

# New and old algorithms for estimating genotype diversity

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## Genotype diversity

An important parameter for species with mixing modes of reproduction

## Current estimators

Richness: e.g. Shannon, Stoddart and Taylor, Gleason

Evenness: e.g. Nei and Simpson

## Good estimator

Considers both richness and evenness

Ranges between 0 and 1

Has high resolution for various species

Be insensitive or less sensitive to sample sizes and replications



## New algorithm

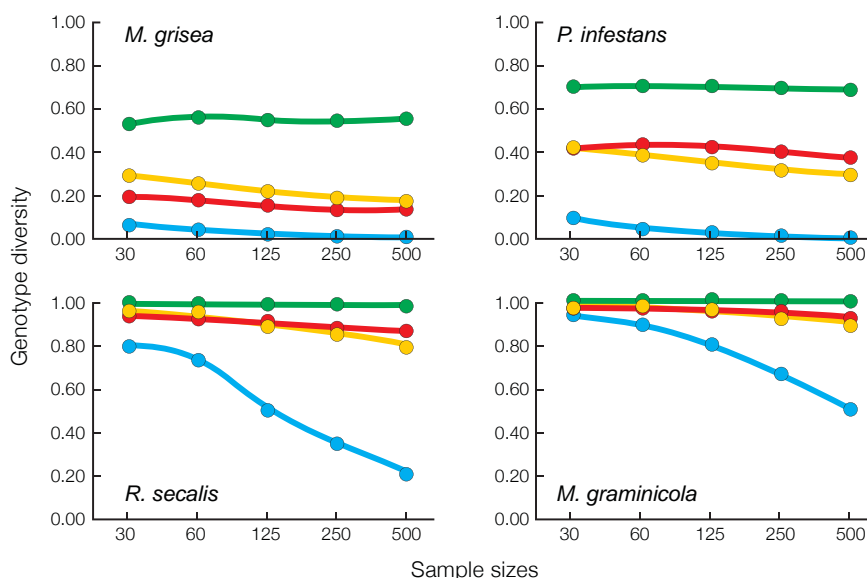
$$\frac{\ln(k)}{\ln(N)} \left[ 1 - \sum_{i=1}^k p_i^2 + \frac{2N-k}{N^2} \right]$$

Where  $N$ ,  $k$  and  $P_i$  are sample size, number of genotypes and the frequency of  $i$ th genotype, respectively.



## Applications

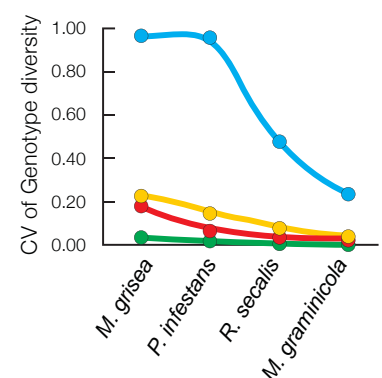
Fig. 1 Genotype diversity



## Key

- New
- Simpson
- Stoddart
- Shannon

Fig. 2 Coefficients of variance over resample



## Conclusions

**Simpson:** Low resolution, least sensitive to resampling

**Stoddart and Taylor:** No resolution for low diversity, very sensitive to resampling

**Shannon:** Good resolution, medium sensitive to resampling

**New:** Better resolution for low diversity and slightly less sensitive to resampling than Shannon