Mixed models

Data with different levels of aggregation (multiple measures of the same individual), the identifier of the level of aggregation (the individual) is included as a random intercept (sometimes random slope).

My work:

Since multiple measures of the same species, species is treated as a random intercept (?) and random slope?

Random slope of environmental variables within species with correlated intercepts

|  |  |
| --- | --- |
| (1|species) | random species intercept |
| (x|species) = (1+x|species) | random slope of env within species with correlated intercept |
| (0+x|species) = (-1+x|species) | random slope of env within species: no variation in intercept |
| (1|species) + (0+x|species) | uncorrelated random intercept and random slope within species |
| (1|site/block) = (1|site)+(1|site:block) | intercept varying among sites and among blocks within sites (nested random effects) |
| site+(1|site:block) | *fixed* effect of sites plus random variation in intercept among blocks within sites |
| (x|site/block) = (x|site)+(x|site:block) = (1 + x|site)+(1+x|site:block) | slope and intercept varying among sites and among blocks within sites |
| (x1|site)+(x2|block) | two different effects, varying at different levels |
| x\*site+(x|site:block) | fixed effect variation of slope and intercept varying among sites and random variation of slope and intercept among blocks within sites |
| (1|species1)+(1|species2) | intercept varying among crossed random effects (e.g. site, year) |

The random intercept (species) allows the separation of total variance in the dependent variable (presence) into a within and between subject (individual) variance component. Fixed predictors (environment and envt:trait interaction) investigate how much of total variation in dependent variable (presence) is explained by the fixed predictor while accounting for intercorrelated measures of the same species.

Model <- lmer (present ~ SST + TSM+ PAR +

depthsp:SST + depthsp:TSM + depthsp:PAR +

wavessp:SST + wavessp:TSM +wavessp:PAR +

turbiditysp:SST + turbiditysp:TSM +turbiditysp:PAR +

(1 + SST + TSM + PAR |species),

data= model.covs,family=binomial(link=logit),

control=list(maxIter=10000))

|  |  |
| --- | --- |
| (1|species) | random species intercept |
| (env|species) =  (1+env|species) | random slope of env within species with correlated intercept |
| (0+env|species) =  (-1+env|species) | random slope of env within species: no variation in intercept |
| (1|species) + (0+env|species) | uncorrelated random intercept and random slope within species |
| (1|site/block) =  (1|site)+(1|site:block) | intercept varying among sites and among blocks within sites (nested random effects) |
| site+(1|site:block) | *fixed* effect of sites plus random variation in intercept among blocks within sites |
| (env|site/block) =  (env|site)+(env|site:block) =  (1 + env|site)+(1+env|site:block) | slope and intercept varying among sites and among blocks within sites |
| (env1|site)+(env2|block) | two different effects, varying at different levels |
| Env\*site+(env|site:block) | *fixed* effect variation of slope and intercept varying among sites and random variation of slope and intercept among blocks within sites |
| (1|species1)+(1|species2) | intercept varying among crossed random effects (e.g. site, year) |

Species presence

Trait presence

Environment

Why aren’t traits their own fixed effects?