

Supporting Information

Article title: Arbuscular mycorrhizal root colonization depends on the spatial structure of the host plants

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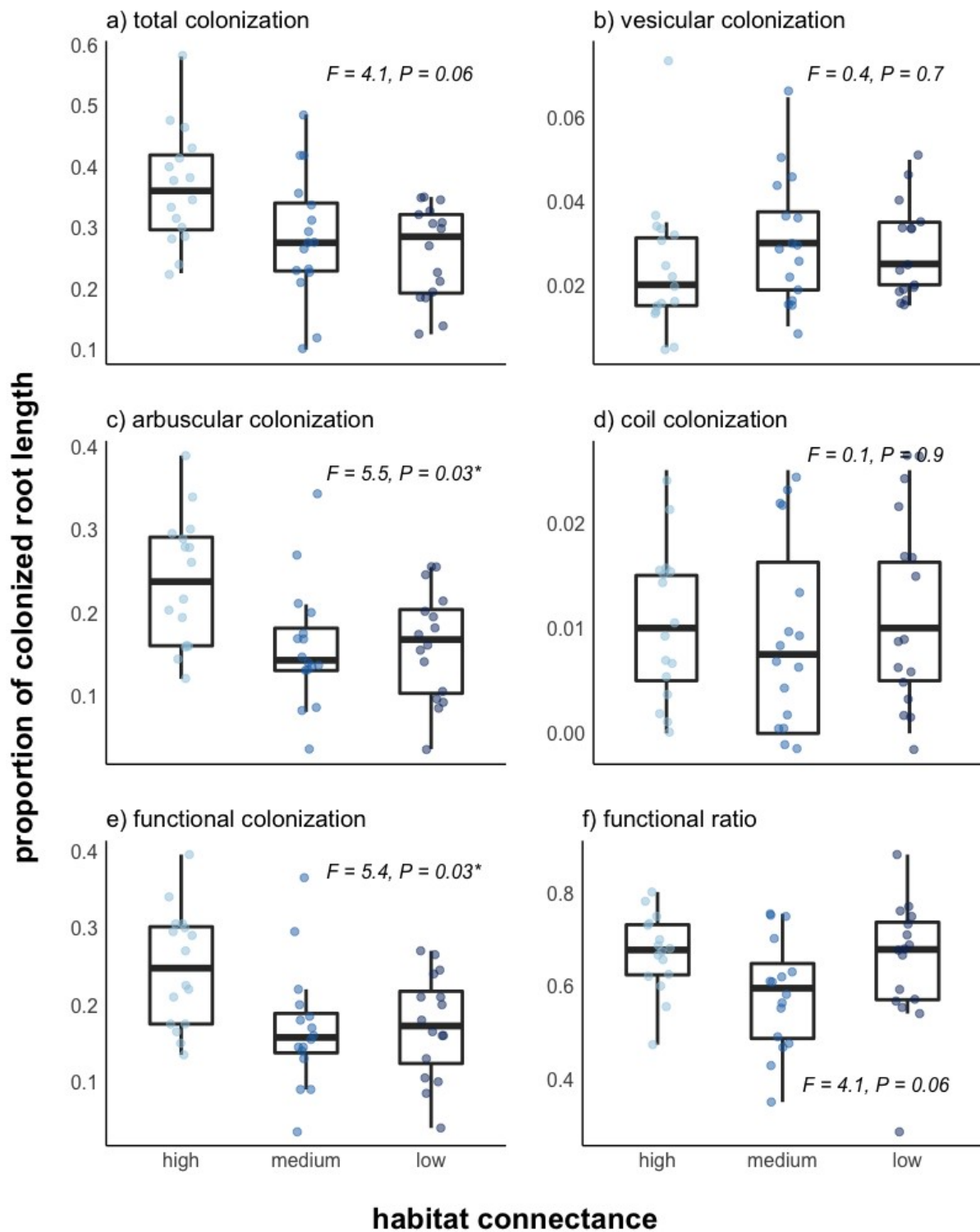


Fig. S1: Overview of the responses of the different colonization measures with habitat connectance (*Experiment One*). The panels display a) total, b) arbuscular, c) coil, d) vesicular, e) functional (additive arbuscular + coil) colonization and f) the functional colonization ratio. Data points in light to darker blue represent the connectance levels 'high', 'medium' and 'low' within mesocosms. Habitat connectance affected arbuscular, functional colonization as well as marginally total colonization and the functional ratio (see inserted F-statistics and full ANOVA model results in the Appendix II: Tests 1.1 - 1.6).

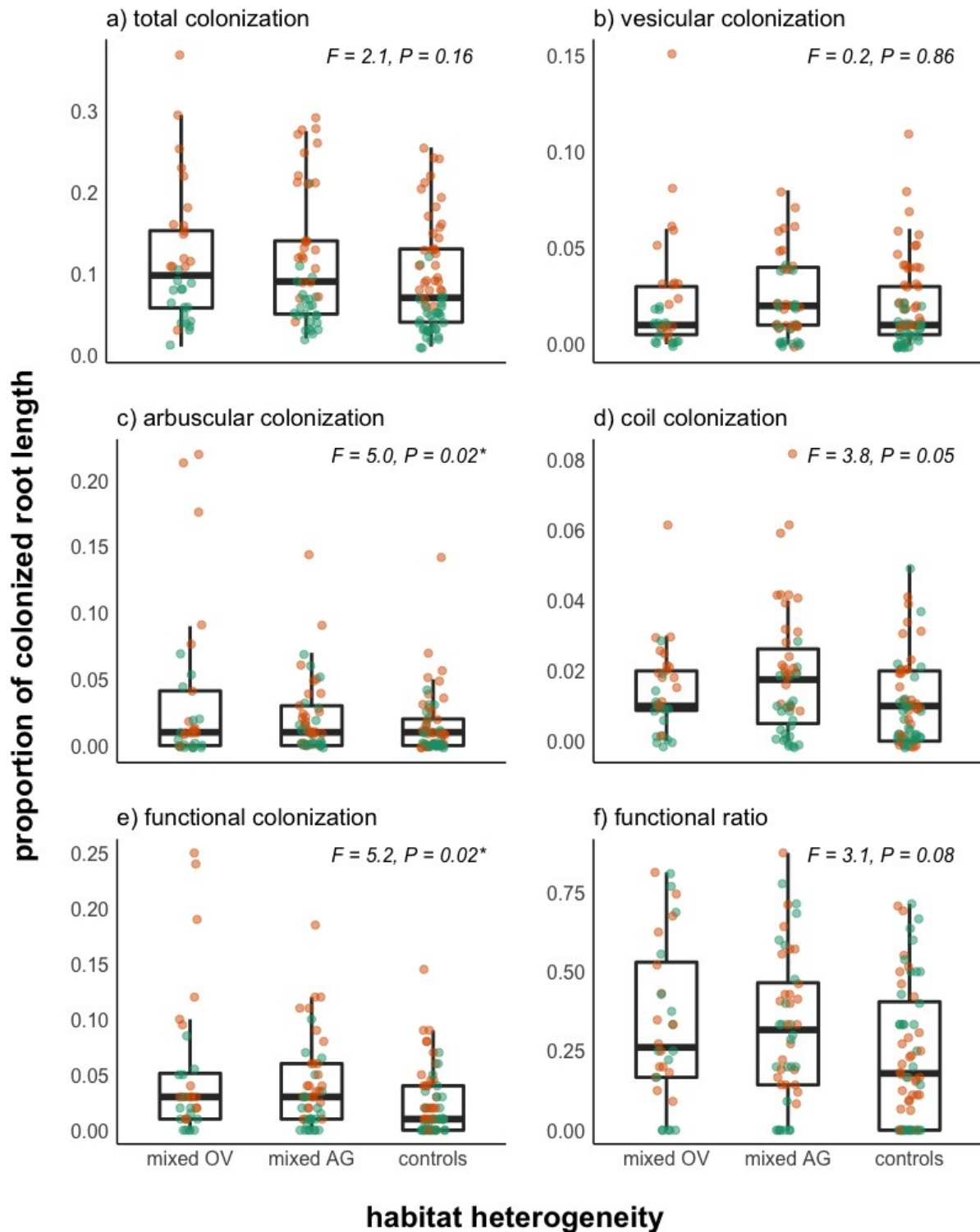


Fig. S2: Overview of the responses of different colonization measures at different levels of habitat heterogeneity (*Experiment Two*). To illustrate differences between mixed micro-landscapes and the one-habitat-type controls, the two control treatments are shown within one boxplot. The panels display a) total, b) arbuscular, c) coil, d) vesicular, e) functional (additive arbuscular + coil) colonization and f) the functional colonization ratio. Phosphorous-fertilized inserts (habitat patches) are shown in green and unfertilized ones in orange. Habitat heterogeneity affected arbuscular and functional colonization (see inserted F-statistics and full ANOVA model results in the Appendix II: Tests 2.1 - 2.6).

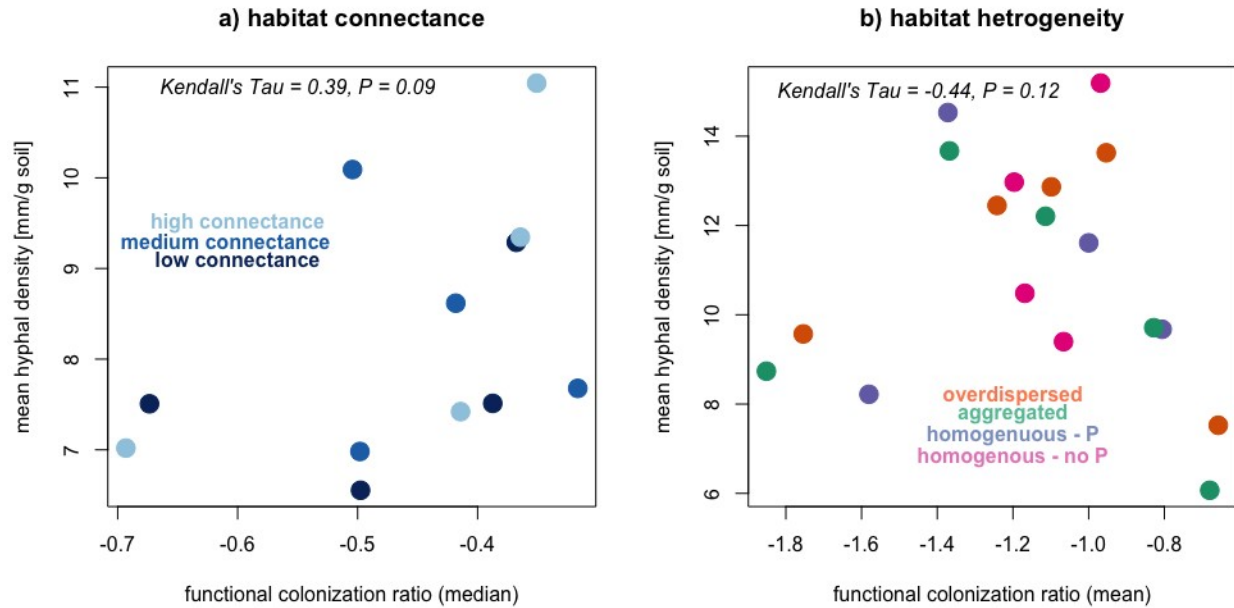


Fig. S3: Mean density of extraradical hyphae (hyphal length in mm per g soil) over functional colonization ratio for a) *Experiment One* (habitat connectance) and b) *Experiment Two* (habitat heterogeneity). Kendall's Tau statistics did not reveal any clear correlation between the mean of hyphal density and the median (a) or mean (b) of the functional colonization ratio. In the full ANOVA models, hyphal density affected the functional ratio in *Experiment One*, but not in *Experiment Two* (see Appendix II: Tests 4.1 - 4.2).

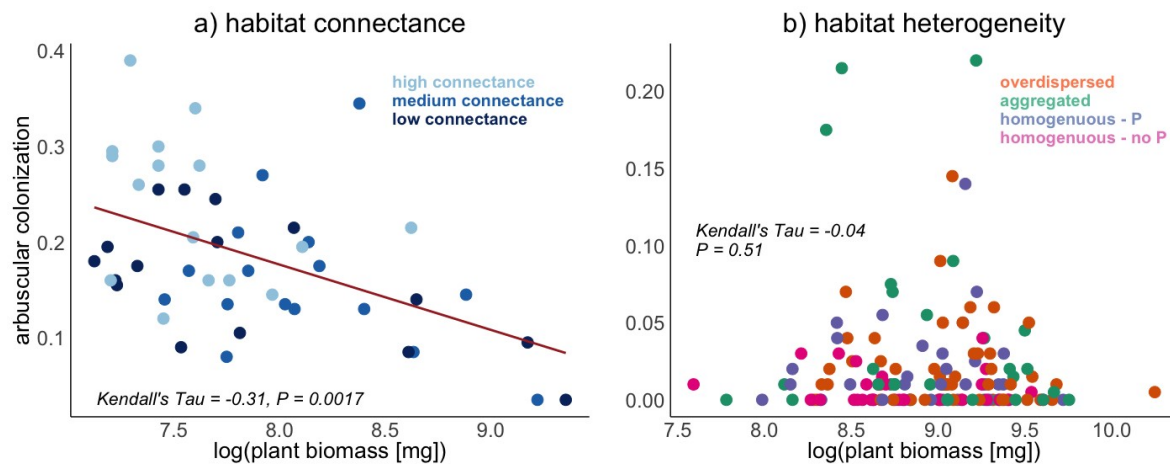


Fig. S4: Proportion of arbuscular colonization per root length and host plant biomass at the respective habitat patches. In *Experiment One* (a) arbuscular colonization was negatively correlated (Kendall's Tau, $P = 0.0017$) with plant biomass indicated by a linear regression line, whereas biomass affected arbuscular colonization only when considering within unit differences ($F = 7.6$, $P = 0.009$, see Appendix II for full ANOVA model results: Test 1.3). There was no effect of biomass on arbuscular colonization in *Experiment Two* (b).

Appendix I: Exploratory study & soil preparation

We used natural soil from an unmanaged grassland in Dallgow-Döberitz near Berlin (Germany, N:52.51°, E:13.14°) dominated by *Tanacetum vulgare*, *Daucus carota* and *Calamagrostis epigejos*. In a probe study, we grew *Plantago lanceolata* (i.e. bait plant) over four weeks to assess the richness of the indigenous AMF community in its roots in four soils via terminal restriction fragment length polymorphism (t-RFLP). To assay AMF community structure, we extracted DNA from 30 µg of freeze-dried root material with the PowerSoil DNA isolation kit (MoBio Laboratories Inc., Carlsbad, CA, USA) and amplified it with the NS31-AML2 primers (Lee et al. 2008, Liu et al., 2011) to which we had adapted (both primers) fluorescent tags and carried out independent restriction digests with two restriction enzymes (i.e. HinfI and HinfII (NlaIII) - under recommended restriction settings). Terminal peaks of purified amplicons (NucleoSpin® Gel and PCR Clean-up, Macherey-Nagel, Düren, Germany) were assayed on an ABI sequencer and were analysed for indigenous AMF richness. We collected fresh soil (with mean values of 0.13 % nitrogen, 1.75 % carbon and a pH of 6.7) from the site prior to each of the experiments. In each case, we sieved the soil with a semi-automatic sieving machine with a 1 cm mesh size to homogenize it and remove rock material. To eliminate AM fungal propagules from the unvegetated compartments, the soil was steam-sterilized at 60°C shortly before the experiment. We subsequently diluted the natural soil with sandbox sand in a proportion of 5:4 (soil:sand) for the unvegetated compartments. For the inserts we used undiluted unsterilized soil.

Appendix II: Model statistics

Abbreviations:

amf = total arbuscular mycorrhizal colonization
 vesicles = vesicular colonization
 arbuscules = arbuscular colonization
 coil = coil colonization
 func = functional colonization (coils + arbuscules)
 ratio = functional colonization ratio (functional over total colonization)
 treatment = Spatial arrangement of host patches
 biomass = aboveground dry biomass
 hyphae = hyphal density

Test 1.1: Exp1 - Total colonization

```
> summary(aov(amf~treatment+biomass+Error(factor(mesocosm)),data=roots2))
```

```
Error: factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.09900 0.04950    4.110 0.0592 .
biomass    1 0.00875 0.00875    0.727 0.4187
Residuals  8 0.09636 0.01204
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1 0.04088 0.04088    5.995 0.0195 *
Residuals 35 0.23865 0.00682
```

Test 1.2: Exp1 - Vesicular colonization

```
> summary(aov(vesicles~treatment+biomass+Error(factor(mesocosm)),data=roots2))
```

```
Error: factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.0002885 0.0001443    0.375 0.699
biomass    1 0.0003989 0.0003989    1.036 0.339
Residuals  8 0.0030808 0.0003851
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1 0.000179 0.0001788    1.069 0.308
Residuals 35 0.005852 0.0001672
```

Test 1.3: Exp1 - Arbuscular colonization

```
> summary(aov(arbuscules~treatment+biomass+Error(factor(mesocosm)),data=roots2))
```

```
Error: factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.06255 0.031277    5.516 0.0312 *
biomass    1 0.00959 0.009589    1.691 0.2297
Residuals  8 0.04536 0.005670
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1 0.03125 0.031250    7.144 0.0113 *
Residuals 35 0.15311 0.004374
```

Test 1.4: Exp1 - Coil colonization

```
> summary(aov(coils~treatment+biomass+Error(factor(mesocosm)),data=roots2))
```

```
Error: factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.0000292 1.458e-05  0.112  0.895
biomass    1 0.0001287 1.287e-04  0.990  0.349
Residuals  8 0.0010400 1.300e-04
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1 3.96e-05 3.962e-05  0.657  0.423
Residuals 35 2.11e-03 6.030e-05
```

Test 1.5: Exp1 - Functional colonization

```
> summary(aov(func~treatment+biomass+Error(factor(mesocosm)),data=roots2))
```

```
Error: factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.06213 0.031065  5.432 0.0323 *
biomass    1 0.01194 0.011940  2.088 0.1865
Residuals  8 0.04575 0.005719
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1 0.03352 0.03352  7.502 0.00963 **
Residuals 35 0.15635 0.00447
```

Test 1.6: Exp1 - Functional colonization ratio

```
> summary(aov(ratio~treatment+biomass+Error(factor(mesocosm)),data=roots2))
```

```
Error: factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.06792 0.03396  4.069 0.0604 .
biomass    1 0.05029 0.05029  6.026 0.0396 *
Residuals  8 0.06676 0.00835
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1 0.1128 0.11283  10.63 0.00248 **
Residuals 35 0.3714 0.01061
```

Test 2.1: Exp2 - Total colonization

```
>
summary(aov(amf~treatment+fertilizer+biomass+Error(as.factor(mesocosm)),data=roots3))
```

```
Error: as.factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.02120 0.01060  2.086 0.163765
fertilizer  1 0.13460 0.13460 26.496 0.000188 ***
biomass    1 0.00013 0.00013  0.026 0.875026
Residuals 13 0.06604 0.00508
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
fertilizer  1 0.2338 0.23382 85.010 9.7e-16 ***
biomass    1 0.0018 0.00183  0.665  0.416
Residuals 124 0.3411 0.00275
```

Aggregated vs. overdispersed

```
> summary(a<-aov(amf~factor(treatment)+fertilizer, data=roots3))
```

```
      Df Sum Sq Mean Sq F value Pr(>F)
factor(treatment)  1 0.00800 0.00800  1.851 0.19142
fertilizer        1 0.06441 0.06441 14.898 0.00126 **
Residuals        17 0.07350 0.00432
```

Test 2.2: Exp2 - Vesicular colonization

```
> summary(aov(vesicles~treatment+fertilizer+biomass+Error(as.factor(mesocosm)),
data=roots3))
```

```
Error: as.factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.000171 0.000086   0.154 0.858741
fertilizer  1 0.011691 0.011691  21.063 0.000507 ***
biomass     1 0.000000 0.000000   0.000 0.982632
Residuals  13 0.007216 0.000555
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
fertilizer  1 0.01128 0.011281  28.046 5.21e-07 ***
biomass     1 0.00005 0.000050   0.126 0.724
Residuals  124 0.04988 0.000402
```

Aggregated vs. overdispersed

```
> summary(a<-aov(vesicles~factor(treatment)+fertilizer, data=roots3))
      Df Sum Sq Mean Sq F value Pr(>F)
factor(treatment)  1 0.0000408 0.0000408   0.242 0.6294
fertilizer         1 0.0012800 0.0012800   7.571 0.0136 *
Residuals         17 0.0028742 0.0001691
```

Test 2.3: Exp2 - Arbuscular colonization

```
> summary(aov(arbuscules~treatment+fertilizer+biomass+Error(as.factor(mesocosm)),
data=roots3))
```

```
Error: as.factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.009991 0.004996   5.043 0.0239 *
fertilizer  1 0.003235 0.003235   3.266 0.0939 .
biomass     1 0.000384 0.000384   0.388 0.5443
Residuals  13 0.012876 0.000990
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
fertilizer  1 0.01431 0.014311  11.688 0.000852 ***
biomass     1 0.00003 0.000028   0.023 0.879020
Residuals  124 0.15183 0.001224
```

Aggregated vs. overdispersed

```
> summary(a<-aov(sqrt(arbuscules)~factor(treatment)+fertilizer, data=roots3))
      Df Sum Sq Mean Sq F value Pr(>F)
factor(treatment)  1 0.05596 0.05596   5.238 0.0352 *
fertilizer         1 0.03935 0.03935   3.682 0.0719 .
Residuals         17 0.18164 0.01068
```

Test 2.4: Exp2 - Coil colonization

```
> summary(aov(coils~treatment+fertilizer+biomass+Error(as.factor(mesocosm)),
data=roots3))
```

```
Error: as.factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
treatment  2 0.001878 0.0009391   3.805 0.050 .
fertilizer  1 0.000657 0.0006566   2.661 0.127
biomass     1 0.000033 0.0000333   0.135 0.719
Residuals  13 0.003208 0.0002468
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
fertilizer  1 0.006661 0.006661  45.188 5.83e-10 ***
biomass     1 0.000181 0.000181   1.231 0.269
Residuals  124 0.018279 0.000147
```

Aggregated vs. overdispersed

```
> summary(a<-aov(sqrt(coils)~factor(treatment)+fertilizer, data=roots3))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
factor(treatment)	1	0.00206	0.002057	0.998	0.33170
fertilizer	1	0.02725	0.027250	13.224	0.00204 **
Residuals	17	0.03503	0.002061		

Test 2.5: Exp2 - Functional colonization

```
> summary(aov(func~treatment+fertilizer+biomass+Error(as.factor(mesocosm)), data=roots3))
```

Error: as.factor(mesocosm)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
treatment	2	0.015738	0.007869	5.200	0.0219 *
fertilizer	1	0.006806	0.006806	4.498	0.0537 .
biomass	1	0.000644	0.000644	0.425	0.5257
Residuals	13	0.019672	0.001513		

Error: Within

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
fertilizer	1	0.04050	0.04050	25.514	1.53e-06 ***
biomass	1	0.00035	0.00035	0.223	0.638
Residuals	124	0.19683	0.00159		

Aggregated vs. overdispersed

```
> summary(a<-aov(sqrt(func)~factor(treatment)+fertilizer, data=data2))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
factor(treatment)	1	0.03278	0.03278	3.870	0.0657 .
fertilizer	1	0.06381	0.06381	7.532	0.0138 *
Residuals	17	0.14401	0.00847		

Test 2.6: Exp2 - Functional colonization ratio

```
> summary(aov(ratio~treatment+fertilizer+biomass+Error(as.factor(mesocosm)), data=roots3))
```

Error: as.factor(mesocosm)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
treatment	2	0.2909	0.14543	3.106	0.079 .
fertilizer	1	0.0037	0.00367	0.078	0.784
biomass	1	0.1754	0.17536	3.745	0.075 .
Residuals	13	0.6087	0.04683		

Error: Within

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
fertilizer	1	0.131	0.13056	2.419	0.122
biomass	1	0.065	0.06547	1.213	0.273
Residuals	124	6.693	0.05398		

Aggregated vs. overdispersed

```
> summary(a<-aov(ratio~factor(treatment)+fertilizer, data=data2))
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
factor(treatment)	1	0.1308	0.13082	2.876	0.108
fertilizer	1	0.0022	0.00221	0.049	0.828
Residuals	17	0.7732	0.04548		

Test 3.1 Exp 1: Hyphal density

```
> summary(aov(hyphae ~ biomass + treatment + Error(as.factor(mesocosm)), data=roots2))
```

Error: as.factor(mesocosm)

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
biomass	1	3.23	3.231	0.336	0.578
treatment	2	6.80	3.399	0.354	0.713
Residuals	8	76.88	9.610		

```
Error: Within
      Df    Sum Sq   Mean Sq F value Pr(>F)
biomass  1 7.500e-31 7.484e-31  0.451  0.506
Residuals 35 5.804e-29 1.658e-30
```

Test 3.2 - Exp 2: Hyphal density

```
> summary(aov(hyphae ~ biomass + treatment + Error(as.factor(mesocosm)),
data=roots3))
```

```
Error: as.factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1   58.7   58.74  1.020  0.330
treatment 2   37.8   18.89  0.328  0.726
Residuals 14  806.4   57.60
```

```
Error: Within
      Df    Sum Sq   Mean Sq F value Pr(>F)
biomass  1 1.870e-28 1.866e-28  1.182  0.279
Residuals 125 1.974e-26 1.579e-28
```

Test 4.1 – Exp 1: Functional ratio accounting for hyphal density

```
> summary(aov(ratio ~ hyphae + treatment + biomass +
Error(factor(mesocosm)),data=roots2))
```

```
Error: factor(mesocosm)
      Df   Sum Sq Mean Sq F value   Pr(>F)
hyphae  1 0.03330 0.03330   8.872 0.02056 *
treatment 2 0.07842 0.03921  10.446 0.00792 **
biomass  1 0.04698 0.04698  12.516 0.00950 **
Residuals 7 0.02627 0.00375
```

```
Error: Within
      Df Sum Sq Mean Sq F value   Pr(>F)
biomass  1 0.1617 0.16173  17.55 0.00018 ***
Residuals 35 0.3225 0.00921
```

Test 4.2 – Exp 2: Functional ratio accounting for hyphal density

```
> summary(aov(ratio ~ hyphae + biomass + treatment + fertilizer +
Error(as.factor(mesocosm)),data=roots3))
```

```
Error: as.factor(mesocosm)
      Df Sum Sq Mean Sq F value Pr(>F)
hyphae  1 0.0147 0.01466  0.303 0.5918
biomass  1 0.0328 0.03282  0.679 0.4259
treatment 2 0.4504 0.22519  4.662 0.0318 *
fertilizer 1 0.0012 0.00118  0.024 0.8784
Residuals 12 0.5796 0.04830
```

```
Error: Within
      Df Sum Sq Mean Sq F value Pr(>F)
biomass  1  0.006 0.00638  0.118 0.7320
fertilizer 1  0.168 0.16810  3.104 0.0805 .
Residuals 124  6.714 0.05415
```