Supplementary

# Power analysis

Our goal was to explore possible effect of biotic factors on commonly used community descriptors of secondary successional forsest. We focused on total bove-ground biomass (TAGB), species richness and abundance, which are strongly related to plant community dynamics (Lohbeck, Poorter, Martínez-Ramos, & Bongers, 2015). Therefore, we performed a manipulative experiment using randomized complete block (RCB) design. For our data we assumed simple one-way classification with single random effect for the block (random intercept model) of the following form:

where, represents community descriptor under treatement within a block , and is a distribution for with variance .

We expected, that experimental blocks separeted by a reasonably small distance, with similar local geological conditions (flat areas within homogenous primary forest matrix), should have low between-block variation in TAGB (Sierra et al., 2007), richness (Fricker et al., 2015), and species turnover rates (Condit et al. 2002). Moreover, to keep the within-block variation low, we planned to sample plant community at (5 5 m) plots, which should ensure that random small scale events during community assembly would not dominate.

To create a random dataset according to the model equation we evaluated each parameter value based on the literature, and we assumed specific magnitudes for each of the experimental treatment effect ( for , see the main text for details). For a single community descriptor (response) three parameter values are required: baseline average value ; within block (local) variation ); and between block (regional) variation .

As mentioned in the main text, for the insecticide (I) treated plots we anticipated a strong increase in TAGB, but at the same time equally strong decrease in richness, and species diversity. Here by strong effects we mean shift in the baseline value of the descriptor of approximately 15% under a given treatment. We expected that high herbivory treatment (H2) would strongly decrease values of all of the considered community characteristics. Similarily we assumed, that predator exclosure and moderate herbivory increase would have negative effect on the community descriptors. However, these effects should be relatively weaker than those of the high herbivory treatment, but at the same time stronger than the effects of predator exclusion. We did not expect fungicide treatment to impact plant biomass, but only to decrese the abundance and species richness of the experimental communities.

Based on the above assumptions we estimated number of blocks optimal to obtain 80% statistical power of our tests. We also explored how different levels of variation between blocks , and residual variation affect the power. We also sensitivity analysis to explore how error of our estimates would affect its value. All randomizations and power calcuations were performed using the *simr* package (Green & MacLeod, 2016) in R.

## Biomass

### Estimates of variation

In a comprehensive review by Martin, Newton, and Bullock (2013) authors compiled data on TAGB values from 607 secondary forest sites. From this dataset we were able to extract only two estimates of TAGB for plant community after one year of regeneration after abandonment. TAGB for these two plots averaged at 12 Mg ha (which gives 30 kg for the experimental plot size used in our study). However, these plots were abandoned pastures, which may negatively affect initial biomass accumulation rates. Different study by Mascaro et al. (2005) in wet tropical forest succession in canopy gaps reported average 78 15 Mg ha (195 kg 25 m) TAGB after one year following a hurricane disturbance. We expected, that TAGB for tropical forest regenerating after small slash-and-burn cultivation within a primary forest matrix, should fall somewhere between the above range. Therefore for the theoretical distribution of plant biomass in a 25 m plots we safely assumed log-normal distribution with = 100 kg.Moreover, by design we tried to minimise unpredicted differences in initial conditions for regeneration, which should keep the variation between and within the blocks small. To capture that assumption we set = = 10.0240476 kg. Fig. 1 shows a distribution of TAGB values under the above assumptions.

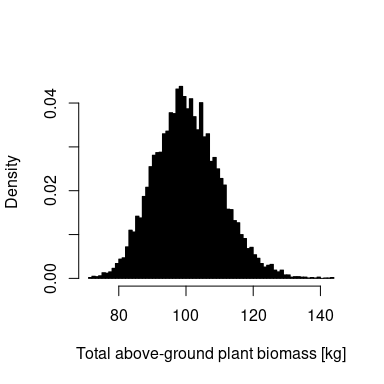
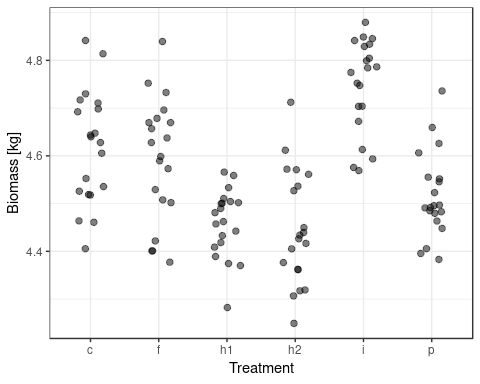


Figure 1. Histogram of 10^{4} values of total above-ground biomass (TAGB) in a hypothesized one year old successional tropical forest community at a experimental plot. Densities follow the log-normal distribution with = 100 kg, and = 10 kg.

### Randomization

With the above approximations of real , , and the effect size of 15 we created a random dataset with an arbitrary number of blocks, each having 6 experimental treatment (including control), and examined sample size necessary to obtain 80% statistical power.



# breaks=c(3,4,5,6,7,8,9,10,11,12)  
pc2 <- powerCurve(bioexp, along = "gard", breaks=c(3,4,5,6,7,8,9,10),   
 nsim=mcrands, progress = F)

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plot(pc2)

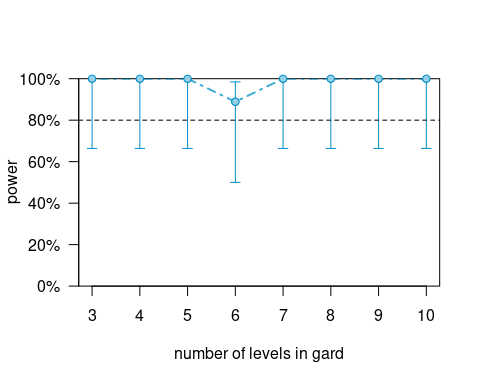


Figure 2. A) Random dataset generated using log-normal mean 100, between-block standard deviation $ = $ 10.02 and within-block standard deviation 10.02. Effect sizes for treatments are: 0 for fungicide treatment (F), -15 for high herbivory increase (H2), 7.5 for predator (P) removal, -11.25 for moderate herbivory increase (H1), and 15 for insecticide treatment (I). B) Power curve for the above dataset with varying number of blocks with confidence intervals for the power estimates based on 9 randomizations.

For the above assumptions we obtained 80% probability of detecting existing effects already with six experimental blocks.

## Species richness and woody plant abundance

### Estimates of variation

We expected to find approximately 30 5 plant species (herbaceous and woody plants) per plot (Leps, personal communication). Based on Whitfeld et al. (2012) and from our personal experience we predicted, that we would find (similarily to the number of species) approximately 30 5 stems per experimental plot. We assumed Poisson distribution for both the number of species and the stem abundance.

### Randomization

We again created a random dataset for number of species and stem abundance. In the same manner we explored the number of blocks necessary to detect 6 species/stems shift in the baseline value at 80% statistical power.



pc2 <- powerCurve(richexp, along = "gard", breaks=c(3,4,5,6,7,8,9,10),   
 nsim=mcrands, progress = F)

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plot(pc2)

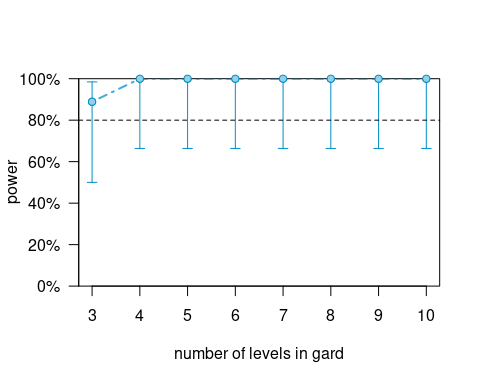
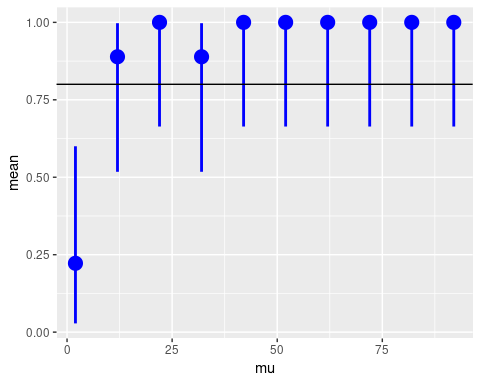
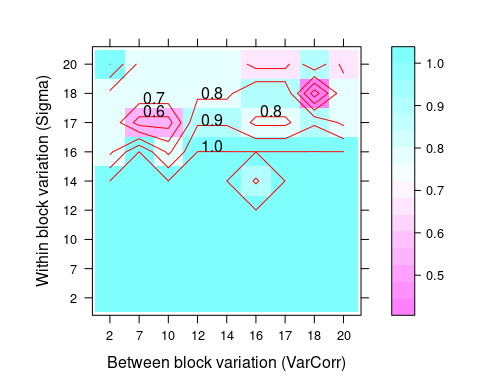


Figure 3. A) Random dataset generated using the Poisson distribution for the mean 30, between-block standard deviation $ = $ 10.02 and within-block standard deviation 10.02. Effect sizes for treatments are: 0 for fungicide treatment (F), -6 for high herbivory increase (H2), 3 for predator (P) removal, -4.5 for moderate herbivory increase (H1), and 6 for insecticide treatment (I). B) Power curve for the above dataset with varying number of blocks with confidence intervals for the power estimates based on 9 randomizations.

## Sample size, within-block and between-block variation

At the last step we analyzed sensitivity of statistical power to the values of our variance estimates. For the TAGB any value of within blocks variation below 15 kg ensures acceptable statistical power. For the richness and abundance an asumptions of the Poisson distribution indicates, that the variance at the plot is equal to the average number of species/stems and between block variation should not affect the power. Therefore, we plotted the power in relation with the average richness/stem abundance for a plot. Statistical power increased with average values for the plot, and estimates above 25 had estimated power larger than 80%. Even after inflating between- and within-block variances we were able to met 80% power requirement for our test.

 Figure 4.

# Evaluation of the treatments efficiency

Despite our considerable effort to define and execute experimental treatments, we identified a few pitfalls in our methods. During evaluation of the effectiveness of the ant eradication treatment, we did not find a significant reduction in ant abundance on the ground. However, harvested vegetation generally had low abundance of small sized, non-predatory canopy ants, suggesting that the ant eradication was successful for aggressive and mobile dominants most likely to attend tuna baits.

Fungicide used in our experiment can potentially accumulate in the soil, which at high concentrations can suppress ammonification and nitrification processes (Walia, Mehta, Guleria, Chauhan, & Shirkot 2014). However, we expected that these undesirable effects would be minimized due to the short half-life times of mancozeb (Xu 2000) and easy biodegradability in tropical soil conditions (Racke et al. 1997). In addition to the predicted increase of arachnid abundance from natural enemy suppression, netting used for the exclosure constructions could potentially boost the abundance of web-building spiders. The number of blocks used for the experiments was limited by the number of suitable locations available and our ability to maintain and sample them. Therefore, some effects may not have been detected and increased sample size could result in higher statistical power of performed tests.

Herbivore damage was significantly reduced only at insecticide treated plots. However, as showed in Poorter, van de Plassche, Willems, and Boot (2004) “accumulated level of herbivory is therefore likely to underestimate the herbivory rate of early successional species, and to overestimate the herbivory rate of late successional species”.

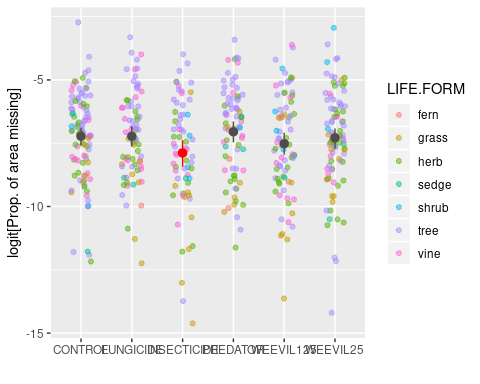


Figure X. Herbivory rates measured as a proportion of leaf area missing due to insect herrbivores feeding Proportional vales were logit transformed to ensure normal error distribution. Points and lines represent mean and 95% bootstraped CIs. Red color indicates significant difference in means compared with the control treratment at the = 0.05.

# Supplementary Literature

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