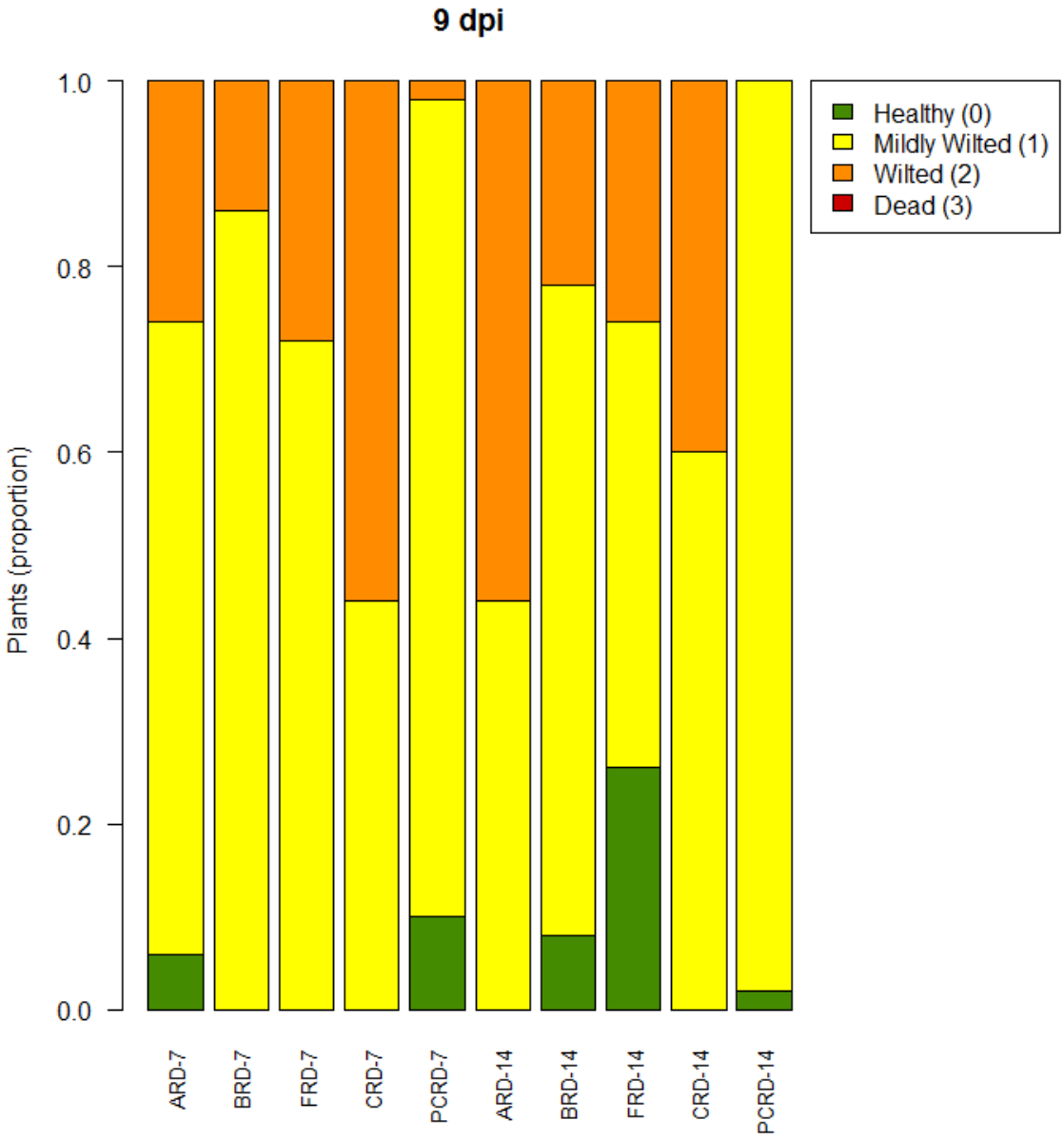
```
##
## Call:
## vglm(formula = cbind(sev0, sev1, sev2, sev3) ~ trt, family =
cumulative(parallel = TRUE),
##     data = green21.2)
##
##
## Pearson residuals:
##    logit(P[Y<=1]) logit(P[Y<=2]) logit(P[Y<=3])
## 79        -0.3093       -0.06512        0.07263
## 80        -0.9391       -0.69321        0.82718
## 81         4.1523        0.05274       -1.50383
## 82        -0.2957        1.87935       -0.85424
## 83        -2.0134        0.12846        1.40888
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept):1  -2.5921     0.4535  -5.716 1.09e-08 ***
## (Intercept):2   0.5506     0.2822   1.951  0.05108 .
## (Intercept):3   1.4590     0.3009   4.849 1.24e-06 ***
## trtARD-14      -3.6603     0.5581  -6.559 5.43e-11 ***
## trtBRD-14      -1.4245     0.3890  -3.662  0.00025 ***
## trtCRD-14      -4.1740     0.6578  -6.345 2.22e-10 ***
## trtFRD-14      -1.0078     0.3825  -2.635  0.00842 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Number of linear predictors:  3
##
## Names of linear predictors:
## logit(P[Y<=1]), logit(P[Y<=2]), logit(P[Y<=3])
##
## Residual deviance: 30.3198 on 8 degrees of freedom
##
## Log-likelihood: -32.7791 on 8 degrees of freedom
##
## Number of iterations: 6
##
## Warning: Hauck-Donner effect detected in the following estimate(s):
## '(Intercept):1', 'trtARD-14', 'trtCRD-14'
##
## Exponentiated coefficients:
##  trtARD-14  trtBRD-14  trtCRD-14  trtFRD-14
## 0.02572535 0.24064016 0.01539099 0.36501361
```

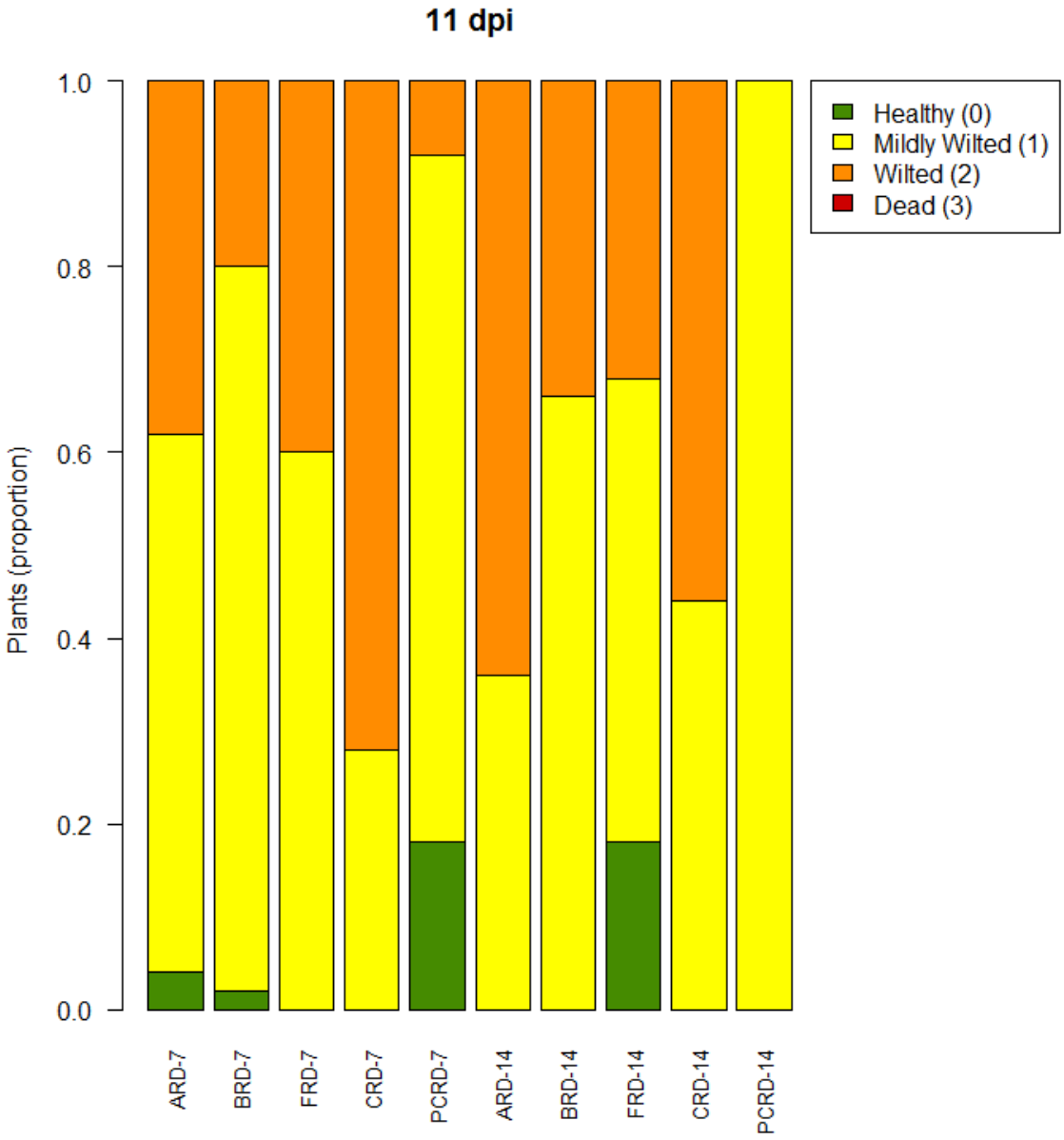
Barplots of disease severity evaluation

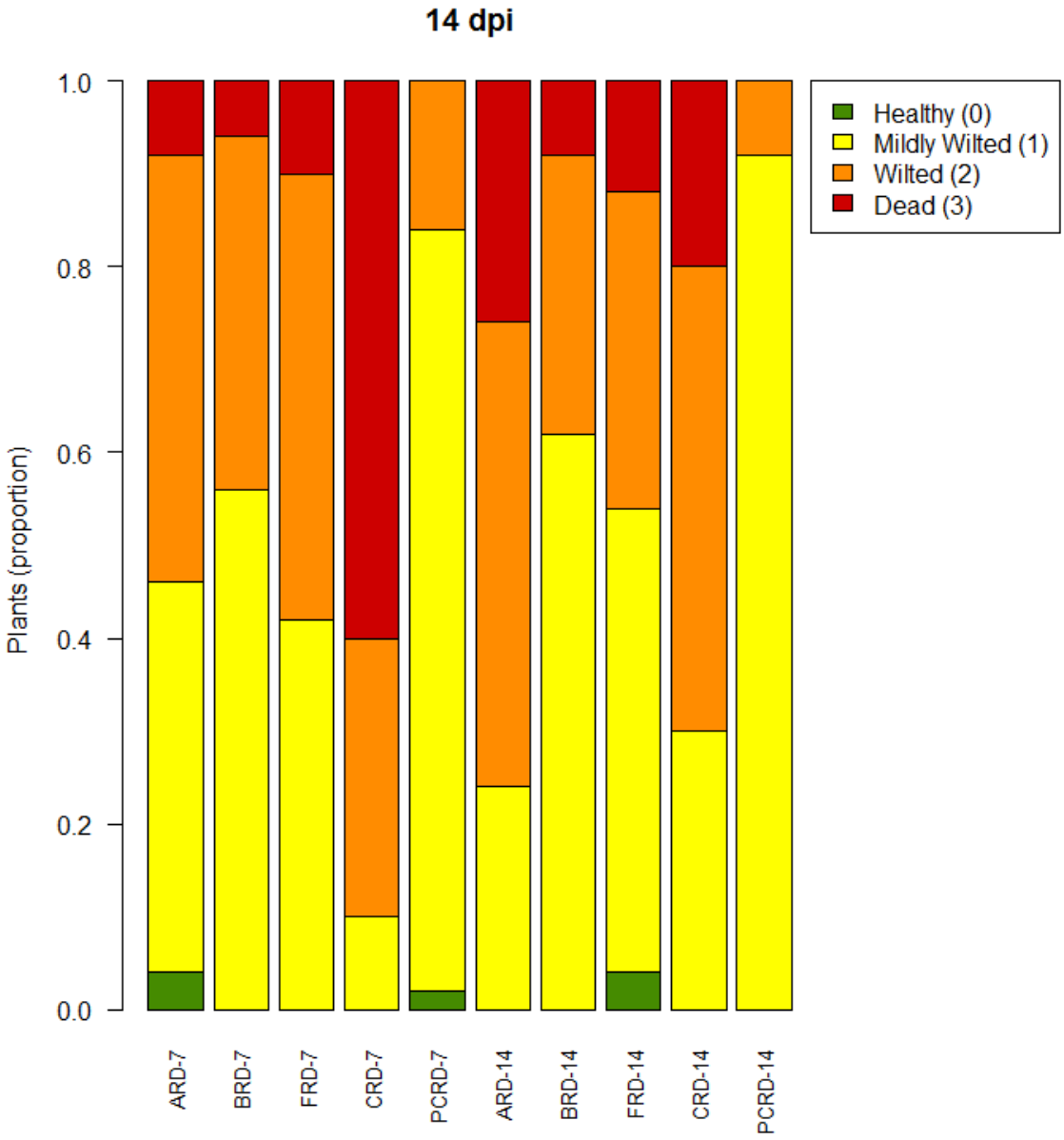
The graphs below present disease severity on 'California Wonder' pepper plants inoculated with *Phytophthora capsici* by root dipping inoculation on 30/04/2018 (treatments RD-7 were done 7 days pre-inoculation and treatments RD-14 14 days pre-inoculation; products used: A, B, F= Fosetyl-al and C; PC= inoculated/non-treated control). Bar plots reflect severity as recorded 7, 9, 11, 14, 16, 18 and 21 days post-inoculation (dpi).

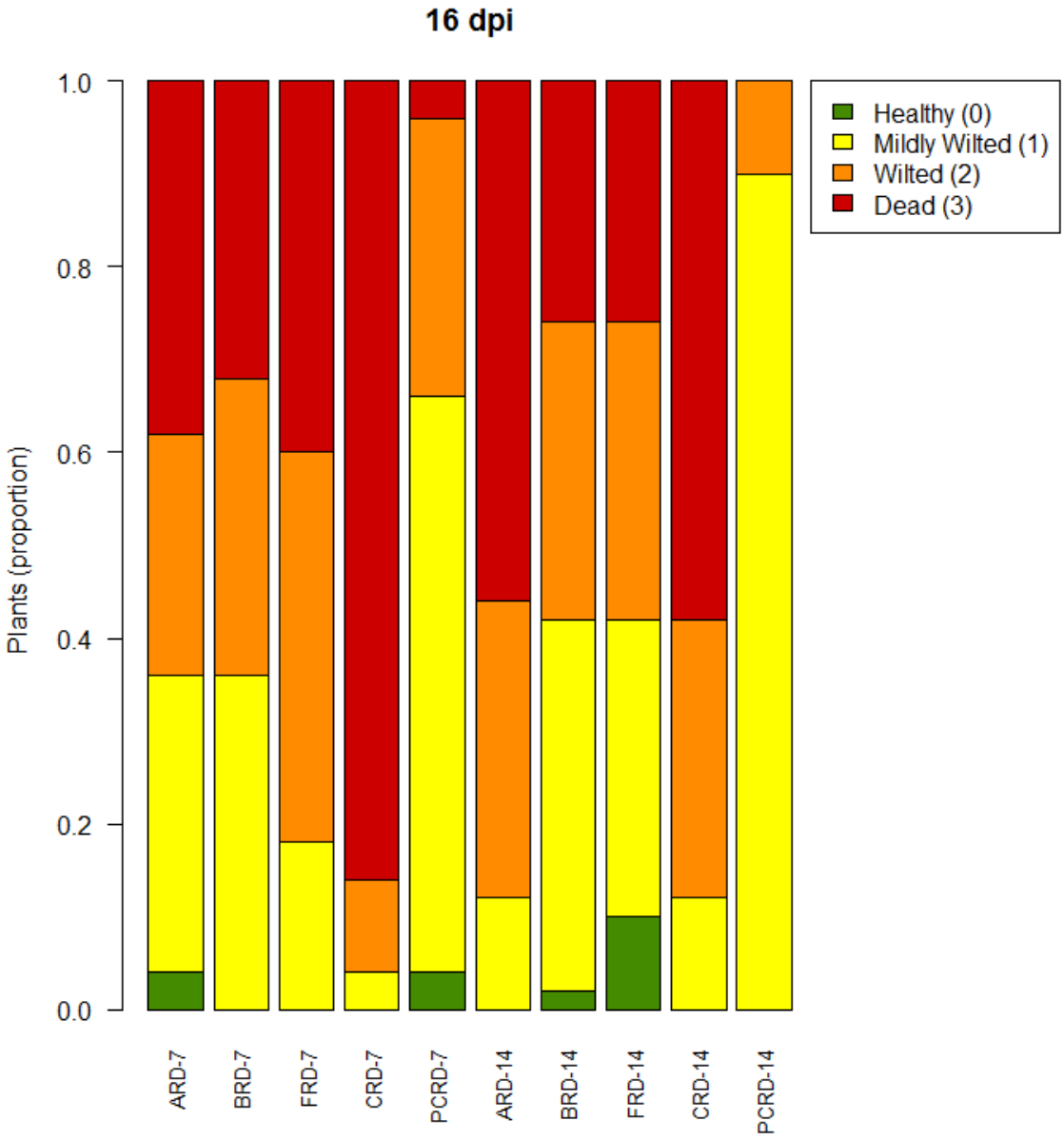
```
perdate1<-subset(perdate,date=="T07")
perdate2<-perdate1[-which(perdate1$trt %in% c("NCRD-7","NCRD-14")),]
m<-ftable(xtabs(~ sev + trt, data = perdate1))
m<-m[, c(2, 4, 8, 6, 12, 10, 1, 3, 7, 5, 11, 9)]
m<-prop.table(m, 2)
m<-m[,-12]
m<-m[,-6]

codes<-c('ARD-7', 'BRD-7', 'FRD-7', 'CRD-7', 'PCRD-7', 'ARD-14', 'BRD-14',
'FRD-14',
         'CRD-14', 'PCRD-14')
leg.txt<-severities<-c('Healthy (0)', 'Mildly Wilted (1)', 'Wilted (2)',
'Dead (3)')
par(mar=c(5.1, 4.1, 4.1, 8.1), las=2,  xpd=TRUE)
barplot(m, main = '7 dpi',
        ylab='Plants (proportion)', names.arg = codes,
        col=c('chartreuse4', 'yellow1', 'darkorange','red3'), cex.names=0.8)
legend("topright", leg.txt, inset=c(-0.35,0), fill=c('chartreuse4','yellow1',
                                                     'darkorange','red3'))
```

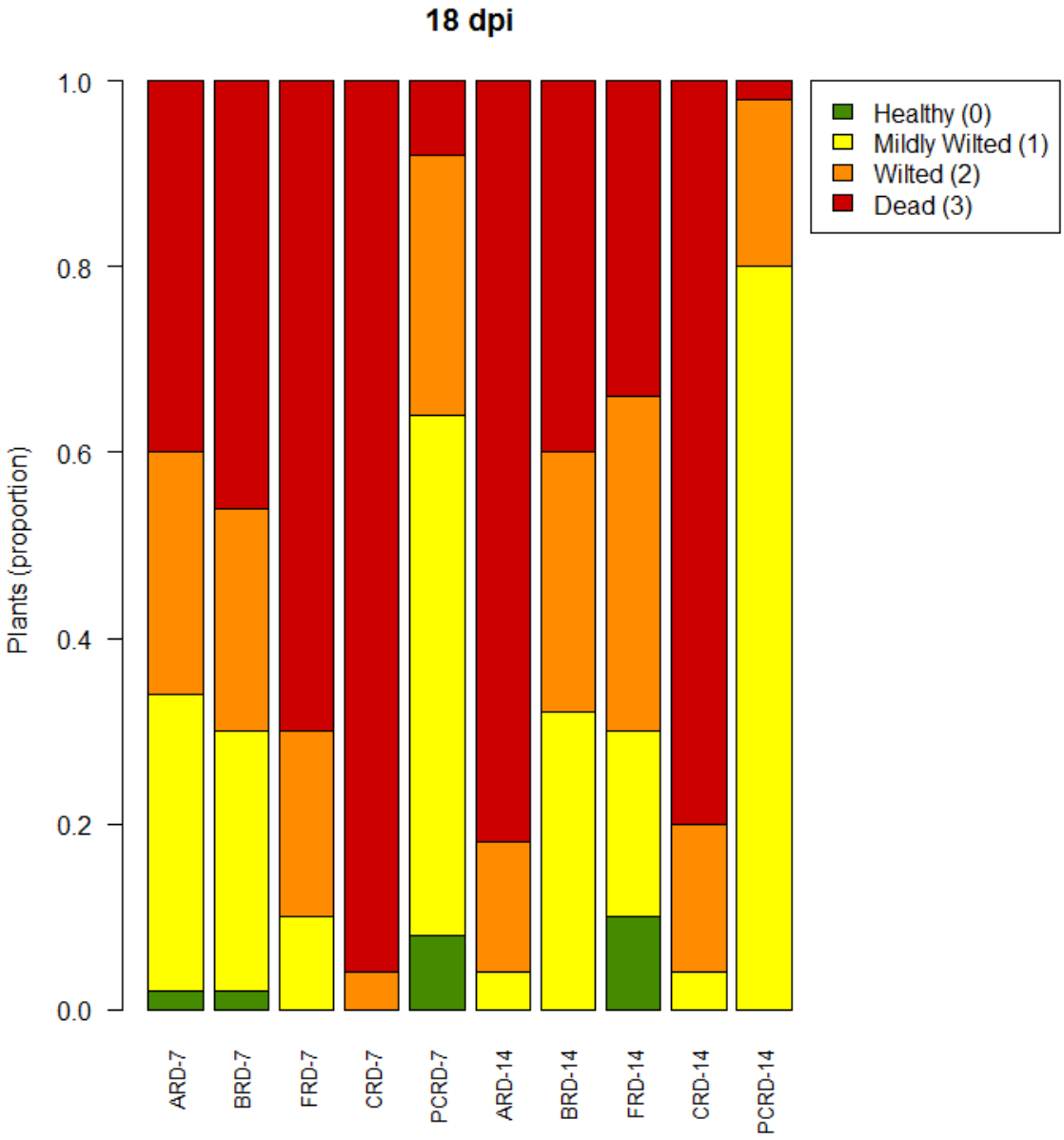

7 dpi
Plants (proportion)
1.0
0.8
0.6
0.4
0.2
0.0
Healthy (0)
Mildly Wilted (1)
Wilted (2)
Dead (3)
ARD-7
BRD-7
FRD-7
CRD-7
PCRD-7
ARD-14
BRD-14
FRD-14
CRD-14
PCRD-14

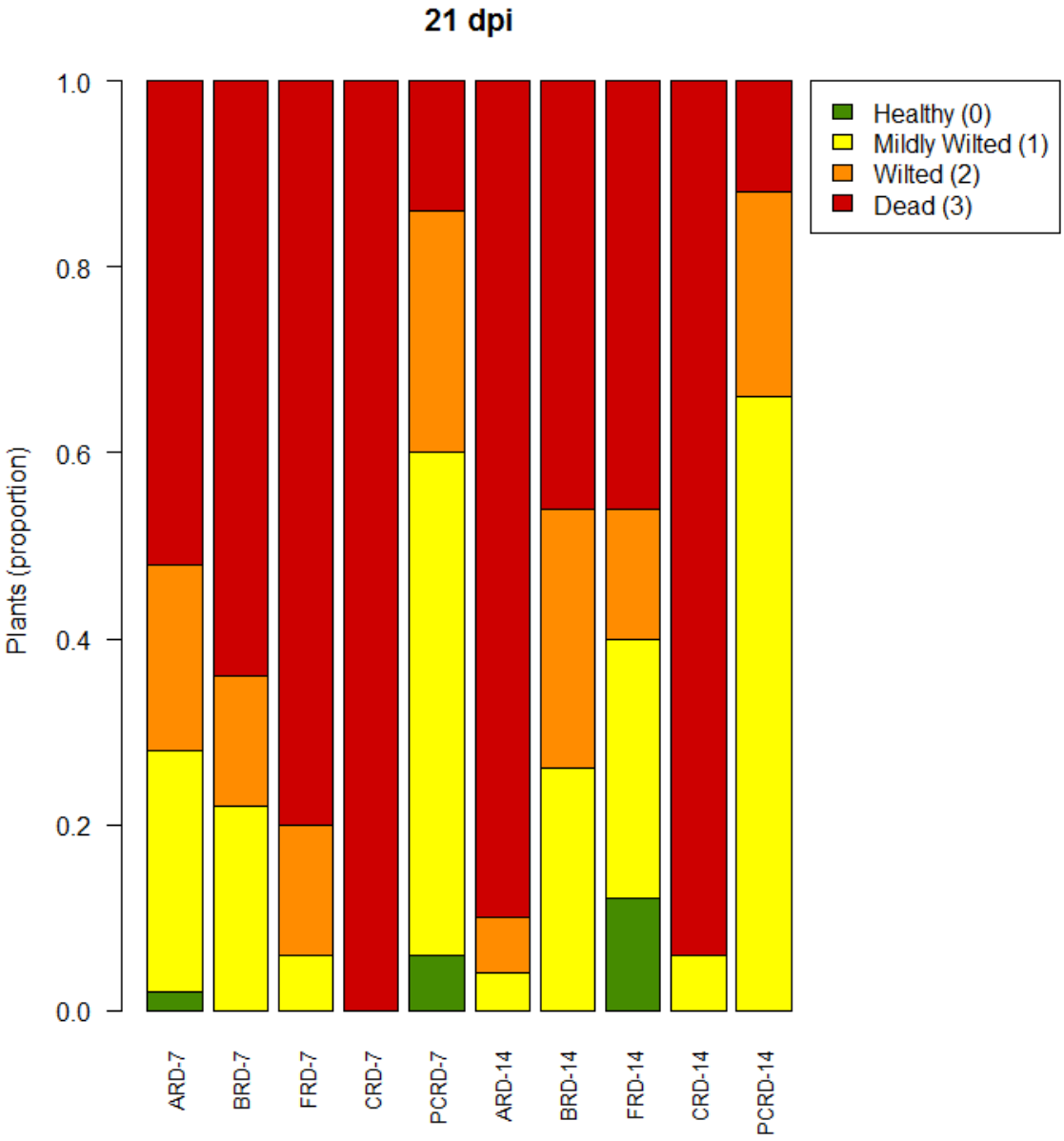

9 dpi
Plants (proportion)
1.0
0.8
0.6
0.4
0.2
0.0
Healthy (0)
Mildly Wilted (1)
Wilted (2)
Dead (3)
ARD-7
BRD-7
FRD-7
CRD-7
PCRD-7
ARD-14
BRD-14
FRD-14
CRD-14
PCRD-14


11 dpi
Plants (proportion)
1.0
0.8
0.6
0.4
0.2
0.0
Healthy (0)
Mildly Wilted (1)
Wilted (2)
Dead (3)
ARD-7
BRD-7
FRD-7
CRD-7
PCRD-7
ARD-14
BRD-14
FRD-14
CRD-14
PCRD-14


14 dpi
Plants (proportion)
1.0
0.8
0.6
0.4
0.2
0.0
Healthy (0)
Mildly Wilted (1)
Wilted (2)
Dead (3)
ARD-7
BRD-7
FRD-7
CRD-7
PCRD-7
ARD-14
BRD-14
FRD-14
CRD-14
PCRD-14


16 dpi
Plants (proportion)
1.0
0.8
0.6
0.4
0.2
0.0
Healthy (0)
Mildly Wilted (1)
Wilted (2)
Dead (3)
ARD-7
BRD-7
FRD-7
CRD-7
PCRD-7
ARD-14
BRD-14
FRD-14
CRD-14
PCRD-14


18 dpi
Plants (proportion)
1.0
0.8
0.6
0.4
0.2
0.0
Healthy (0)
Mildly Wilted (1)
Wilted (2)
Dead (3)
ARD-7
BRD-7
FRD-7
CRD-7
PCRD-7
ARD-14
BRD-14
FRD-14
CRD-14
PCRD-14


21 dpi
Plants (proportion)
1.0
0.8
0.6
0.4
0.2
0.0
Healthy (0)
Mildly Wilted (1)
Wilted (2)
Dead (3)
ARD-7
BRD-7
FRD-7
CRD-7
PCRD-7
ARD-14
BRD-14
FRD-14
CRD-14
PCRD-14

Proportional odds assumption

The proportional odds assumption was not rejected by the chi squared χ^2 test ($P > 0.05$) in the ordinal logistic regression of disease severity in most evaluation dates of trial 2.1. The goodness of fit was also satisfactory for the same evaluation dates that satisfied the proportional odds assumption, with deviance/df ratios from 0.64 to 3.56. The evaluation dates with poor model fit were the ones that did not meet the proportional odds assumption. Poor goodness of fit was evident by the fact that the residual deviance/df ratio would exceed the value of 10. These datasets correspond to the evaluations of the treatments of group RD-14 (product treatments 14 days before the inoculation) on 9, 11, 16, 18 and 21 dpi. The proportional odds assumption was not examined for the dataset corresponding to the evaluation of the treatments of group RD-14 21 dpi because the non proportional odds model could not be run for this dataset.

Data collected 7 days post-inoculation (7dpi) (07.1 corresponds to group RD-07 and 07.2 to group RD-14)

```
fit07.1non<-vglm(cbind(sev0,sev1,sev2,sev3)~trt,
                 family=cumulative(parallel = FALSE ),data=green07.1)
fit07.2non<-vglm(cbind(sev0,sev1,sev2,sev3)~trt,
                 family=cumulative(parallel = FALSE ),data=green07.2)

(test07.1 <- lrtest(fit07.1, fit07.1non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   4 -19.048
## 2   0 -15.245 -4 7.606     0.1071

(test07.2 <- lrtest(fit07.2, fit07.2non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   4 -18.598
## 2   0 -15.152 -4 6.8923     0.1417
```

Data collected 9 days post-inoculation (9dpi) (09.1 corresponds to group RD-07 and 09.2 to group RD-14)

```
(test09.1 <- lrtest(fit09.1, fit09.1non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   4 -16.727
## 2   0 -12.277 -4 8.8985    0.06369 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(test09.2 <- lrtest(fit09.2, fit09.2non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   4 -34.861
## 2   0 -12.967 -4 43.787  7.102e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Data collected 11 days post-inoculation (11dpi) (11.1 corresponds to group RD-07 and 11.2 to group RD-14)

```
(test11.1 <- lrtest(fit11.1, fit11.1non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   4 -16.397
## 2   0 -14.143 -4 4.5072     0.3417

(test11.2 <- lrtest(fit11.2, fit11.2non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df Chisq Pr(>Chisq)
## 1   4 -32.942
## 2   0 -10.452 -4 44.98  4.014e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Data collected 14 days post-inoculation (14dpi) (14.1 corresponds to group RD-07 and 14.2 to group RD-14)

```
(test14.1 <- lrtest(fit14.1, fit14.1non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -23.899
## 2   0 -19.056 -8 9.6854     0.2878

(test14.2 <- lrtest(fit14.2, fit14.2non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -24.285
## 2   0 -18.439 -8 11.692     0.1655
```

Data collected 16 days post-inoculation (16dpi) (16.1 corresponds to group RD-07 and 16.2 to group RD-14)

```
(test16.1 <- lrtest(fit16.1, fit16.1non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -26.746
## 2   0 -21.100 -8 11.293     0.1856

(test16.2 <- lrtest(fit16.2, fit16.2non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -34.388
## 2   0 -20.129 -8 28.518  0.0003851 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Data collected 18 days post-inoculation (18dpi) (18.1 corresponds to group RD-07 and 18.2 to group RD-14)

```
(test18.1 <- lrtest(fit18.1, fit18.1non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -22.867
## 2   0 -20.238 -8 5.2573     0.7298

(test18.2 <- lrtest(fit18.2, fit18.2non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -33.058
## 2   0 -18.943 -8 28.231  0.0004323 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Data collected 21 days post-inoculation (21dpi) (21.1 corresponds to group RD-07 and 21.2 to group RD-14)

```
(test21.1 <- lrtest(fit21.1, fit21.1non))

## Likelihood ratio test
##
## Model 1: cbind(sev0, sev1, sev2, sev3) ~ trt
## Model 2: cbind(sev0, sev1, sev2, sev3) ~ trt
##   #Df  LogLik Df  Chisq Pr(>Chisq)
## 1   8 -19.898
## 2   0 -17.357 -8 5.0802      0.749

#(test21.2 <- lrtest(fit21.2, fit21.2non))
```

Probabilities and odds ratios

The tables below present the probabilities and odds ratios of the proportional odds logistic regression model for disease severity on 'California Wonder' pepper plants inoculated with *Phytophthora capsici* by root dipping inoculation (treatments RD-7 were done 7 days before inoculation and treatments RD-14 14 days before inoculation; products used: A, B, F= Fosetyl-al and C; PC= inoculated/non-treated control).

Data collected 7 days post-inoculation (7dpi) (07.1 corresponds to group RD-07 and 07.2 to group RD-14)

```
#T07
green07.1<-subset(green,date=="T07" & green$trt %in% c("ARD-7","BRD-7","FRD-
7","CRD-7",
                                                       "PCRD-7"))
green07.2<-subset(green,date=="T07" & green$trt %in% c("ARD-14","BRD-
14","FRD-14",
                                                       "CRD-14", "PCRD-14"))
green07.1<-within(green07.1,trt<-relevel(trt,ref="PCRD-7"))
green07.2<-within(green07.2,trt<-relevel(trt,ref="PCRD-14"))
fit07.1<-vglm(cbind(sev0,sev1,sev2,sev3)~trt,
              family=cumulative(parallel=TRUE),data=green07.1)
fit07.2<-vglm(cbind(sev0,sev1,sev2,sev3)~trt,
              family=cumulative(parallel=TRUE),data=green07.2)
#T07 1.1
m<-fit07.1
trt <- data.frame(trt = c("ARD-7","BRD-7","FRD-7","CRD-7", "PCRD-7"))
predict(m, trt, type = "response")

##         sev0      sev1       sev2
## 1 0.18475575 0.7592107 0.05603352
## 2 0.13697709 0.7848883 0.07813461
## 3 0.04534886 0.7339582 0.22069295
## 4 0.01395841 0.4987832 0.48725837
## 5 0.32498362 0.6478341 0.02718228

codes <- data.frame(trt = c("ARD-7","BRD-7","FRD-7","CRD-7", "PCRD-7"))
sev3 <-matrix(0, 5, 1)
newdat1 <- cbind(codes, predict(m, trt, type = "response"), sev3)
exp(coef(m))

## (Intercept):1 (Intercept):2      trtARD-7      trtBRD-7      trtCRD-7
##    0.48144554   35.78867448    0.47072045    0.32966924    0.02940314
##      trtFRD-7
##    0.09866759

ci <- confint(m)
exp(cbind(OR = coef(m), ci))

##                         OR       2.5 %      97.5 %
## (Intercept):1  0.48144554  0.26991040  0.85876574
## (Intercept):2 35.78867448 15.37252727 83.31936568
```

```
## trtARD-7       0.47072045  0.19711936  1.12407903
## trtBRD-7       0.32966924  0.13345237  0.81438648
## trtCRD-7       0.02940314  0.01084614  0.07970987
## trtFRD-7       0.09866759  0.03677159  0.26475039
```

```
table<-exp(cbind(OR = coef(m), ci))
table<-round(table[,c(1,2,3)],digits=2)
table<-table[-c(1,2),]
cur <- rbind(table[1:4,], NA)
newdat2<-round(newdat1[,c(2,3,4,5)],digits=3)
newdat2$Odds <-as.character(paste(cur[,1], ' (', cur[,2],'-', cur[,3], ')',
sep=''))
newdataT07_1.1<-cbind(codes, newdat2)
newdataT07_1.1
```

```
##      trt  sev0  sev1  sev2 sev3             Odds
## 1  ARD-7 0.185 0.759 0.056    0  0.47 (0.2-1.12)
## 2  BRD-7 0.137 0.785 0.078    0 0.33 (0.13-0.81)
## 3  FRD-7 0.045 0.734 0.221    0 0.03 (0.01-0.08)
## 4  CRD-7 0.014 0.499 0.487    0  0.1 (0.04-0.26)
## 5 PCRD-7 0.325 0.648 0.027    0
```

Data collected 7 days post-inoculation (7dpi) (07.2 corresponds to group RD-14)

```
##       trt  sev0  sev1  sev2 sev3             Odds
## 1  ARD-14 0.031 0.551 0.419    0 0.02 (0.01-0.06)
## 2  BRD-14 0.122 0.736 0.142    0  0.1 (0.04-0.24)
## 3  FRD-14 0.095 0.726 0.179    0 0.03 (0.01-0.07)
## 4  CRD-14 0.039 0.601 0.360    0 0.07 (0.03-0.18)
## 5 PCRD-14 0.587 0.397 0.016    0
```

Data collected 9 days post-inoculation (9dpi) (09.1 corresponds to group RD-07)

```
##      trt  sev0  sev1  sev2 sev3             Odds
## 1  ARD-7 0.014 0.762 0.224    0  0.11 (0.03-0.4)
## 2  BRD-7 0.021 0.821 0.158    0 0.17 (0.05-0.62)
## 3  FRD-7 0.010 0.703 0.287    0 0.03 (0.01-0.09)
## 4  CRD-7 0.003 0.435 0.561    0 0.08 (0.02-0.29)
## 5 PCRD-7 0.111 0.858 0.032    0
```

Data collected 9 days post-inoculation (9dpi) (09.2 corresponds to group RD-14)

```
##       trt  sev0  sev1  sev2 sev3             Odds
## 1  ARD-14 0.015 0.419 0.566    0  0.1 (0.04-0.24)
## 2  BRD-14 0.068 0.722 0.210    0  0.48 (0.2-1.19)
## 3  FRD-14 0.122 0.756 0.122    0 0.18 (0.07-0.44)
## 4  CRD-14 0.026 0.558 0.416    0 0.92 (0.37-2.27)
## 5 PCRD-14 0.131 0.755 0.114    0
```

Data collected 11 days post-inoculation (11dpi) (11.1 corresponds to group RD-07)

```
##      trt  sev0  sev1  sev2 sev3             Odds
## 1  ARD-7 0.020 0.613 0.367    0  0.11 (0.04-0.3)
## 2  BRD-7 0.041 0.742 0.217    0 0.22 (0.08-0.62)
## 3  FRD-7 0.017 0.573 0.410    0 0.02 (0.01-0.07)
## 4  CRD-7 0.005 0.274 0.721    0 0.09 (0.03-0.25)
## 5 PCRD-7 0.161 0.781 0.058    0
```

Data collected 11 days post-inoculation (11dpi) (11.2 corresponds to group RD-14)

```
##       trt  sev0  sev1  sev2 sev3             Odds
## 1  ARD-14 0.006 0.351 0.642    0 0.06 (0.02-0.16)
## 2  BRD-14 0.021 0.626 0.354    0  0.2 (0.07-0.52)
## 3  FRD-14 0.042 0.752 0.206    0 0.08 (0.03-0.22)
## 4  CRD-14 0.009 0.427 0.564    0  0.41 (0.16-1.1)
## 5 PCRD-14 0.097 0.806 0.097    0
```

Data collected 14 days post-inoculation (14dpi) (14.1 corresponds to group RD-07)

```
##      trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-7 0.007 0.474 0.431 0.087 0.19 (0.08-0.47)
## 2  BRD-7 0.010 0.547 0.377 0.066 0.26 (0.11-0.63)
## 3  FRD-7 0.006 0.417 0.469 0.108    0.01 (0-0.04)
## 4  CRD-7 0.000 0.060 0.358 0.582 0.15 (0.06-0.37)
## 5 PCRD-7 0.036 0.792 0.153 0.018
```

Data collected 14 days post-inoculation (14dpi) (14.2 corresponds to group RD-14)

```
##       trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-14 0.001 0.247 0.483 0.268 0.04 (0.01-0.11)
## 2  BRD-14 0.005 0.608 0.316 0.071 0.18 (0.07-0.52)
## 3  FRD-14 0.004 0.543 0.362 0.091 0.05 (0.02-0.15)
## 4  CRD-14 0.001 0.309 0.477 0.212 0.14 (0.05-0.39)
## 5 PCRD-14 0.028 0.868 0.090 0.014
```

Data collected 16 days post-inoculation (16dpi) (16.1 corresponds to group RD-07)

```
##      trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-7 0.011 0.303 0.364 0.322  0.22 (0.1-0.48)
## 2  BRD-7 0.012 0.323 0.363 0.301 0.24 (0.11-0.53)
## 3  FRD-7 0.007 0.215 0.345 0.432 0.02 (0.01-0.05)
## 4  CRD-7 0.001 0.034 0.106 0.859  0.14 (0.06-0.3)
## 5 PCRD-7 0.048 0.626 0.231 0.095
```

Data collected 16 days post-inoculation (16dpi) (16.2 corresponds to group RD-14)

```
##       trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-14 0.003 0.137 0.290 0.570 0.03 (0.01-0.08)
## 2  BRD-14 0.012 0.395 0.354 0.239 0.14 (0.06-0.33)
## 3  FRD-14 0.014 0.424 0.345 0.217 0.03 (0.01-0.08)
## 4  CRD-14 0.003 0.129 0.282 0.586 0.16 (0.07-0.38)
## 5 PCRD-14 0.082 0.749 0.127 0.042
```

Data collected 18 days post-inoculation (18dpi) (18.1 corresponds to group RD-07)

```
##      trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-7 0.020 0.297 0.303 0.380 0.24 (0.11-0.51)
## 2  BRD-7 0.016 0.254 0.295 0.435 0.19 (0.09-0.41)
## 3  FRD-7 0.005 0.102 0.190 0.703    0.01 (0-0.03)
## 4  CRD-7 0.001 0.011 0.028 0.960 0.06 (0.03-0.14)
## 5 PCRD-7 0.079 0.583 0.212 0.127
```

Data collected 18 days post-inoculation (18dpi) (18.2 corresponds to group RD-14)

```
##       trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-14 0.001 0.046 0.131 0.821 0.02 (0.01-0.04)
## 2  BRD-14 0.010 0.270 0.351 0.369 0.13 (0.06-0.29)
## 3  FRD-14 0.012 0.312 0.354 0.322 0.02 (0.01-0.05)
## 4  CRD-14 0.001 0.052 0.144 0.803 0.16 (0.07-0.36)
## 5 PCRD-14 0.071 0.681 0.178 0.070
```

Data collected 21 days post-inoculation (21dpi) (21.1 corresponds to group RD-07)

```
##      trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-7 0.013 0.249 0.233 0.506  0.21 (0.1-0.46)
## 2  BRD-7 0.008 0.172 0.197 0.624 0.13 (0.06-0.29)
## 3  FRD-7 0.003 0.078 0.114 0.805        0 (0-Inf)
## 4  CRD-7 0.000 0.000 0.000 1.000 0.05 (0.02-0.13)
## 5 PCRD-7 0.056 0.566 0.197 0.180
```

Data collected 21 days post-inoculation (21dpi) (21.2 corresponds to group RD-14)

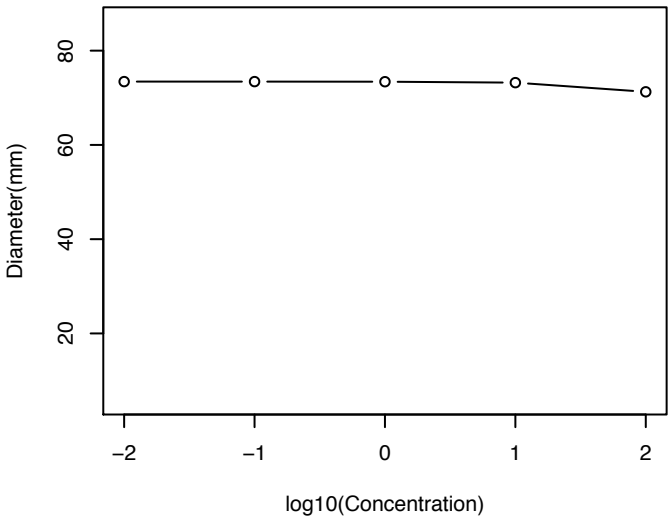
```
##       trt  sev0  sev1  sev2  sev3             Odds
## 1  ARD-14 0.002 0.041 0.057 0.900 0.03 (0.01-0.08)
## 2  BRD-14 0.018 0.277 0.214 0.491 0.24 (0.11-0.52)
## 3  FRD-14 0.027 0.361 0.223 0.389    0.02 (0-0.06)
## 4  CRD-14 0.001 0.025 0.036 0.938 0.37 (0.17-0.77)
## 5 PCRD-14 0.070 0.565 0.177 0.189
```

Annex III

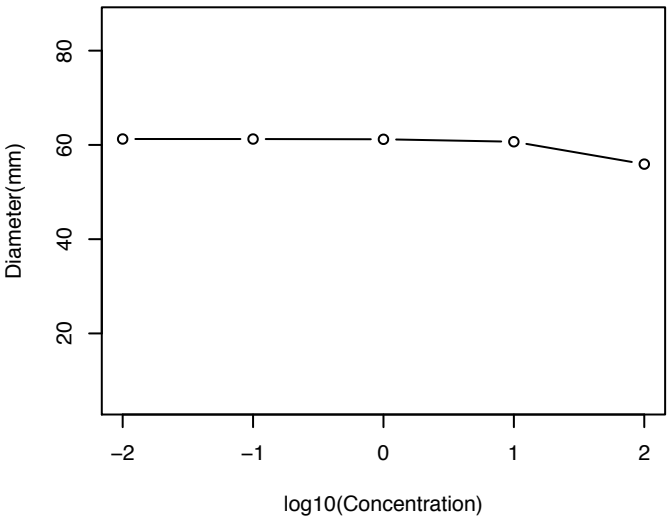
Regression lines representing the generalized lineal models ran for all product-pathogen combinations of the experiment. These involved the pathogens *Phytophthora capsici*, *P. citrophthora*, *Fusarium solani*, *Verticillium dahliae* and *Alternaria alternata*, grown in different product concentrations. Concentrations tested ranged from 0 ppm to 100 ppm.

L01

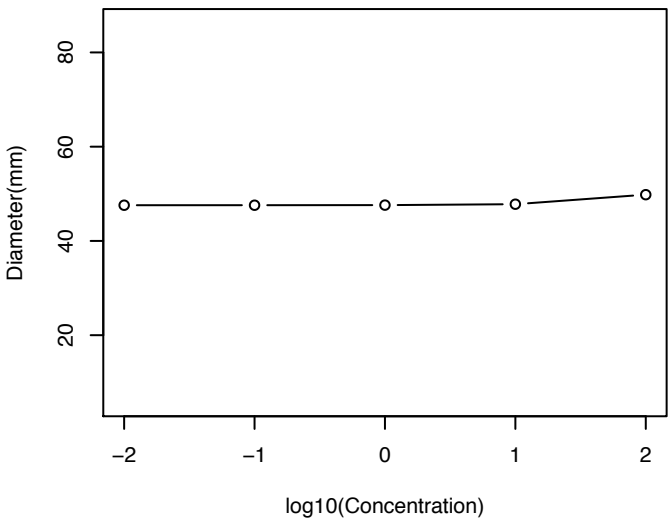
Phytophthora citrophthora



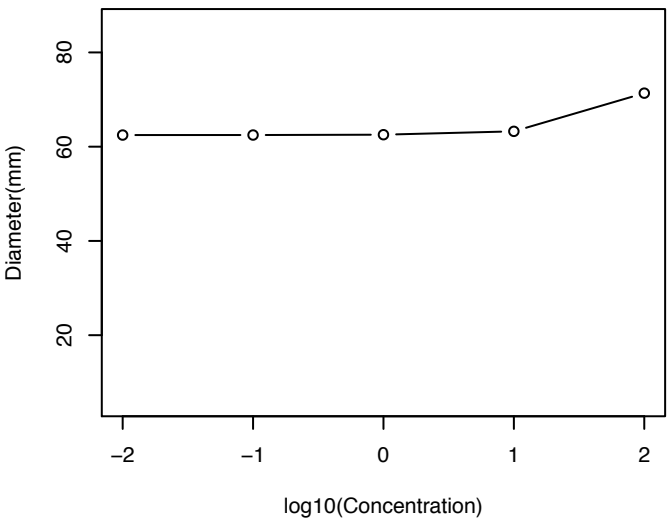
Phytophthora capsici



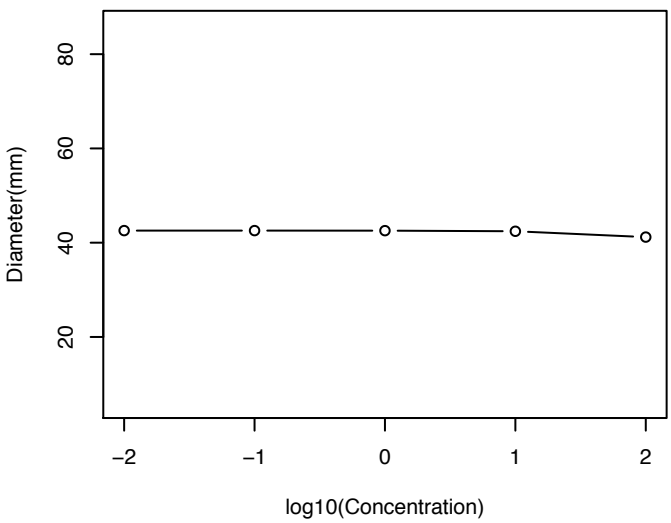
Alternaria alternata



Fusarium solani

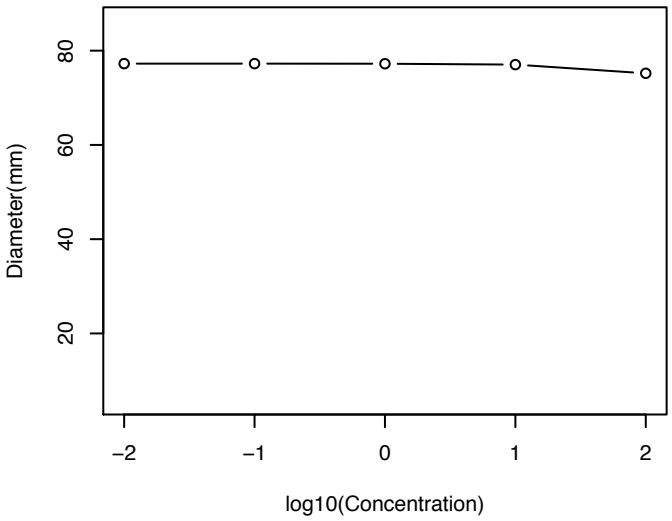


Verticillium dahliae

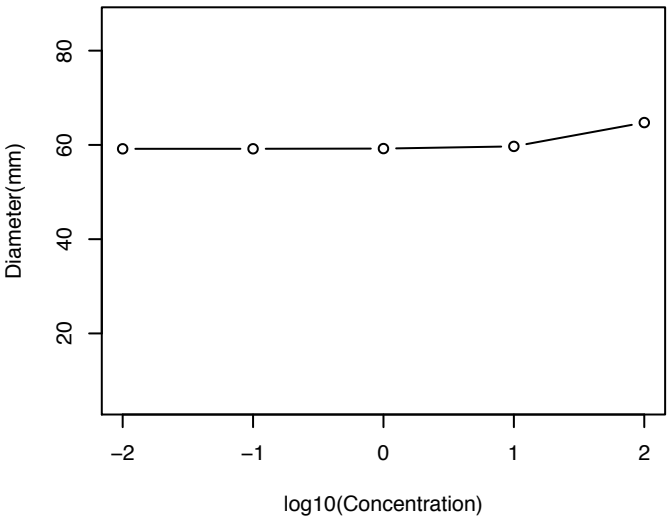


L02

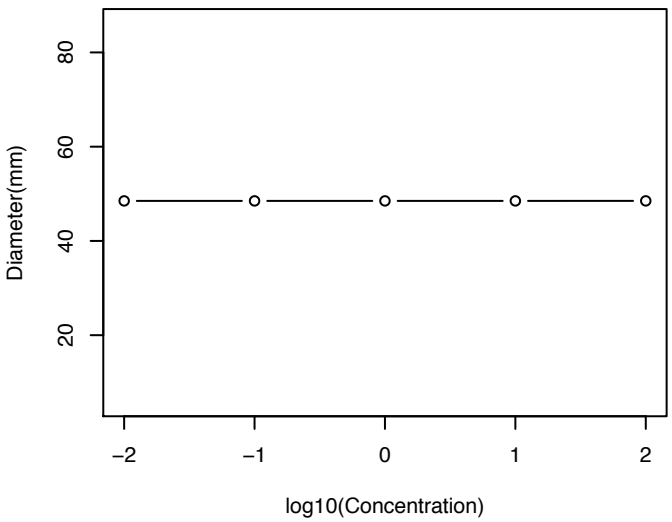
Phytophthora citrophthora



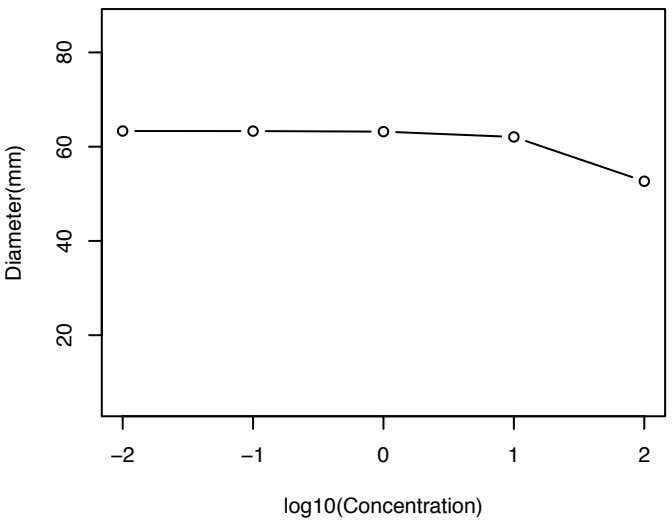
Phytophthora capsici



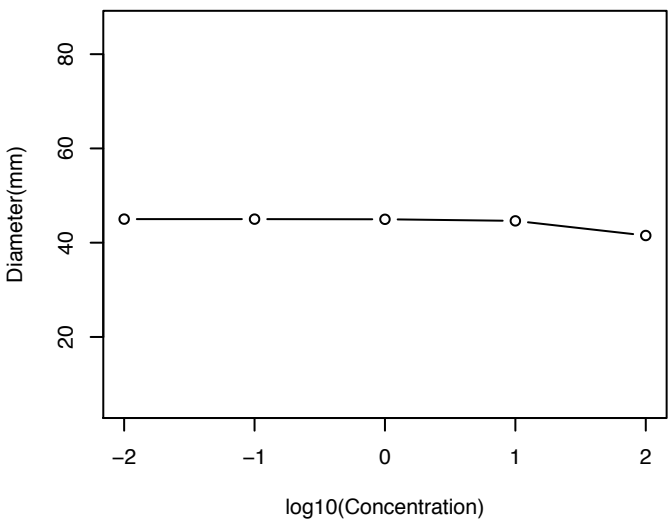
Alternaria alternata



Fusarium solani

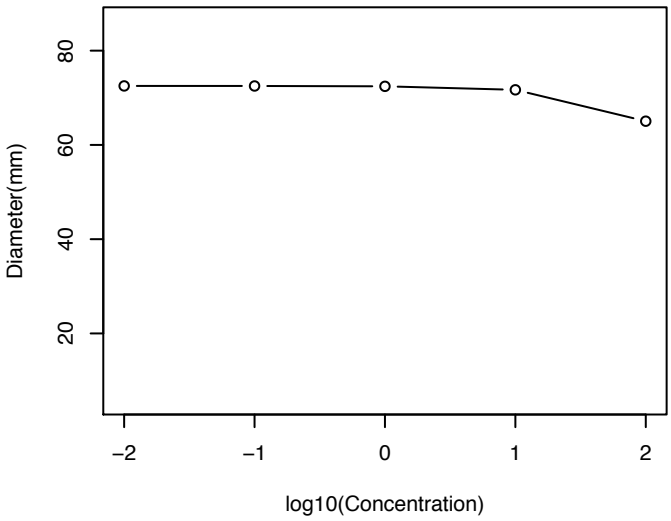


Verticillium dahliae

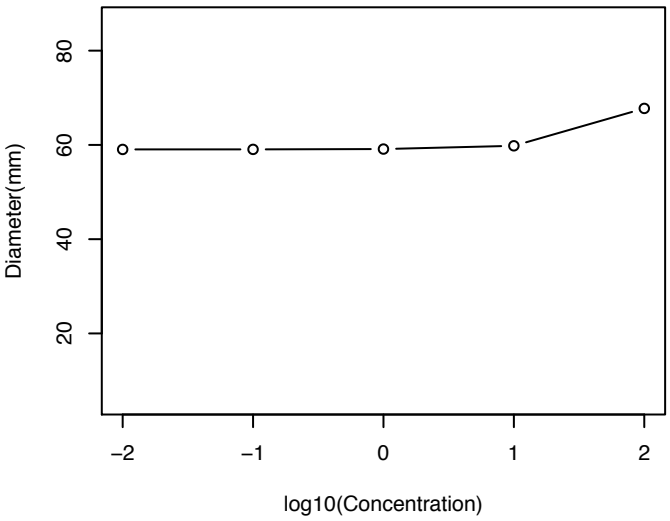


L03

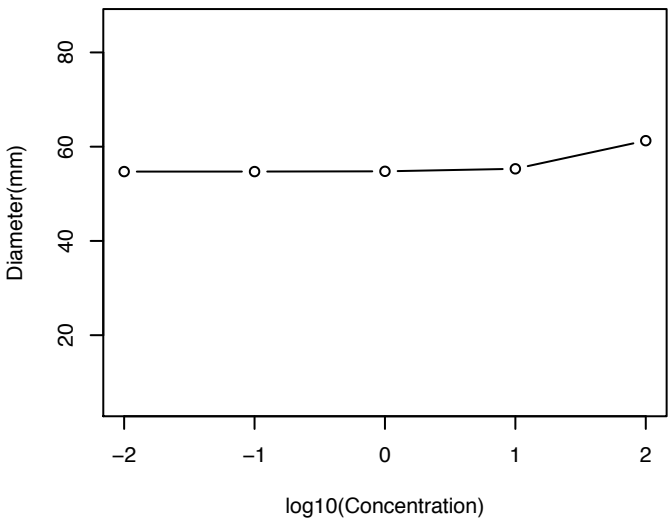
Phytophthora citrophthora



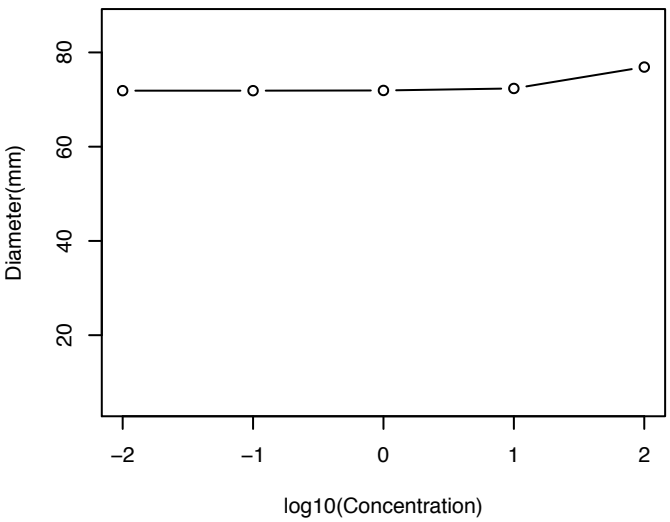
Phytophthora capsici



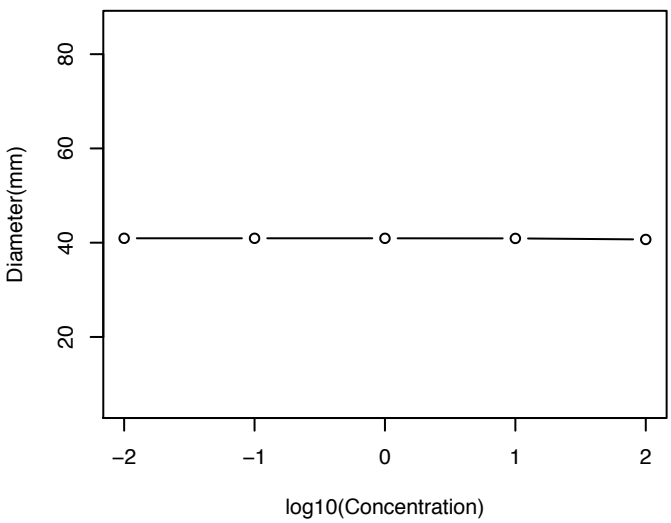
Alternaria alternata



Fusarium solani

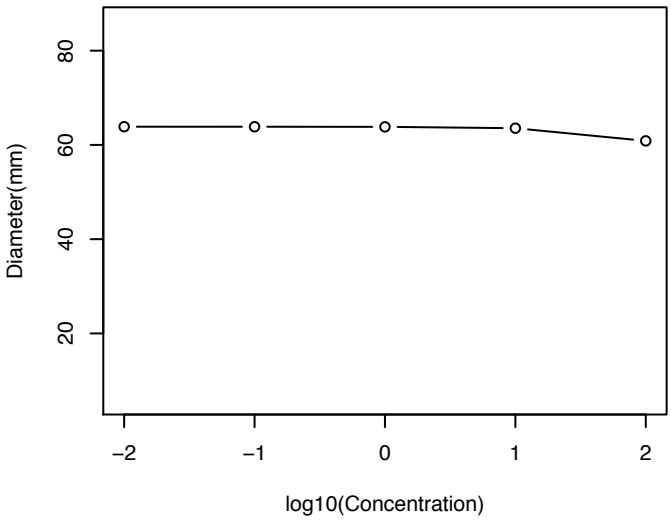


Verticillium dahliae

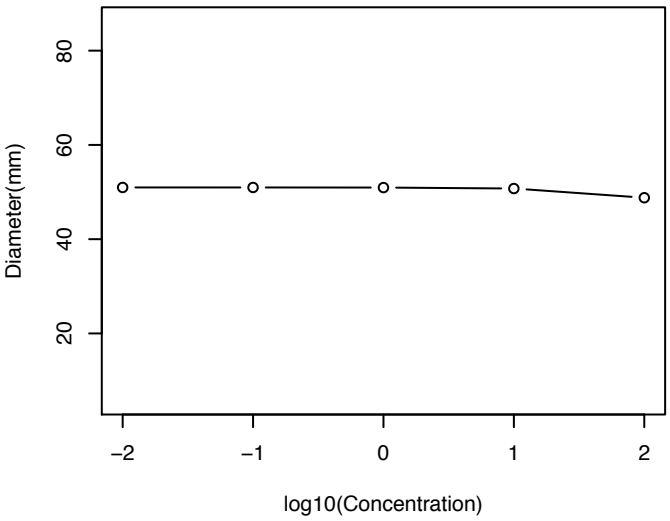


L04

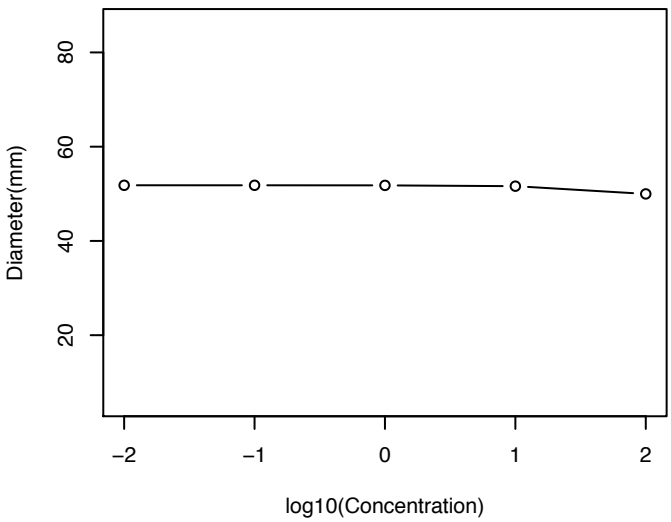
Phytophthora citrophthora



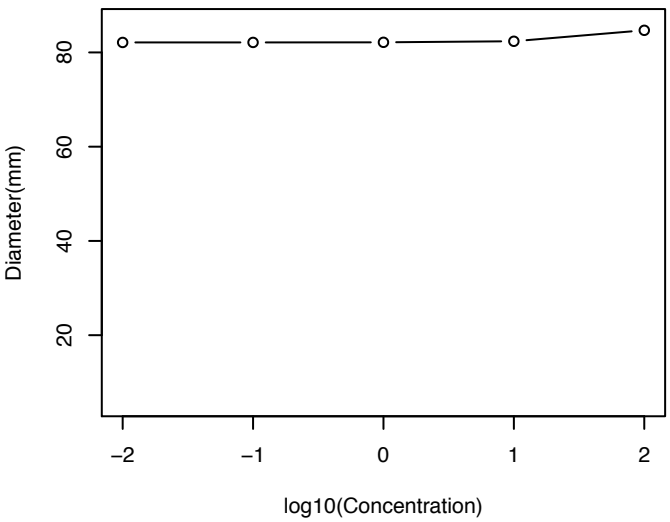
Phytophthora capsici



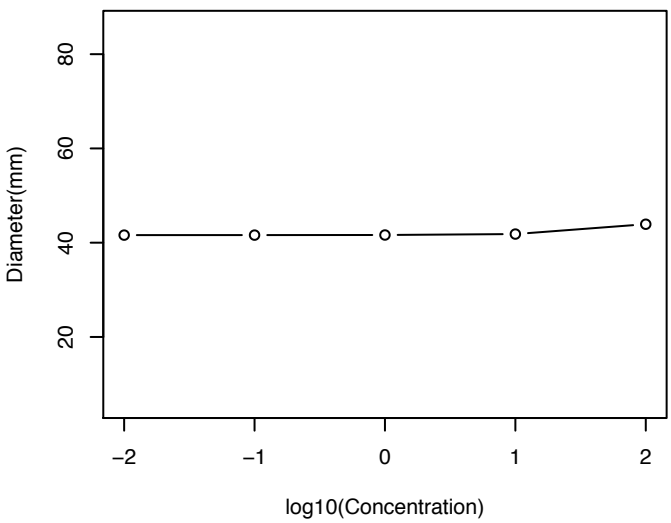
Alternaria alternata



Fusarium solani

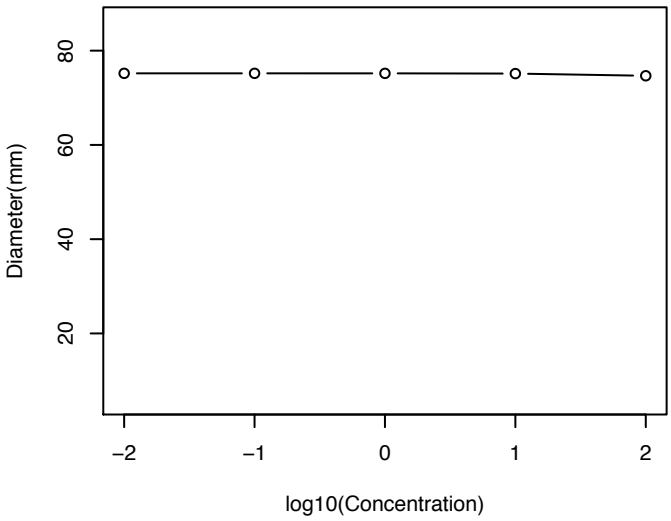


Verticillium dahliae

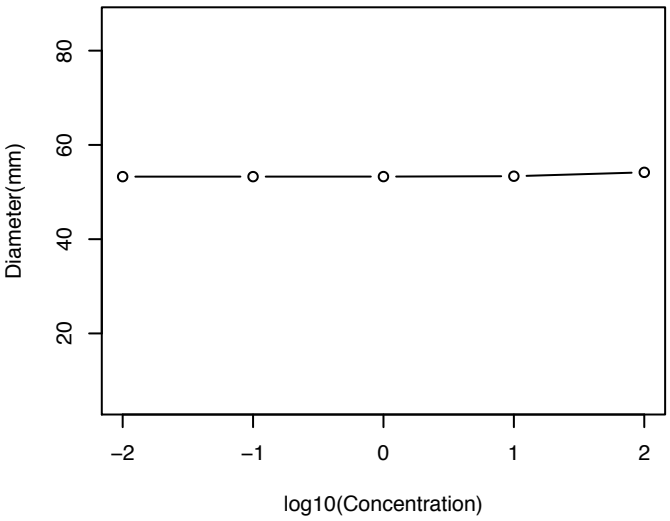


L05

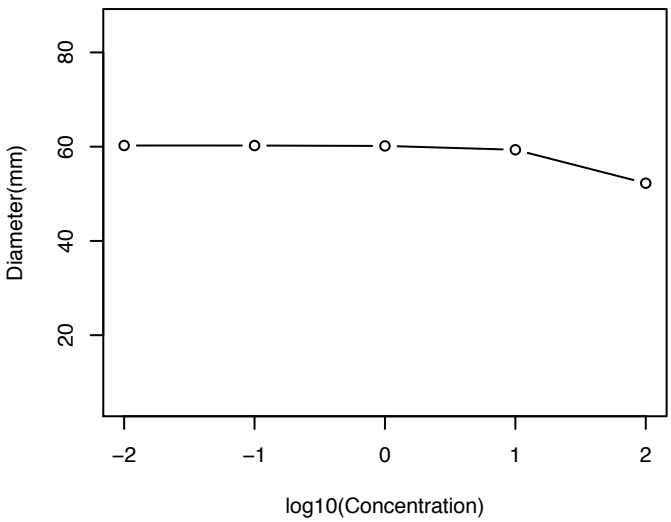
Phytophthora citrophthora



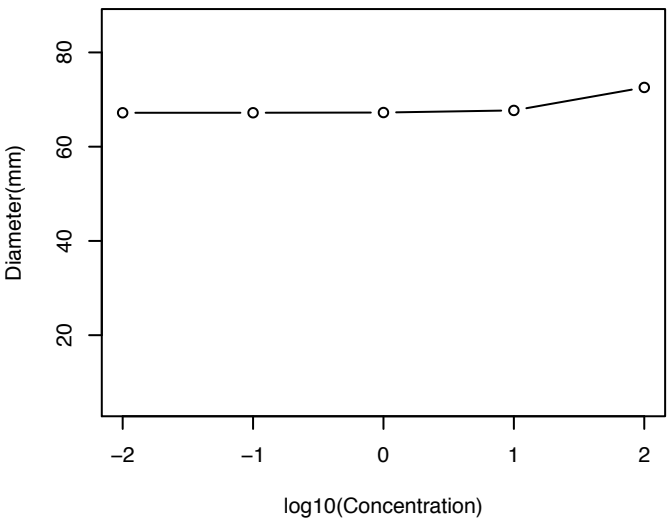
Phytophthora capsici



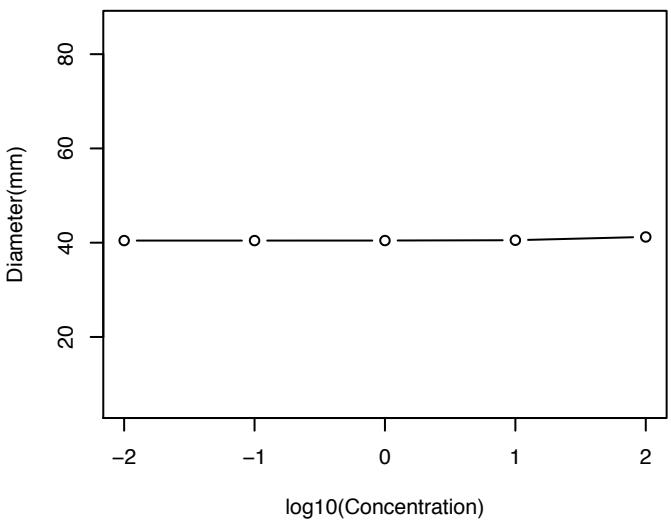
Alternaria alternata



Fusarium solani

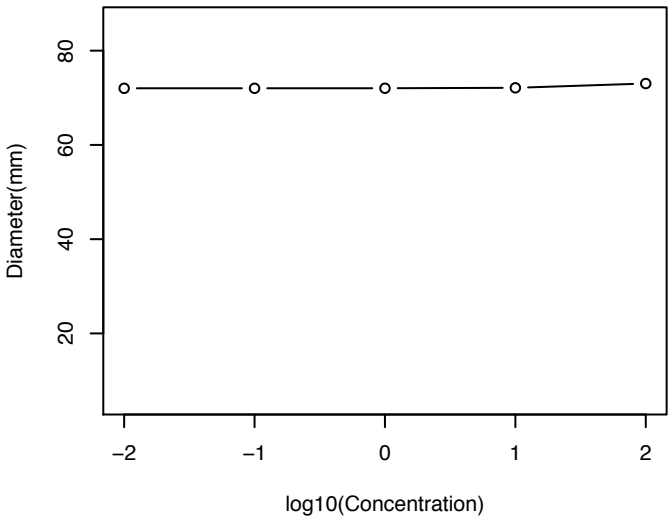


Verticillium dahliae

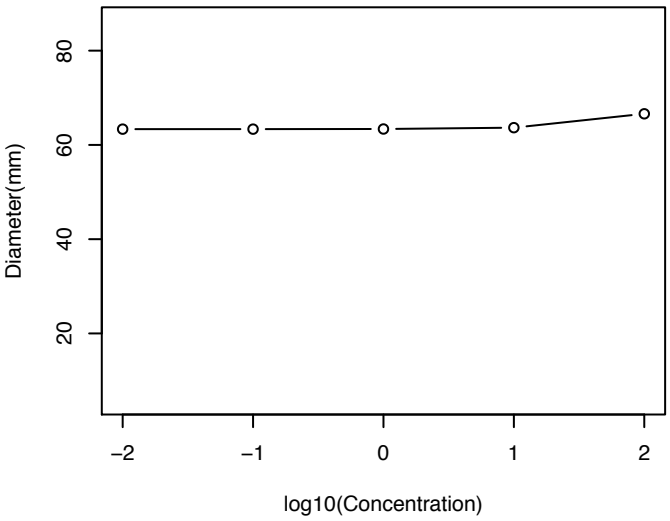


L06

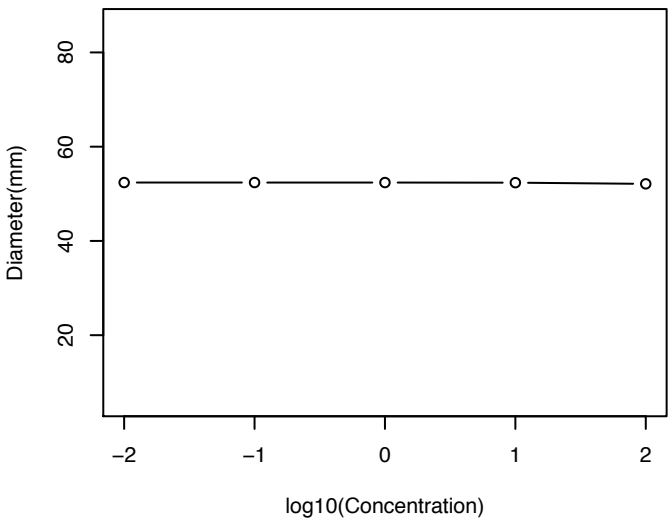
Phytophthora citrophthora



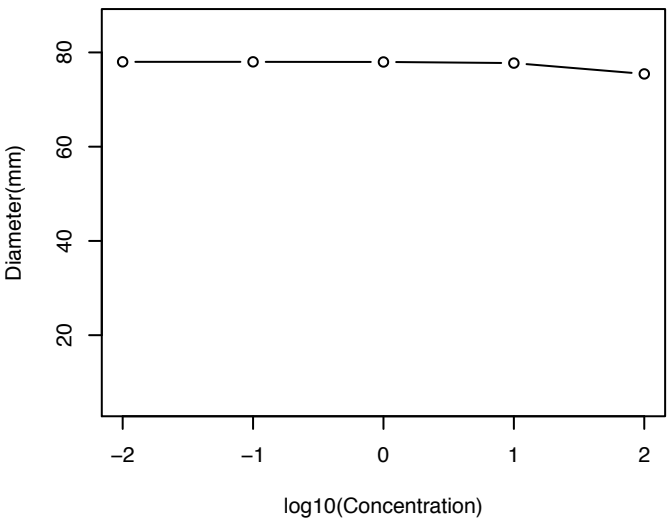
Phytophthora capsici



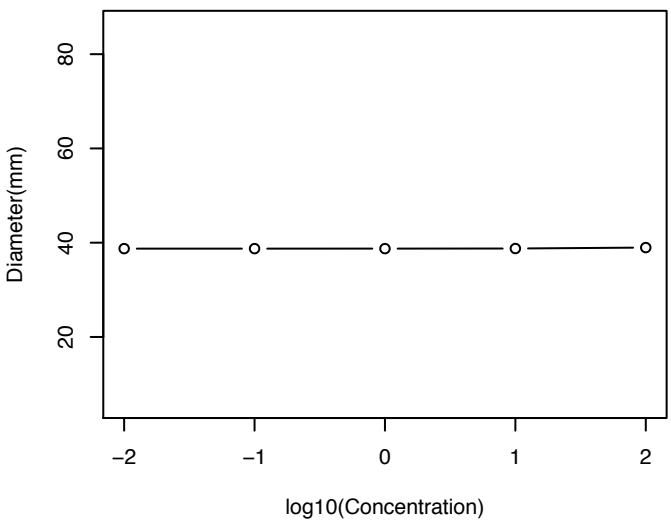
Alternaria alternata



Fusarium solani

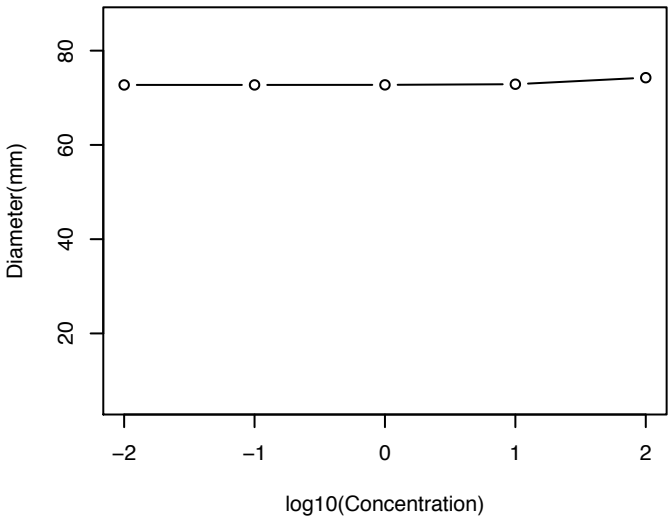


Verticillium dahliae

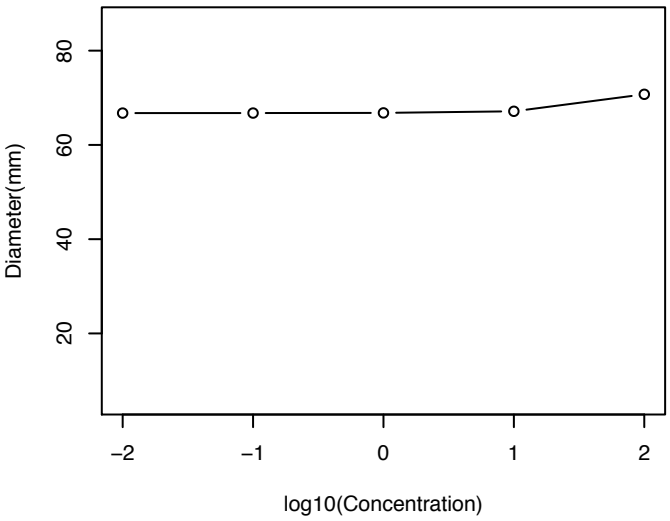


L07

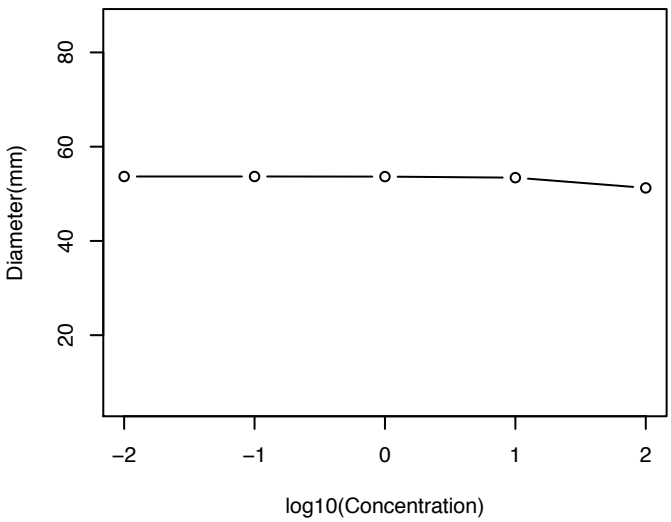
Phytophthora citrophthora



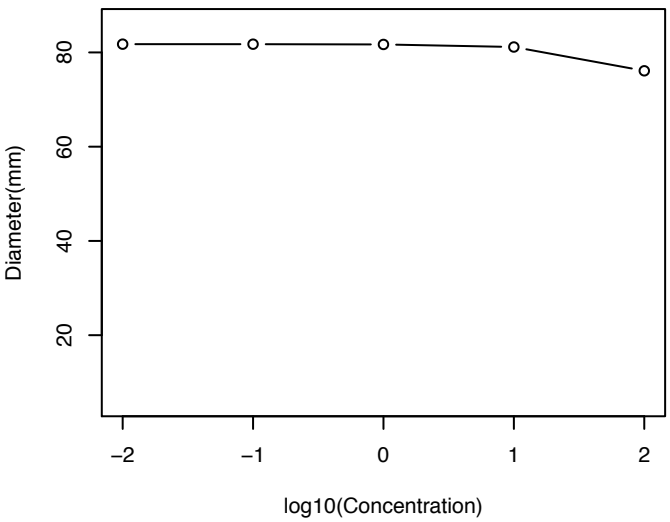
Phytophthora capsici



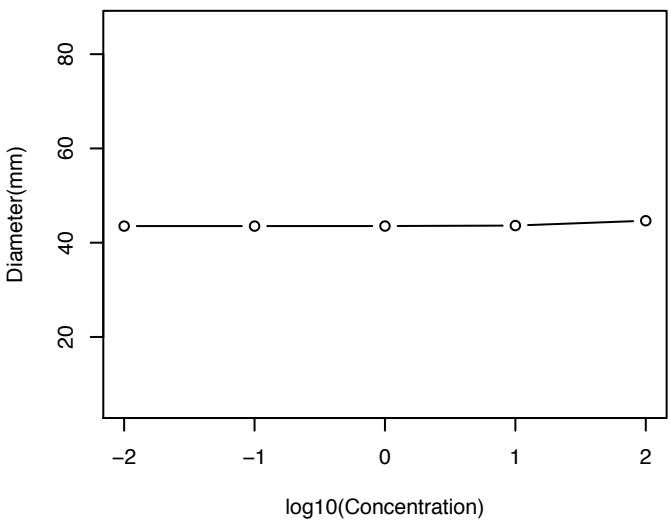
Alternaria alternata



Fusarium solani

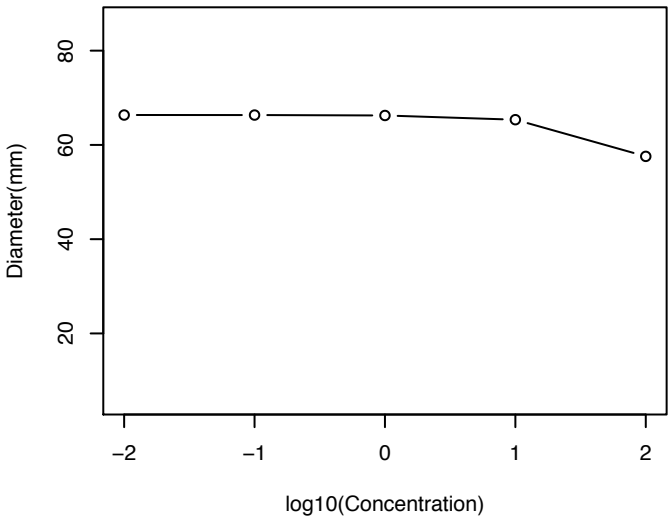


Verticillium dahliae

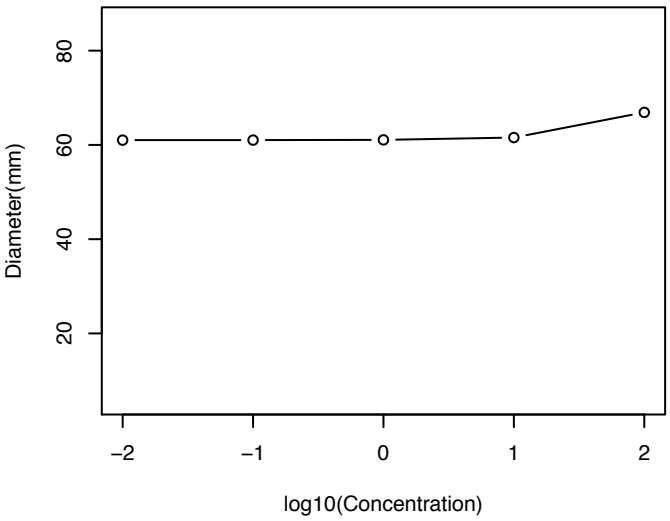


L08

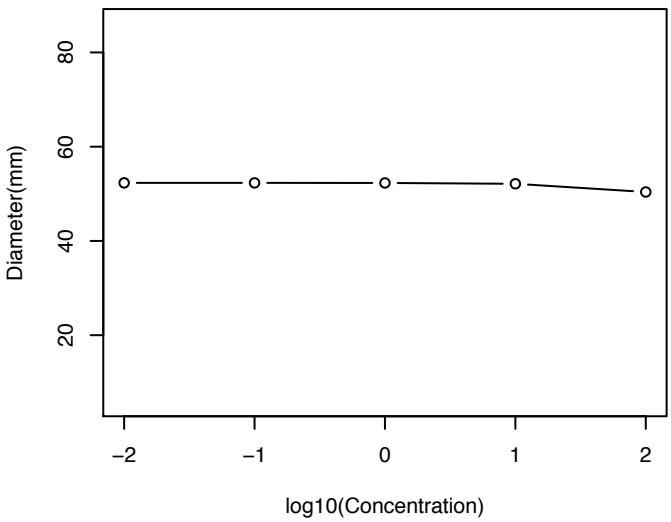
Phytophthora citrophthora



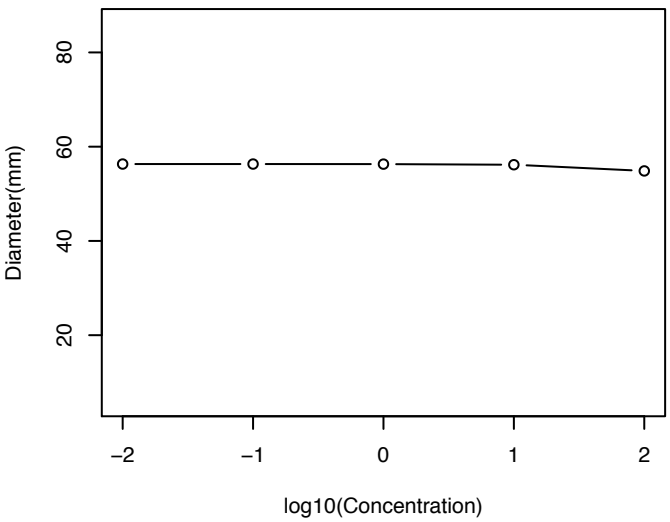
Phytophthora capsici



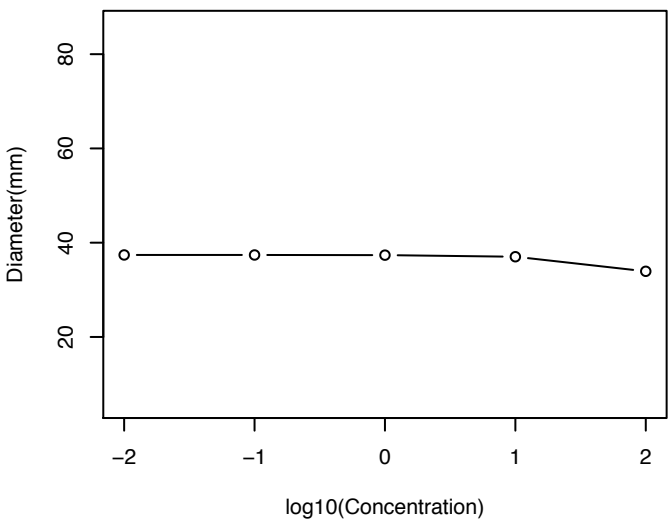
Alternaria alternata



Fusarium solani

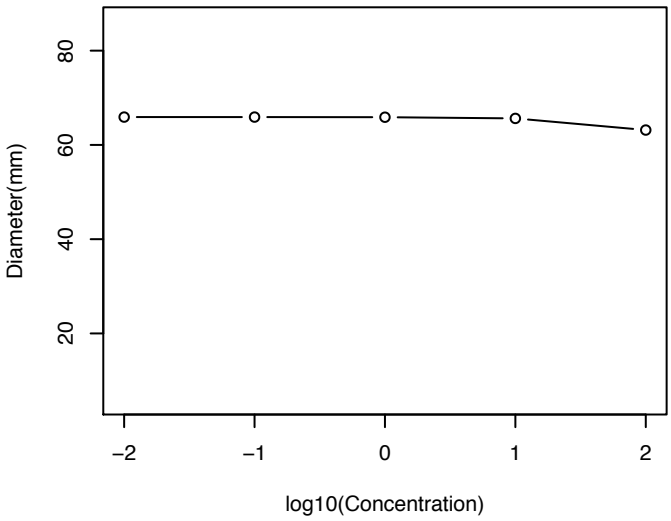


Verticillium dahliae

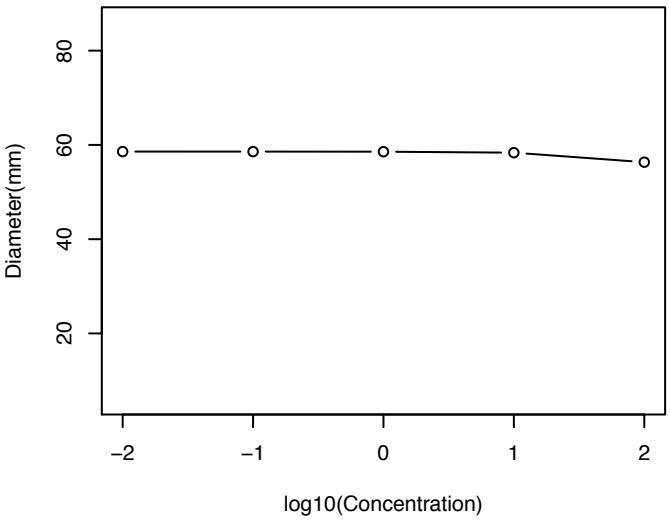


L09

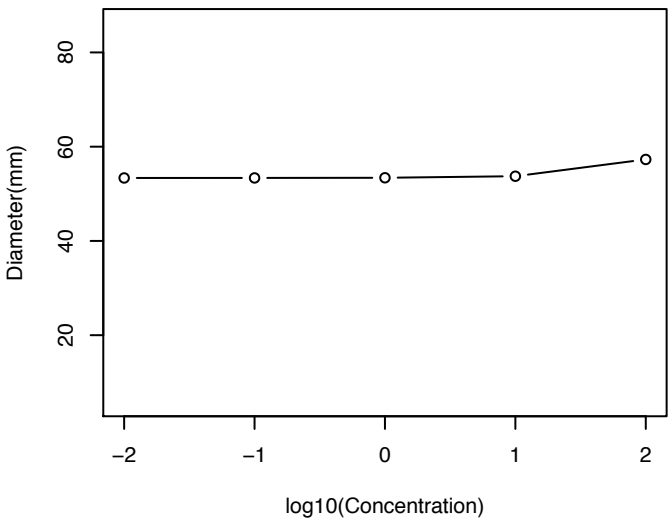
Phytophthora citrophthora



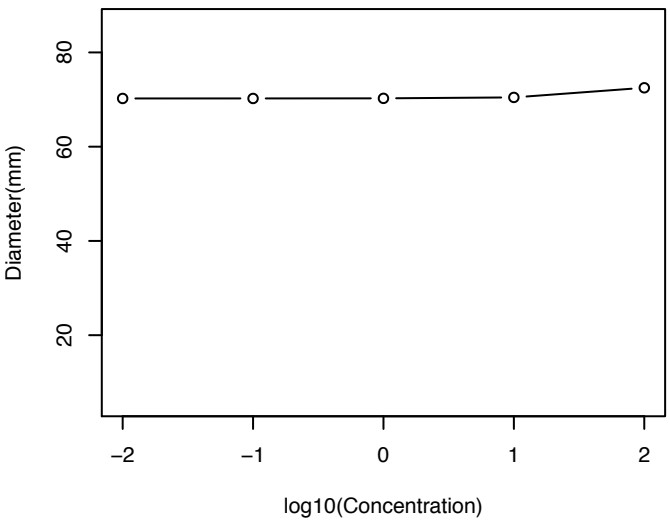
Phytophthora capsici



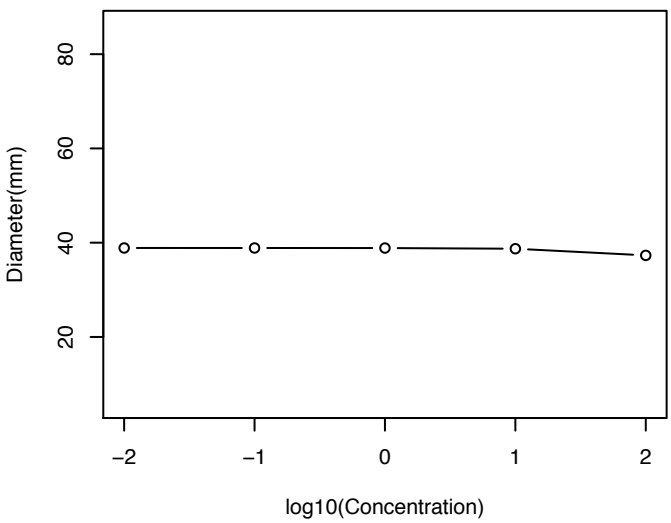
Alternaria alternata



Fusarium solani

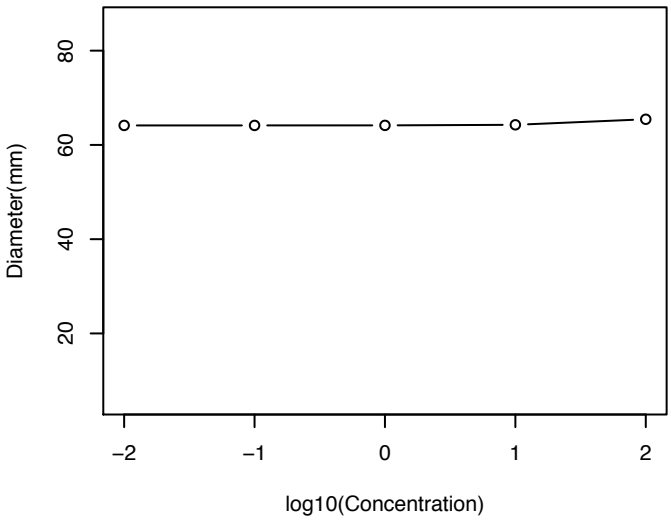


Verticillium dahliae

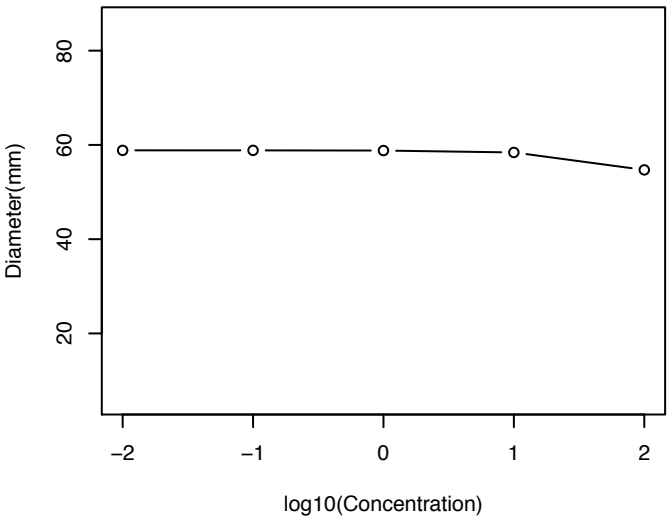


L10

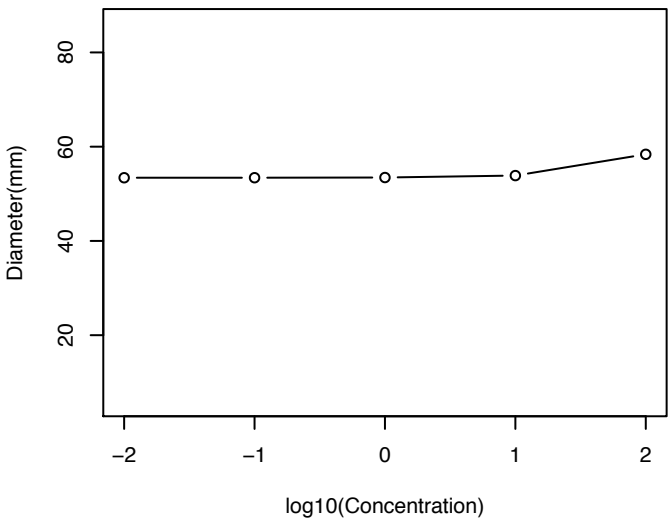
Phytophthora citrophthora



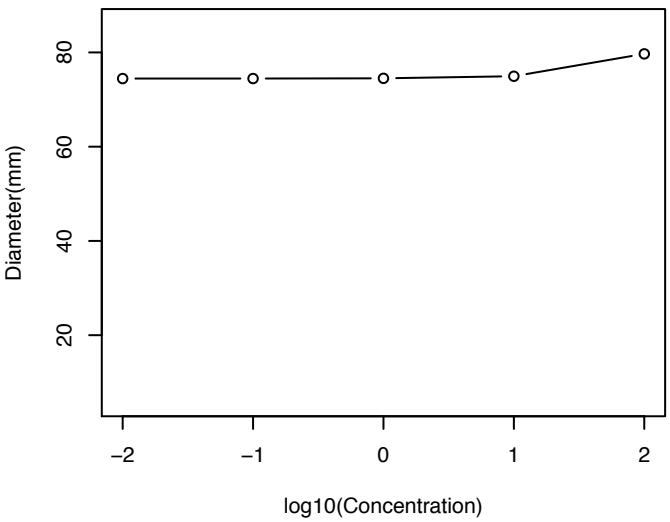
Phytophthora capsici



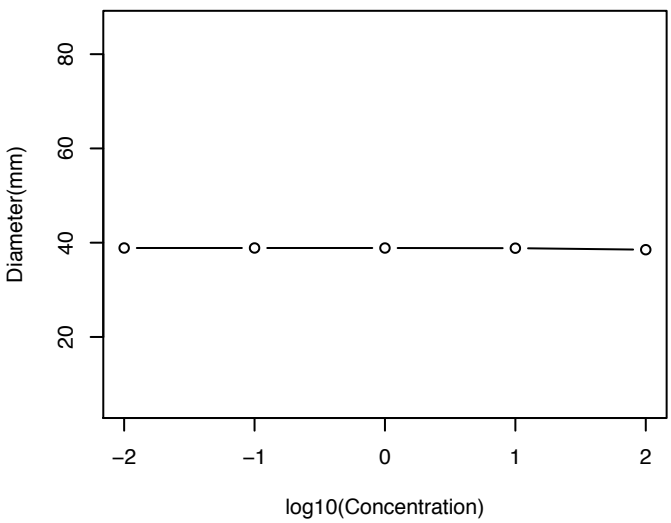
Alternaria alternata



Fusarium solani

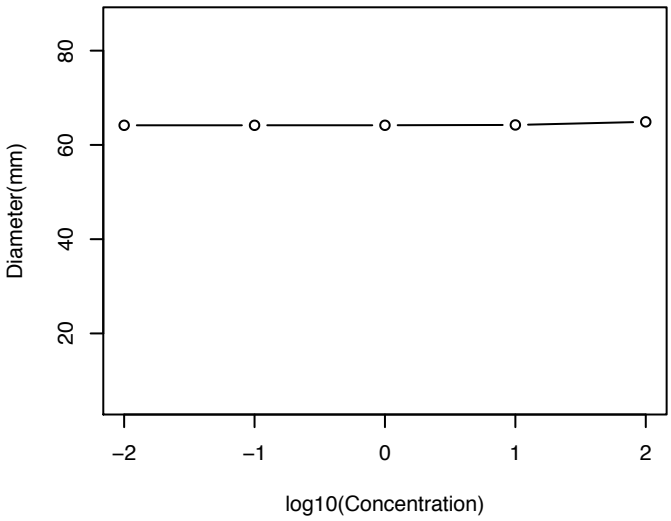


Verticillium dahliae

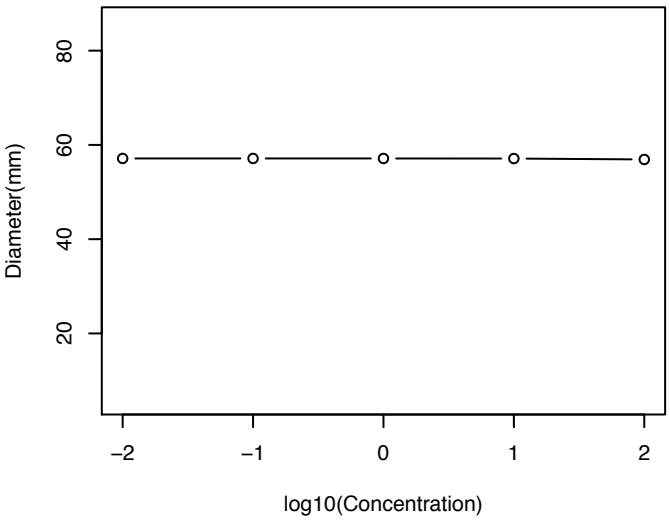


L11

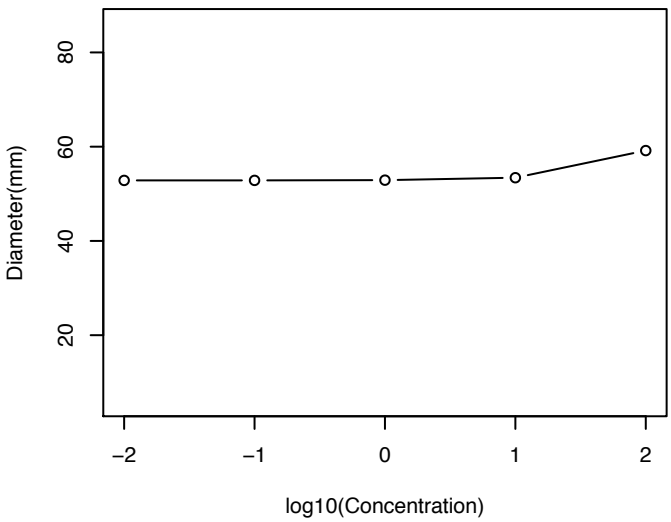
Phytophthora citrophthora



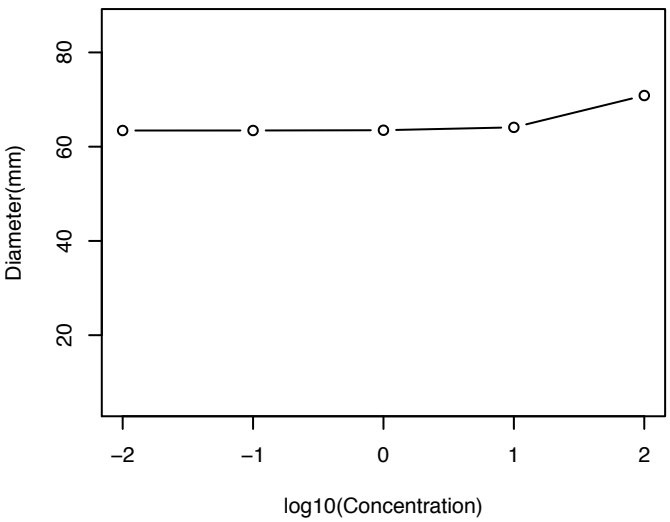
Phytophthora capsici



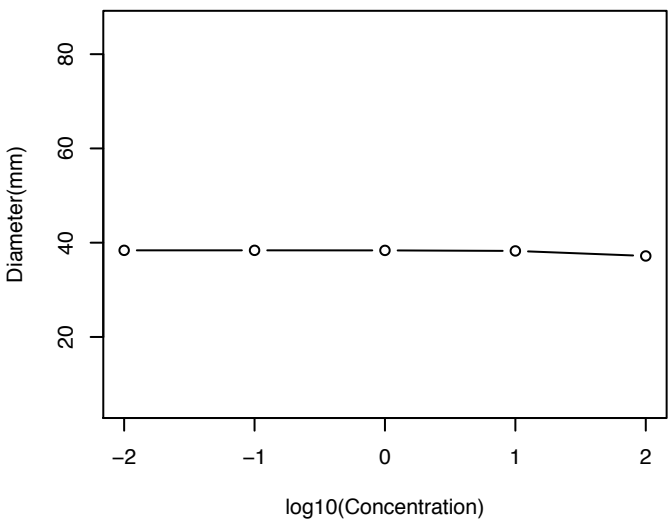
Alternaria alternata



Fusarium solani

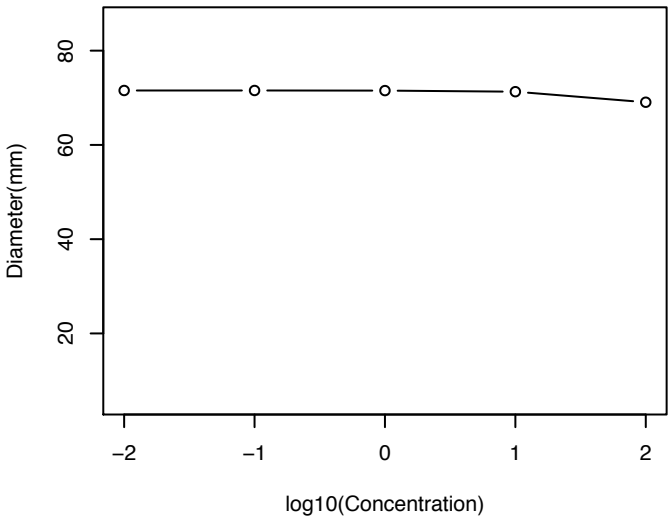


Verticillium dahliae

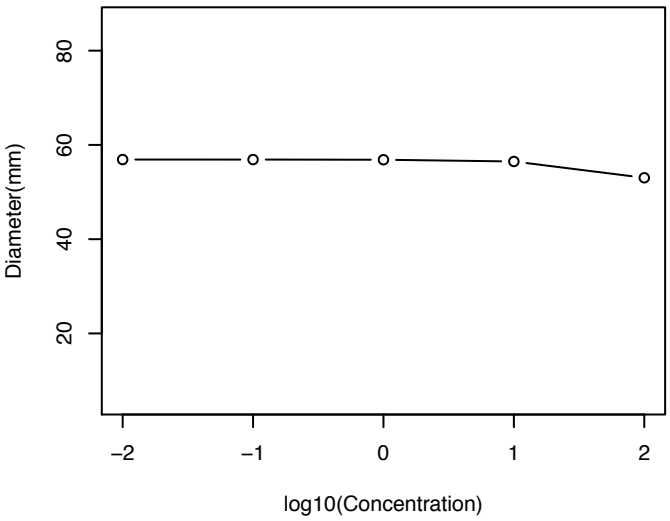


L12

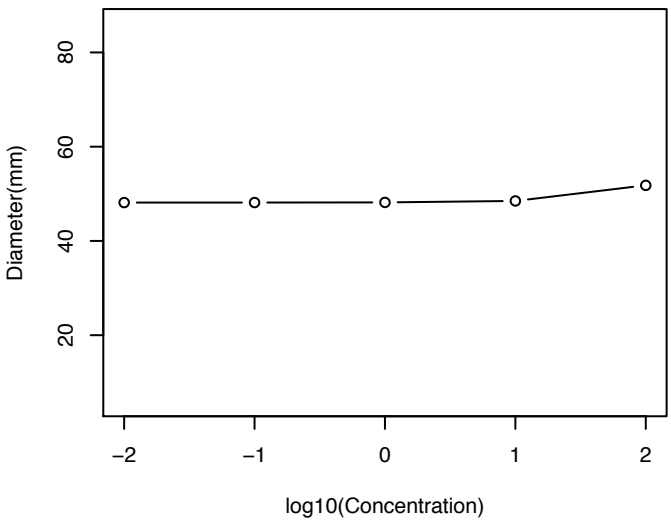
Phytophthora citrophthora



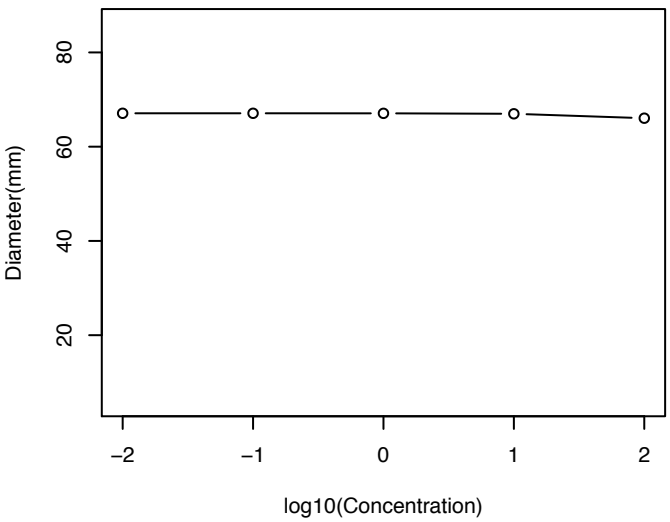
Phytophthora capsici



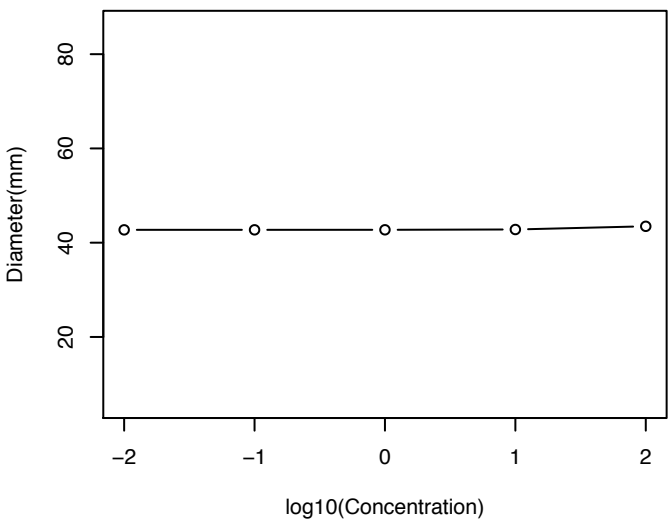
Alternaria alternata



Fusarium solani

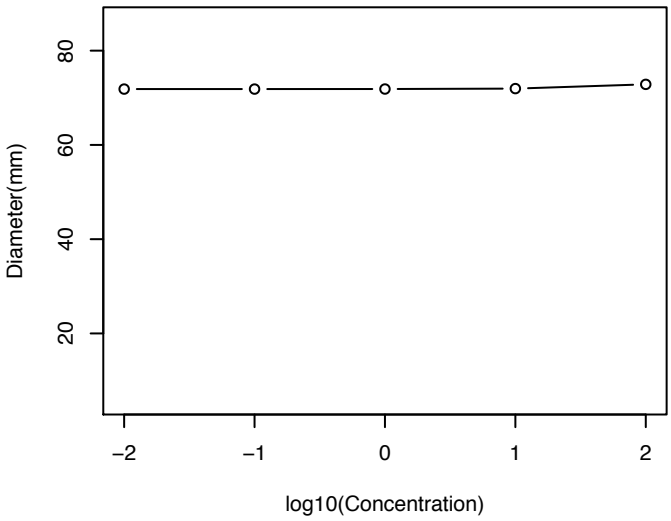


Verticillium dahliae

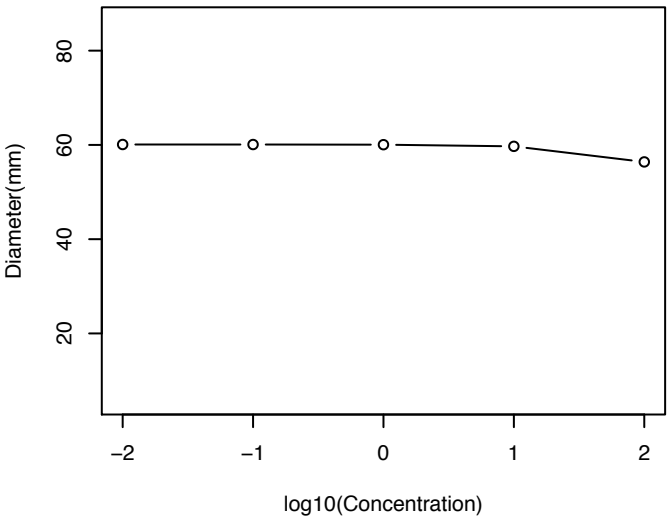


L13

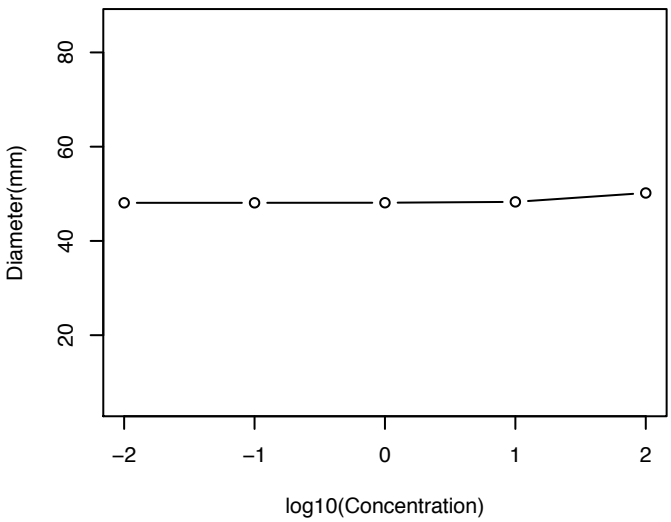
Phytophthora citrophthora



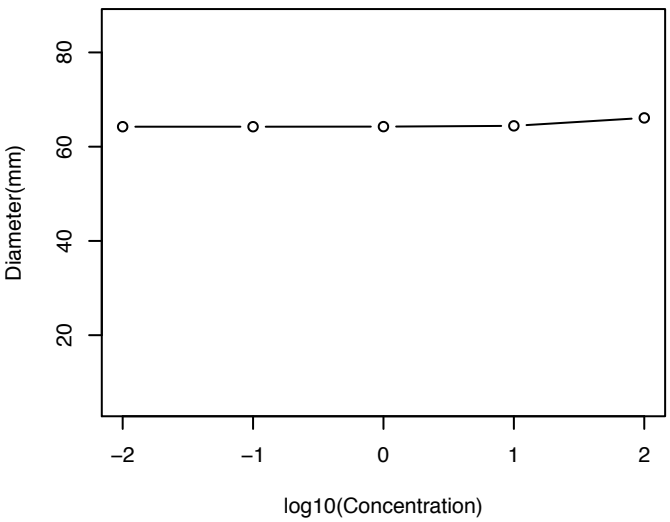
Phytophthora capsici



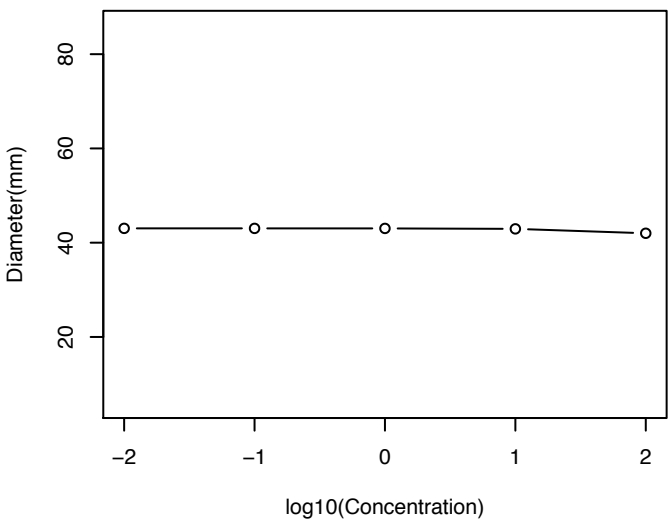
Alternaria alternata



Fusarium solani

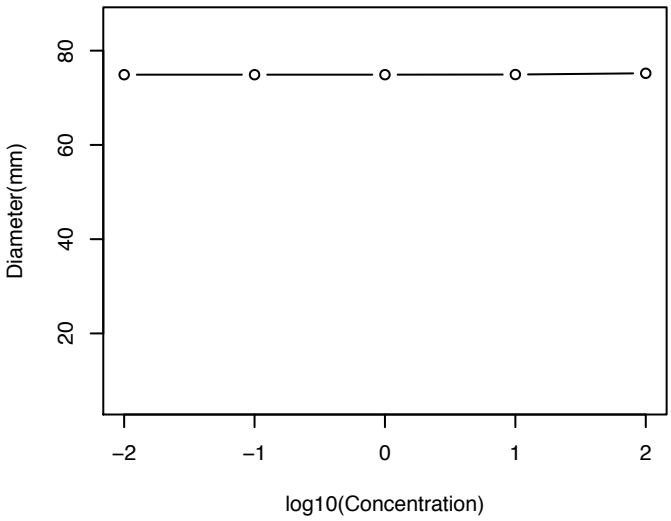


Verticillium dahliae

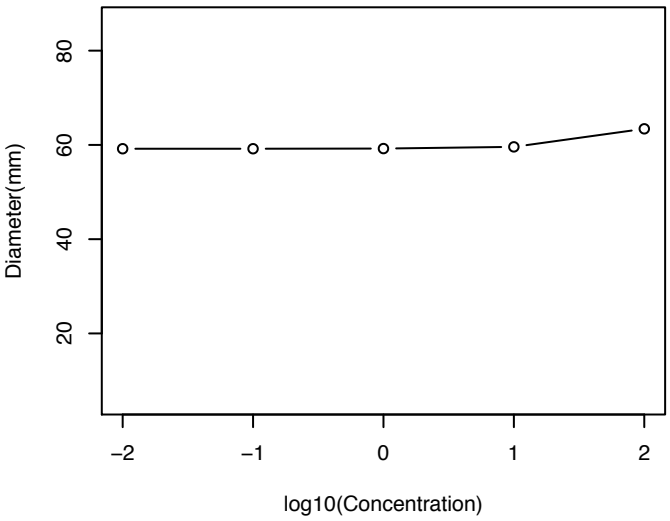


A

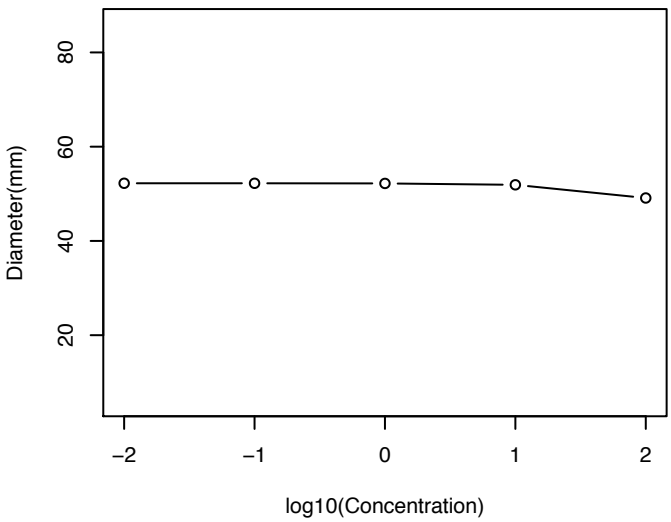
Phytophthora citrophthora



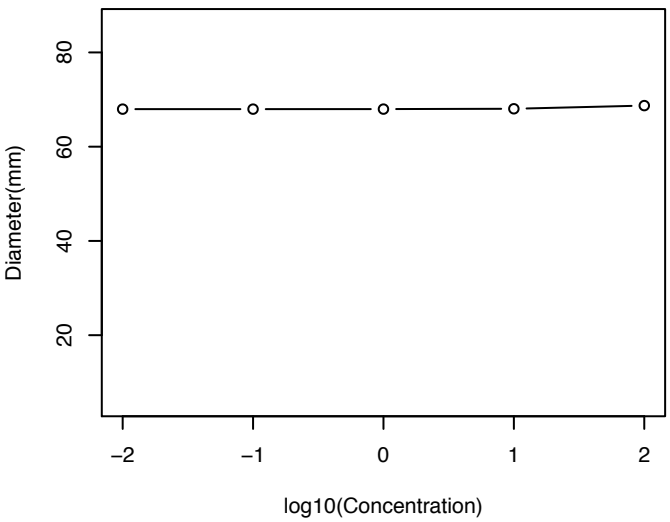
Phytophthora capsici



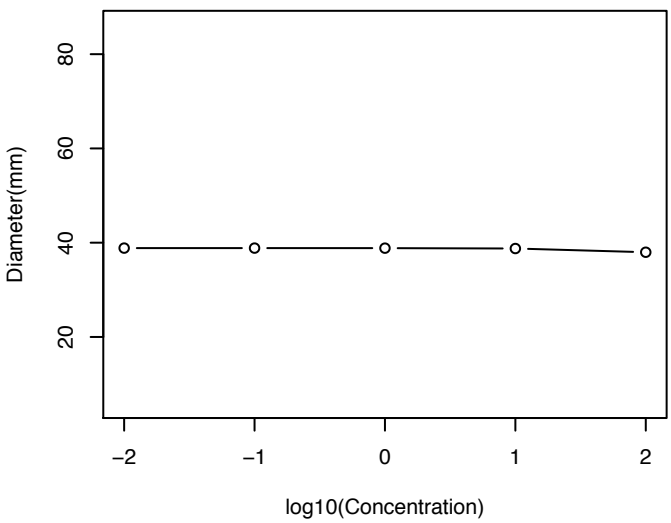
Alternaria alternata



Fusarium solani

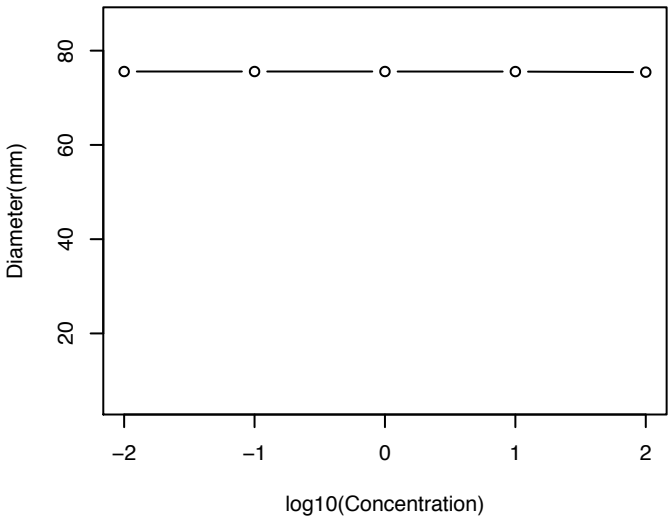


Verticillium dahliae

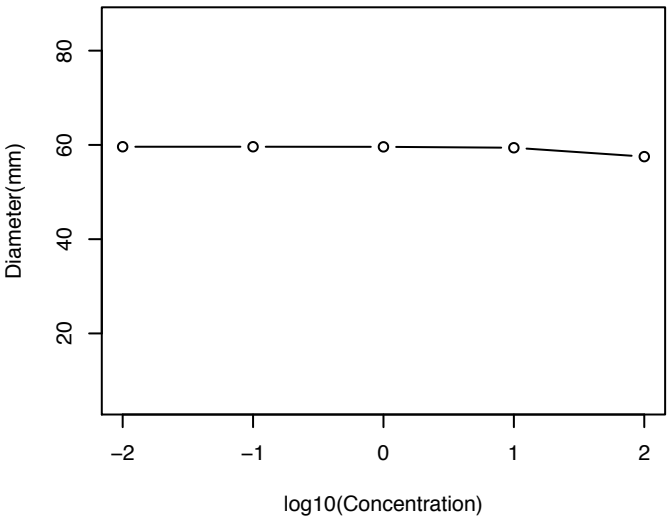


B

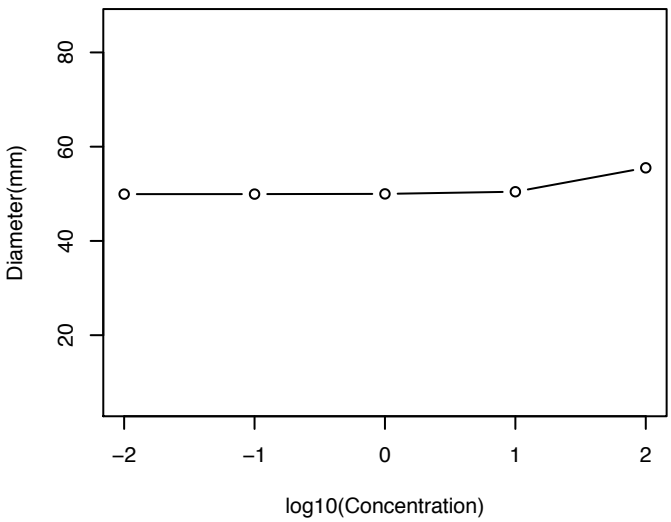
Phytophthora citrophthora



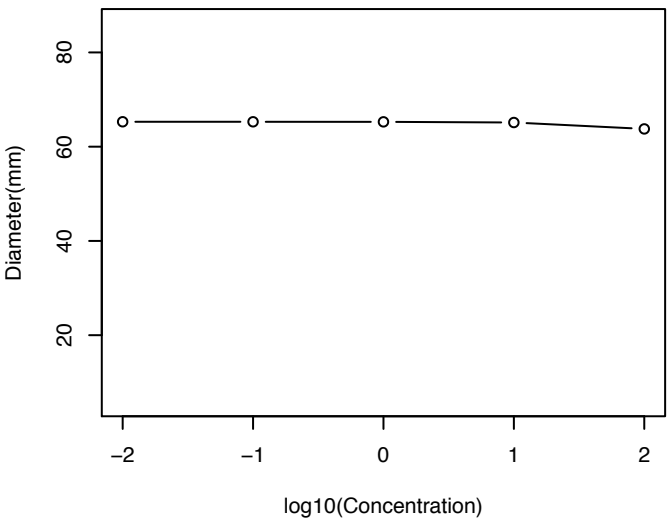
Phytophthora capsici



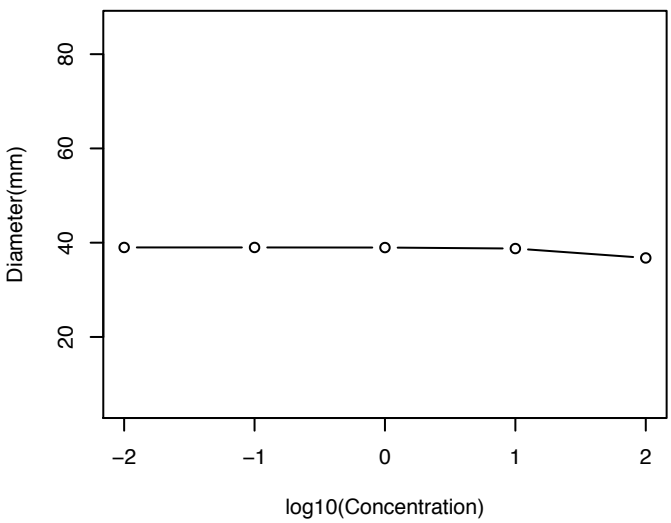
Alternaria alternata



Fusarium solani

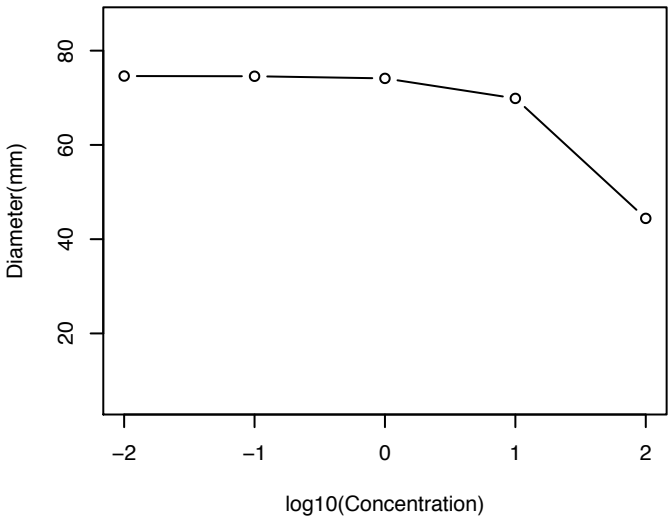


Verticillium dahliae

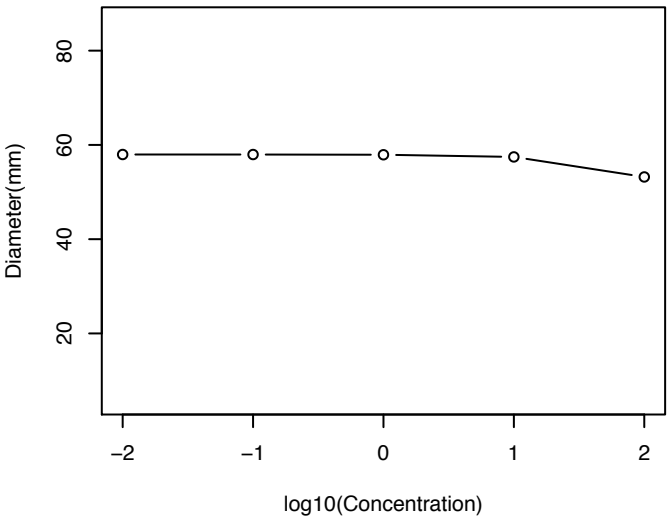


Fosetyl–Al

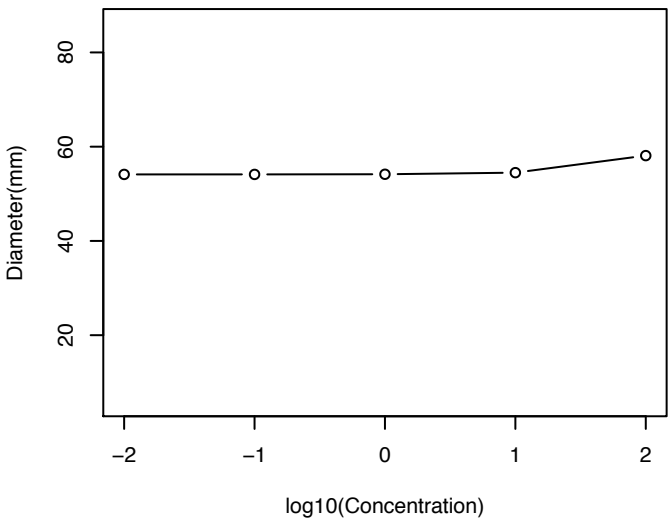
Phytophthora citrophthora



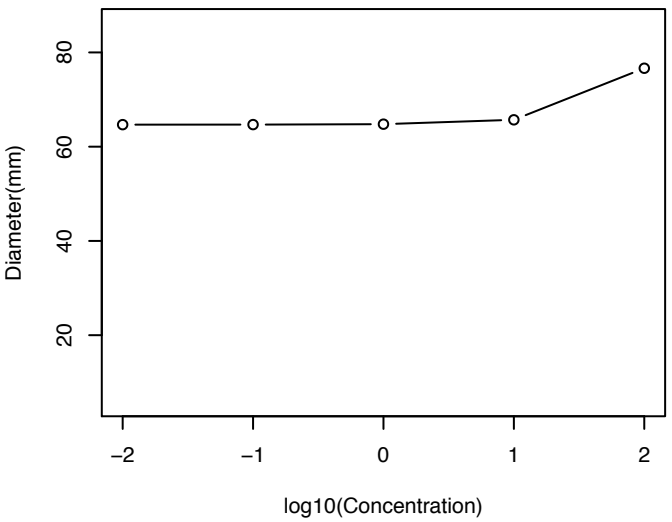
Phytophthora capsici



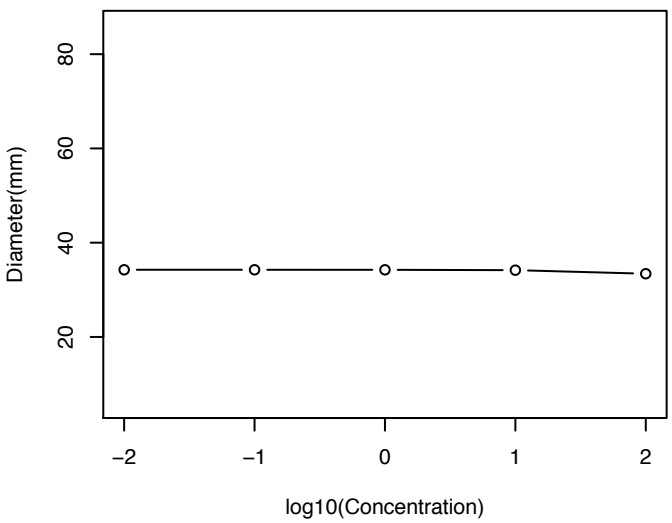
Alternaria alternata



Fusarium solani

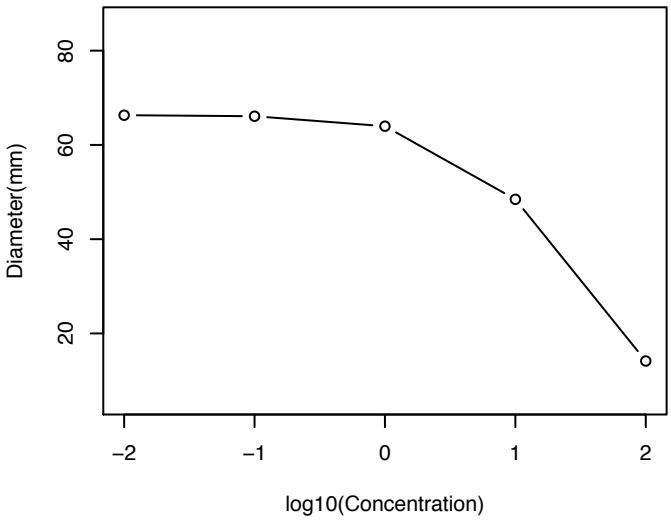


Verticillium dahliae

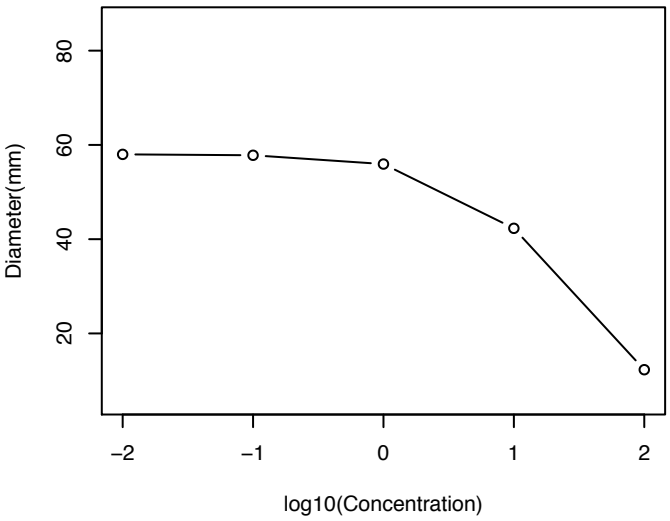


c

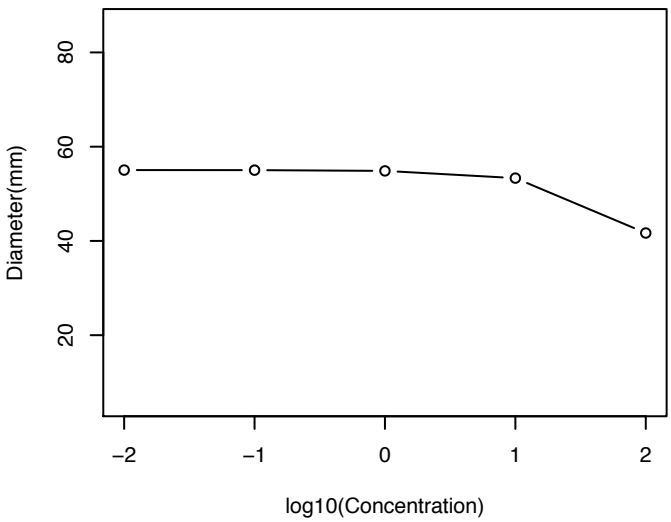
Phytophthora citrophthora



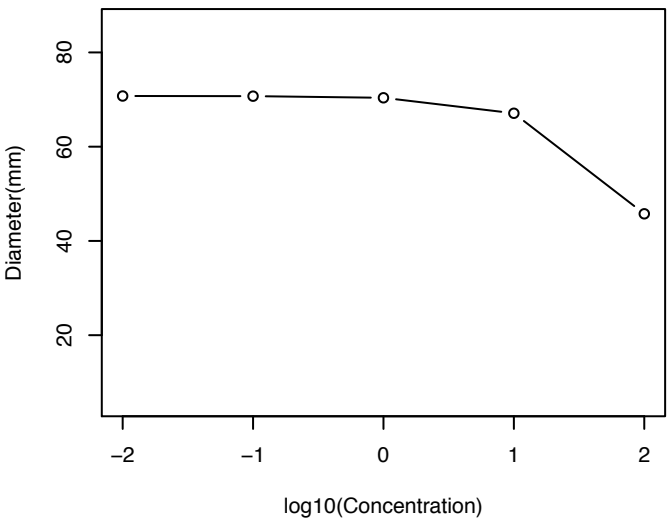
Phytophthora capsici



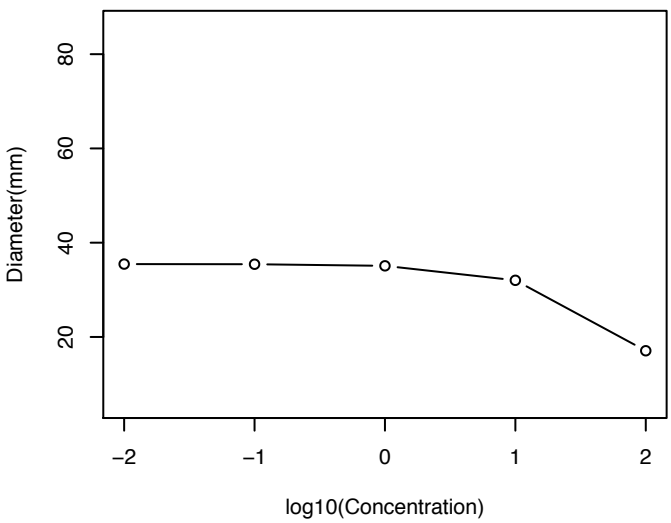
Alternaria alternata



Fusarium solani

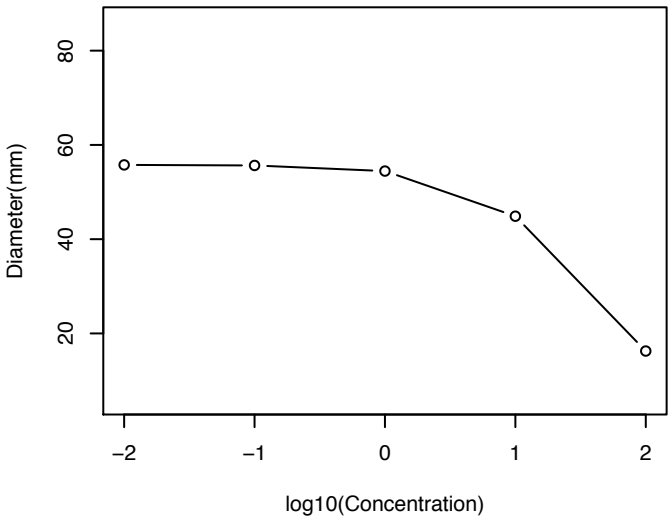


Verticillium dahliae

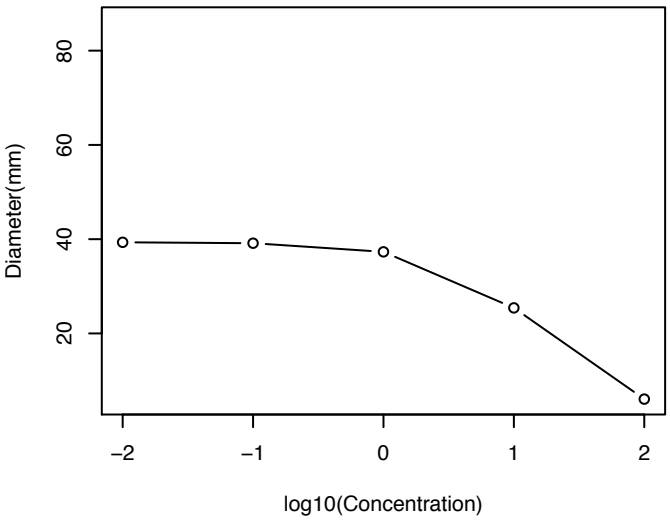


Mefenoxam

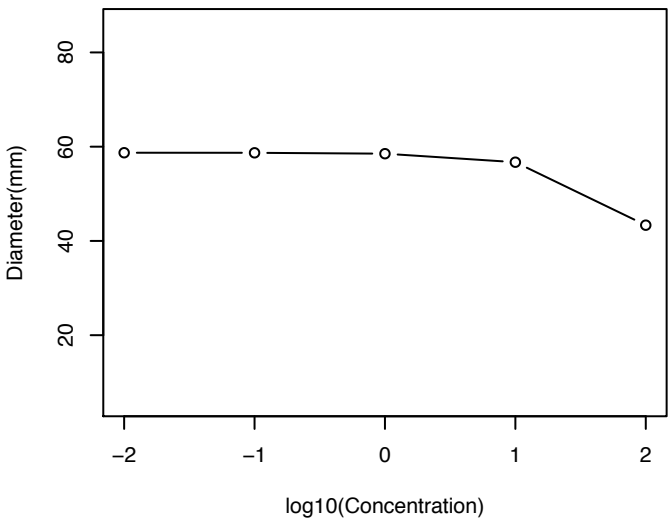
Phytophthora citrophthora



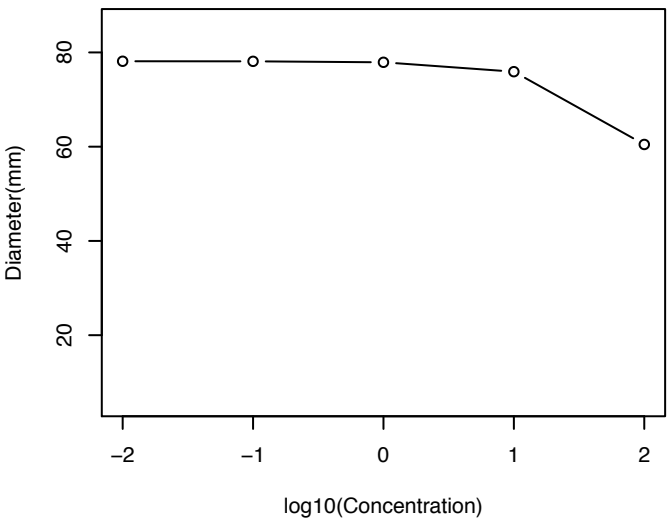
Phytophthora capsici



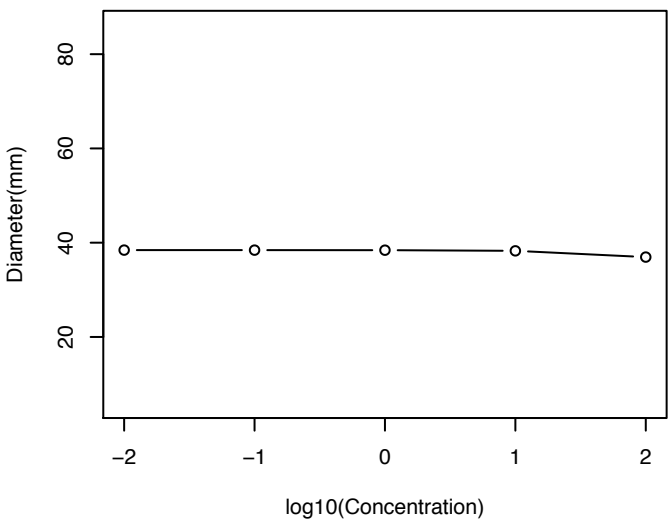
Alternaria alternata



Fusarium solani

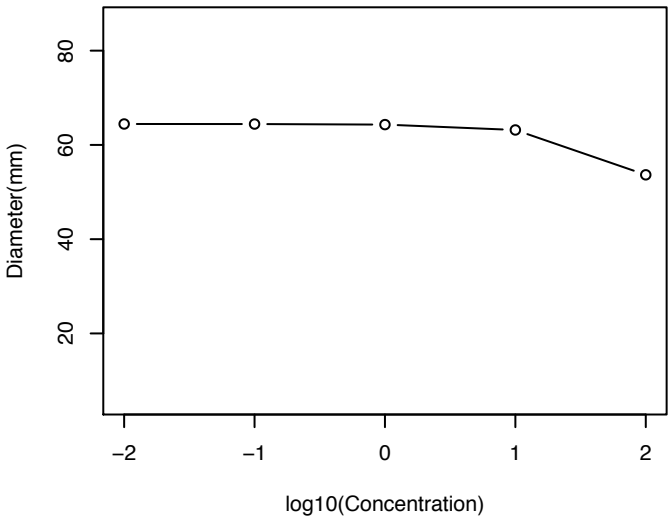


Verticillium dahliae

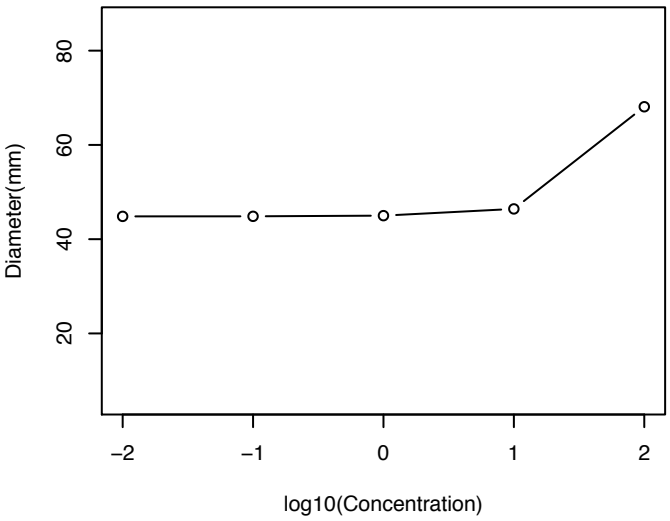


Pyraclostrobin

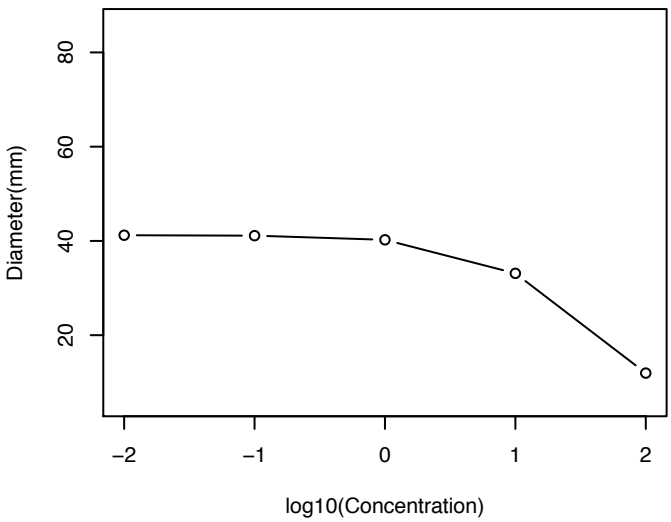
Phytophthora citrophthora



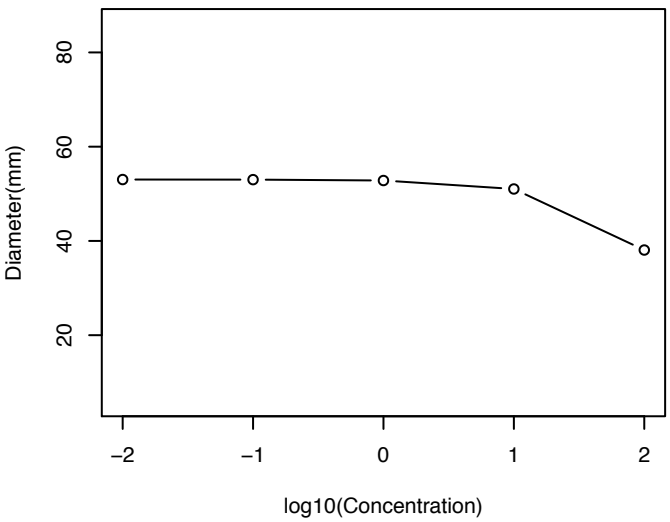
Phytophthora capsici



Alternaria alternata



Fusarium solani



Verticillium dahliae