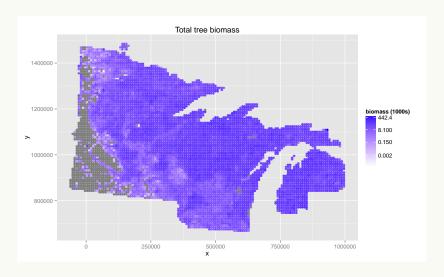
Spatial smoothing of zero-inflated abundance data

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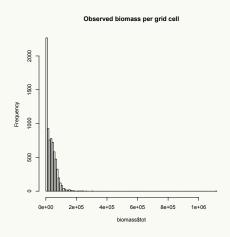
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A look at the data



A look at the data

The data is non-negative with a long right tail, suggesting a log transformation or a gamma model.



A look at the data

The data is the total tree biomass per grid cell from the Public Land Survey of the upper midwest.

- Observations are at corner points (90 per grid cell)
- Want to know the actual biomass on the grid cell from these local samples
- Goal is to calculate the total biomass of each taxon across the upper midwest
- Many grid cells have zero observed biomass

Our approach

Recall our approach

Want a model for which power-law variation (long right tail) and exact zeroes are handled naturally, not as an exception.

- We use the Tweedie family of distribution
- Tweedie distribution has a tuning parameter that slides smoothly from Poisson to Gamma distribution
- Estimate that tuning parameter via MLE

Drawing biomass samples

- Create a model for each taxon
- ▶ Use MLE matching to estimate $\hat{\theta}$
- Use parametric bootstrap to get draws from biomass
- distribute draws from the "total" taxon based on the relative biomass of the other taxa

Complications

- Smoothing biomass via a GAM for Wisconsin with 500 knots:
 - Too few knots
 - Takes too long to complete (some taxa never finished running)
- Possible solution: adapt R-INLA for Tweedie likelihood

Complications

- ► Incomplete taxa:
 - Cherries
 - Willow
 - Walnuts
 - Hickory
 - Fir
 - Spruce
 - Cedar
 - Hemlock
 - Pine
 - Birches

Complications

- ▶ Complete taxa:
 - tot
 - Beech
 - Ironwoods
 - Basswood
 - Ashes
 - Elms
 - Poplar
 - Tamarack
 - Maple
 - Oaks