Multilevel Urban Tree Allometric equations

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Model

likelihood

$$y_{iqsc} \sim Gamma(\mu_{iqsc}, \alpha_y)$$

$$\mu_i = \beta_{igsc}^0 + \beta_{igsc}^1 (1 - \exp(-\beta_{igsc}^2 x_i^{\beta_{3sc[i]}}))$$

where:

 y_{igsc} is the diameter at breast height of tree i and has a gamma distribution with mean, μ_{igsc} , and shape, α_{y} .

i = 1, ..., n_{sc} ; where n_{sc} is the number of trees sampled for species, s, and city, c. g = 1, ..., G; where G is the number of genera (G) s = 1, ..., S_g ; where S_g is the number of species in genus g.

 $\beta_{\mathrm{igsc}}^{0}$ is the intercept, or the diameter of a tree at time of transplanting.

 β_{igsc}^1 (plus $\beta_{0\text{igsc}}$) is the asymptote of the sigmoidal weibull curve. For most species there are no data near the true asymptote and so this parameter should be considered a highly uncertain estimate of the real maximum dbh of a tree. Pragmatically, it models/causes the slowing of the diameter growth of a tree as it ages.

 β_{igsc}^2 and β_{igsc}^3 affect the rate of growth. β_{igsc}^2 provides flexibility to have slow or fast growth at young ages.

All β 's must be positive and they are likely correlated with one another, especially β_{igsc}^1 and β_{igsc}^3 . Without very old trees that are close to their asymptotic dbh, it is harder to separate these two parameters.

for each beta, j = 0,1,2, genus, g, species, s, and each city, c.

$$\beta_{igsc}^j = \beta_0^j + \gamma_{igs}^j + \delta_{ic}^j$$

for $beta^3$

$$\beta_{igsc}^3 = \beta_0^3 + \tau_1 * Precip_c + \tau_2 * GDD_c + \tau_3 * (Precip_c * GDD_c) + \gamma_{igs}^3 + \delta_{ic}^3$$

where β_0^j is the mean for β coefficient β_j . γ_{js} is the contribution of genetic (species) effect for species s on β_j . δ_{jc} is the city effect for city c on β_j .

Species effect:

$$\gamma_{igs}^j \sim N(\gamma_{ig}^j, \sigma_{is}^j)$$

Genus effect:

$$\gamma_{jg[i]} \sim N(0, \sigma_{jg[i]})$$

for each j. City random effect:

$$\delta_{jc} \sim N(0, \sigma_{jc[i]})$$

Priors:

Just describe the priors roughly, gamma, half normal etc. Then put the details in an appendix.

Priors were selected to be slightly informative and make very biologically unreasonable

parameters improbable. The quantity of data overwhelms the priors, but the relatively narrow priors also helps with sampling.