

## Annex B: Bd infection intensity treatment group comparison using linear mixed models.

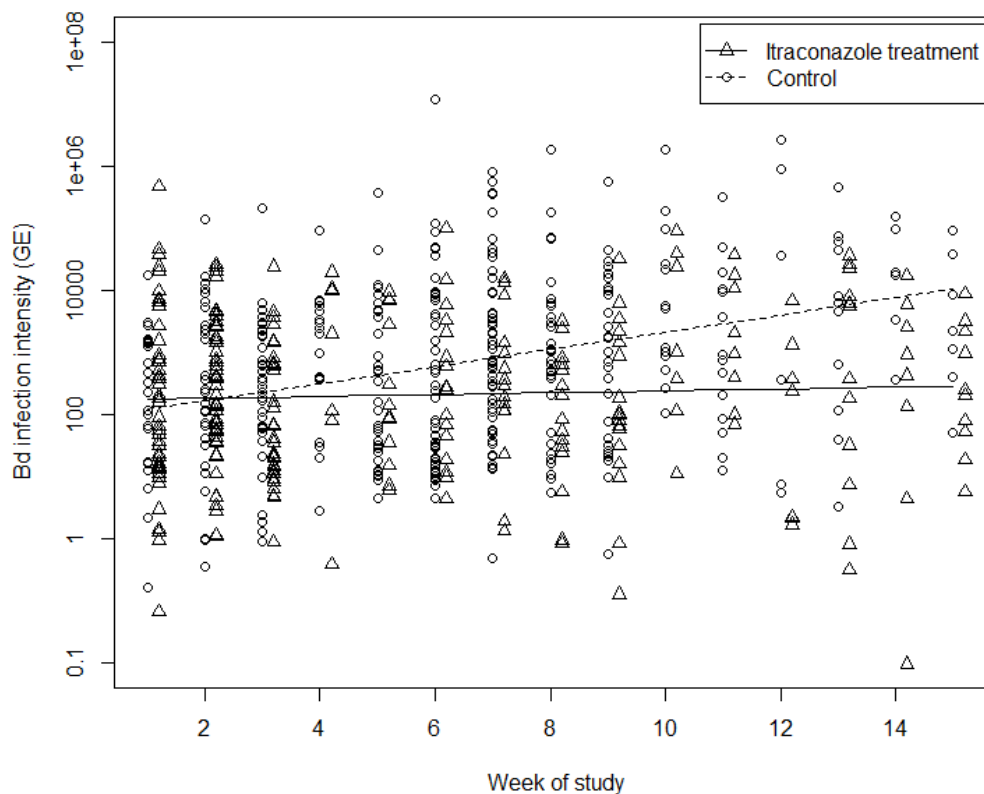
### During treatment comparison (weeks 1-15):

Bd infection intensities in the IT and control groups were compared using a linear mixed model constructed with package {lme4} (Bates et al. 2015) in R. Treatment group and time were included as fixed effects and frog ID was included as a random effect. Models are ranked using AIC corrected for small sample size (AICc). Standard errors for variable estimates were produced using 10000 simulations of the model in the {arm} package (Gelman and Su 2015) in R.

**Table 1: Model selection table for linear mixed effects model of Bd infection intensity (Genomic equivalents) comparison between the IT and control groups during treatment (weeks 1-15). Model selection was carried out using AICc.**

Fixed effects	Random effects	K	AICc	Delta AICc	AICc Weight	Log likelihood
Group*Time	Frog ID	6	2147.125	0.0000	0.9997	-1067.496
Group+Time	Frog ID	5	2163.159	16.0340	0.0003	-1076.532
Group	Frog ID	4	2171.464	24.3394	0.0000	-1081.700
Time	Frog ID	4	2182.987	35.8620	0.0000	-1087.462
.	Frog ID	3	2196.183	49.0577	0.0000	-1095.072

During the treatment period, there is clear support for the top model over the other models (AICc weight = 0.9997). We therefore use only parameter estimates from this model in the graph below.



**Figure 1. Bd infection intensity comparison (Genomic equivalents) between the IT and control groups during the treatment period.** The y-axis is logged in order to display data which varies over many orders of magnitude. Linear mixed model prediction for top model (treatment group\*time) is plotted. IT group data are plotted with an x-offset of +0.1 for display purposes.

### Post treatment comparison (weeks 16-24):

**Table 2: Model selection table for linear mixed effects model of Bd infection intensity (Genomic equivalents) comparison between the IT and control groups after treatment (weeks 16-24). Model selection was carried out using AICc.**

Fixed effects	Random effects	K	AICc	Delta AICc	AICc Weight	Log likelihood
.	Frog ID	3	685.4048	0.0000	0.5772	-339.6334
Group	Frog ID	4	686.2000	0.7953	0.3878	-338.9844
Time	Frog ID	4	692.5821	7.1773	0.0160	-342.2211
Group+Time	Frog ID	5	693.1020	7.6972	0.0123	-341.4810
Group*Time	Frog ID	6	694.3212	8.9164	0.0067	-340.9150

As no model received overwhelming support (AICc weight of top model = 0.5772), we considered all models with a delta AIC <7 for inference (Burnham & Anderson, 2002). The top model had no variation in group or time, and the only model with a delta AIC <7 included group dependency. There was, however, very weak evidence for a group difference in Bd infection intensity in the post treatment period (summed Akaike weight=0.401; evidence ratio=0.7). The model averaged estimate for the difference in Bd infection intensity between the control and IT groups was 1.45 GE (Unconditional SE=1.82), suggesting that any difference was not ecologically important and after treatment ended, there was no prolonged benefit of treatment with itraconazole.

#### References:

Bates, D., Machler, M., Bolker, B., and Walker, S. 2015. Fitting linear mixed-effects models using {lme4}. *Journal of Statistical Software* **67**: 1-48. doi:10.18637/jss.v067.i01

Burnham, K.P., and Anderson, D.R. 2002. *Model selection and multimodel inference: a practical information-theoretic approach*. Springer-Verlag, New York.

Gelman, A., and Su, Y-S. 2015. *arm: data analysis using regression and multilevel/heirachical models*. R package version 1.8-6. <http://CRAN-R-project.org/package=arm>