Species richness estimation revisited – An effective computation method

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Materials covered in this presentation will be uploaded to `https://github.com/songsqian/missingSP`

In This Talk

- A Bayesian hierarchical model for Estimating biodiversity/species richness
    - An efficient computation strategy
    - Capable of pooling data from multiple sources
- Model evaluation (comparing to other existing methods)
- Potential of evaluating biodiversity changes over time and space
- Discussions

Species Richness – difficult to observe and estimate

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  - Physically
  - Analytically
- Species richness is always an approximation
  - We can never observe the true richness

A Mixture Model – Data format

- Fisher et al (1943)
- Data format –
  - y_i – number of individuals from species/taxon i
  - Often recorded as n_j number of species (n) with j individual(s) in the sample.

A Mixture Model – Parametric model

- A Poisson-gamma mixture model

$$\begin{aligned} y_i \mid \lambda_i &\sim \mathit{Pois}(\lambda_i) \\ \lambda_i &\sim \mathit{gamma}(\alpha, \beta) \end{aligned}$$

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- Predictive distribution of y_i: a negative binomial (NB) model

$$\pi(y_i) = \int_{\lambda_i} \pi(y_i \mid \lambda_i)\pi(\lambda_i) d\lambda_i$$

$$\Pr(y_i = k) = \frac{\Gamma(\alpha + k)}{\Gamma(\alpha) k!} \left(\frac{\beta}{\beta + 1}\right)^{\alpha} \left(\frac{1}{\beta + 1}\right)^{k}$$

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- Reparameterizing: $\mu = \alpha/\beta$ and $r = \alpha$:

$$\Pr(y_i = k) = \frac{\Gamma(r + k)}{\Gamma(r) k!} \left(\frac{r}{\mu + r}\right)^{r} \left(\frac{\mu}{\mu + r}\right)^{k}$$

Meanings of μ and r

- μ – mean of y, average number of individuals among all species
- r – the dispersion parameter, measuring the differences/variance in number of individuals among species
    - A larger r – more evenly distributed and less clustering
    - A smaller r – more clustering

A Mixture Model – Species richness

- Under the NB model

$$\Pr(y = 0) = p_0 = \left(\frac{r}{\mu + r}\right)^r$$

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- Under the NB model

$$\Pr(y = 0) = p_0 = \left(\frac{r}{\mu + r}\right)^r$$

- The total number of species S:

$$S = S_{obs} + S_0 = S_{obs} + Sp_0$$

or

$$S = S_{obs}/(1 - p_0)$$

A Mixture Model – Hierarchical modeling

- Combining data from multiple sources (l)

$$\begin{aligned} y_{il} &\sim NB(\mu_l, r_l) \\ \log(\mu_l) &\sim N(\theta, \tau^2) \end{aligned}$$

Data for Model Evaluation

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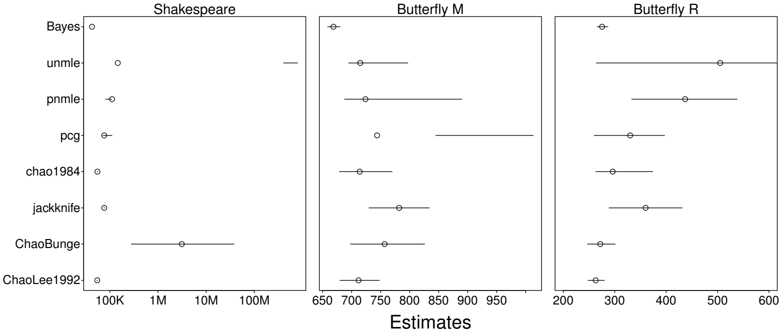
- Shakespeare's Vocabulary – A total of 884,647 words in Shakespeare's known works tabulated in n_j for $j = 1, \cdots, 100$. For words with > 100 appearances: one recorded as appeared 1,305 times and 845 appeared 815 times.

Model Evaluation – Comparisons

Comparing to 7 methods included in R package `SPECIES`



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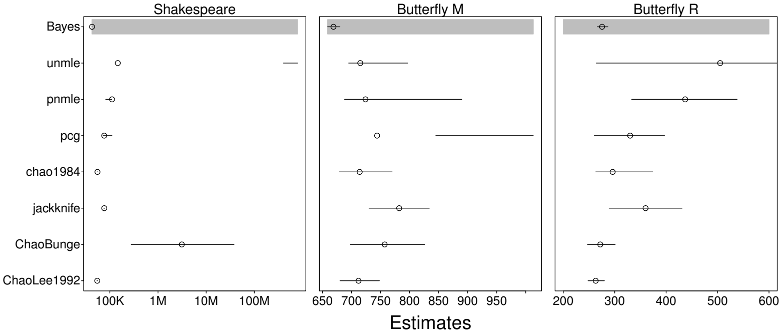
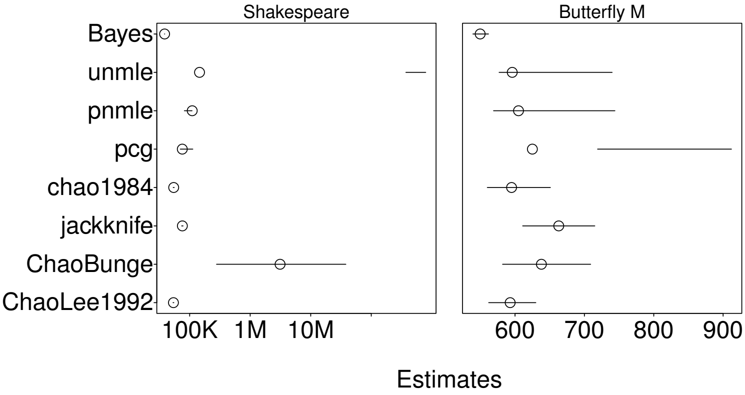


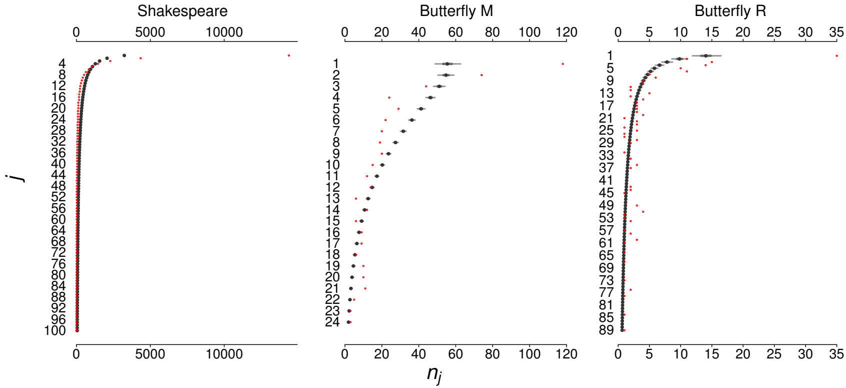
Model Evaluation – Comparisons

Using only accurately recorded data from SK and Butterfly M



Model Evaluation – Goodness-of-fit

Posterior simulation: model predicted number of species n_j with $j, j = 1, 2, 3, ..., J$ specimens



Data for Illustrating BHM

- USGS trawl fishing data for evaluating fish recruitment

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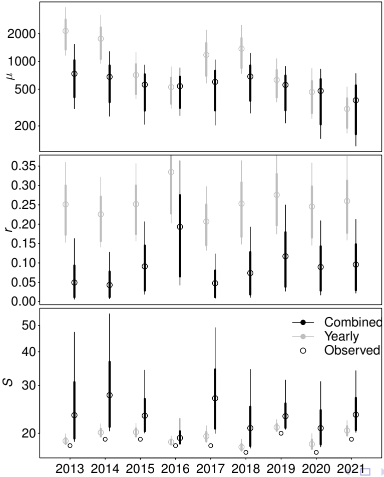
- USGS trawl fishing data for evaluating fish recruitment
  - Data used 2013-2021, age-0 catch data
  - Numbers of species represented in each year's data are small ($\sim 10 - 20$)

Combining Data – BHM

Comparing results from BHM and individual year fits



Conclusions

- Estimated S is comparable to competing MLE-based methods when data were recorded accurately
- Much faster computation and smaller estimation uncertainty
- Combining data from similar sources is effective in evaluating changes in community structure

Parametric versus Nonparametric

- Parametric models are more sensitive to data error than nonparametric ones
- Issues with the Butterfly M and Shakespeare data sets are no longer important – record all samples accurately

The Dispersion Parameter r

- Likely overestimated (underestimate the dispersion) with small sample size
- BHM is a sensible way to share information among multiple sources of data

“True” Richness Impossible

- Cannot compare the model estimate to the observed – true richness unobservable
- Model parameters μ and *r* describe species composition structure
  - Changes of μ and *r* over time or space can be more informative

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Thank You

Questions/Comments?

Computational details are at `github.com/songsqian/missingSp`