

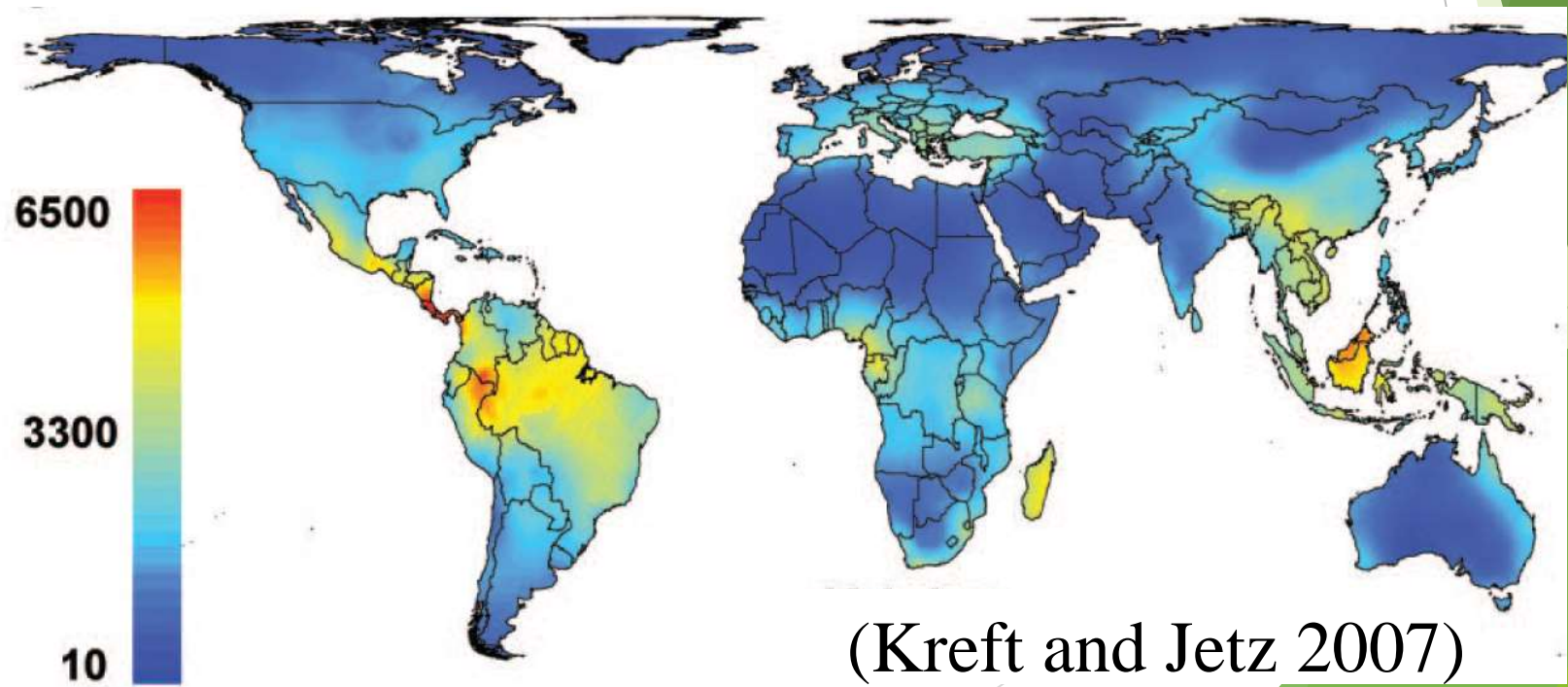
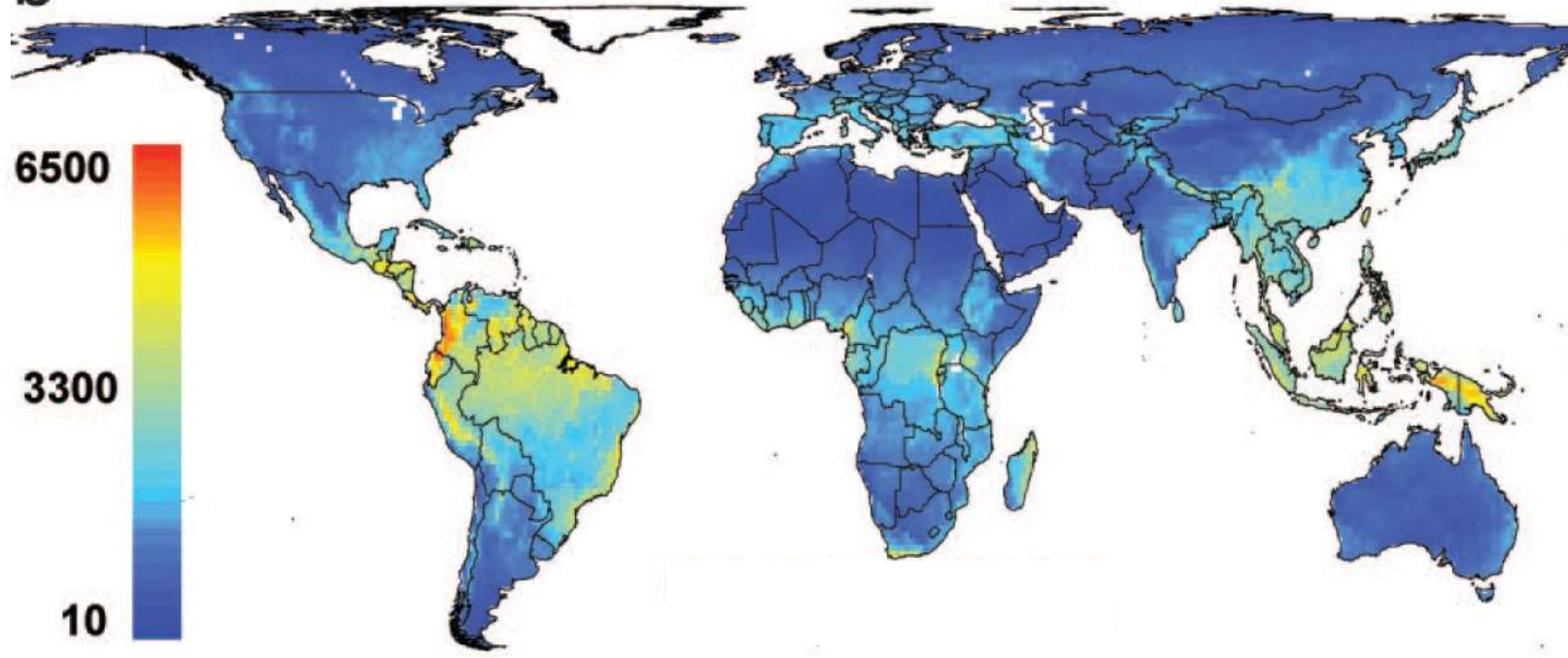
Estimation of broad-scale species richness: individual-based or spatially-constrained rarefaction?

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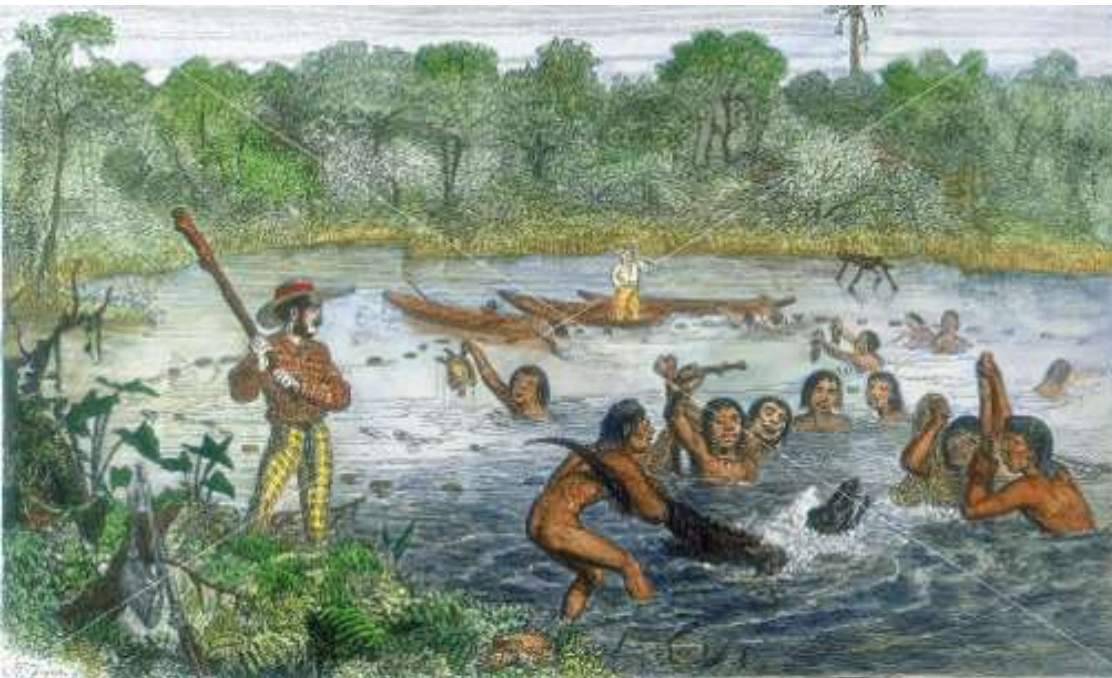
Vascular plant richness



(Kreft and Jetz 2007)

The Wallacean shortfall:

“paucity of information on the geographic variation of nature”
(Lomolino et al. 2010)



Alfred Russell Wallace and Henry Walter Bates hanging out in 1848 by Belém (Pará), Brazilian Amazonia.



Individual-based rarefaction

The simplest rarefaction approach to estimate broad-scale species richness using data from natural history museum and herbarium specimens is known as individual-based rarefaction (Gotelli & Colwell 2001).

Under this approach $E[S_n]$ is estimated from multiple random samples of n specimens drawn from the pool of N specimens collected in a sampling unit.

Ideally, the pool of N specimens collected in a sampling unit would be a random sample from the (potentially very large) set of individuals occurring in the sampling unit.

Spatially-constrained rarefaction

Spatially constrained rarefaction aims to control for the spatial arrangement of sampling activities across a sampling unit (Chiarucci et al. 2009, Bacaro et al. 2012).

In spatially constrained rarefaction the spatial proximity of individuals is considered when drawing subsets of n individuals from the pool of all N individuals.

In particular, these subsets are obtained by drawing individuals that are near each other in geographic space.

Research hypothesis:

When estimating broad-scale species richness using data from natural history museum and herbarium specimens, spatially-constrained rarefaction is less biased than individual-based rarefaction, because it reduces over estimation of species richness due to spatial aggregation of sampling activities.

Definitions

$E[sn.r]$

$E[Sn.scr]$

$Sn.a$

Study system and general methods

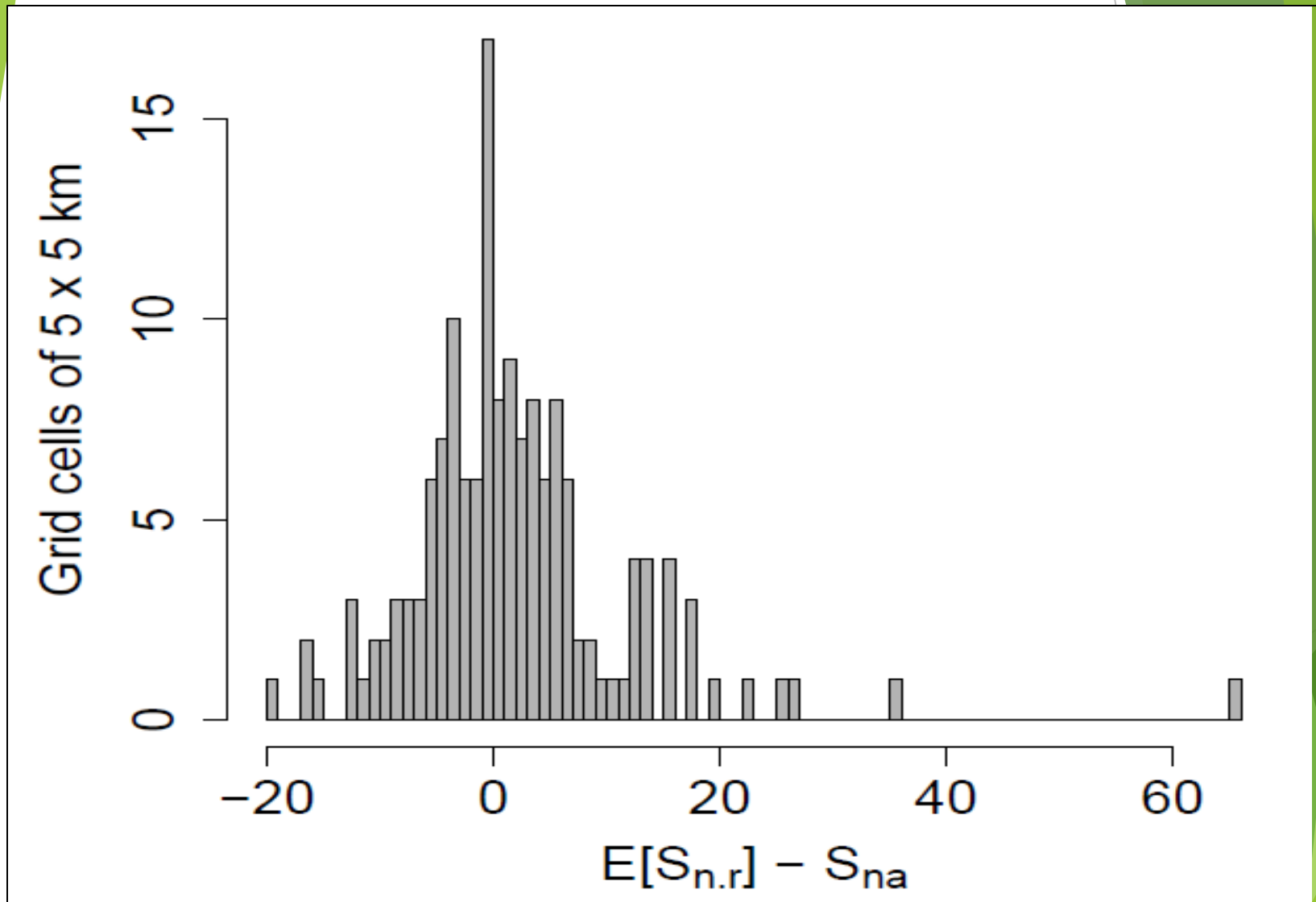
- The Nicaragua flora
 - The flora of Nicaragua is highly diverse, for our study system we used the entire vascular plant flora which includes both woody and herbaceous species.
- Data source and cleaning
 - Tropicos database
 - What was excluded for the data
- The spatial scale and number of grid cells used
 - 5km x 5km grid cells
 - At least 200 specimen records
- How species richness was estimated
 - Use of accumulation curves
 - Individual rarefaction
 - Spatial constrained rarefaction

Prediction 1

on average, across grid cells, $E[S_{nr}] - S_{na} > 0$

The first prediction states that, on average across grid cells, $E[S_{nr}]$ is larger than S_{na} . This prediction derives from the fact that accurate rarefaction curves are statistical expectations of accumulation curves (Gotelli & Colwell 2001).

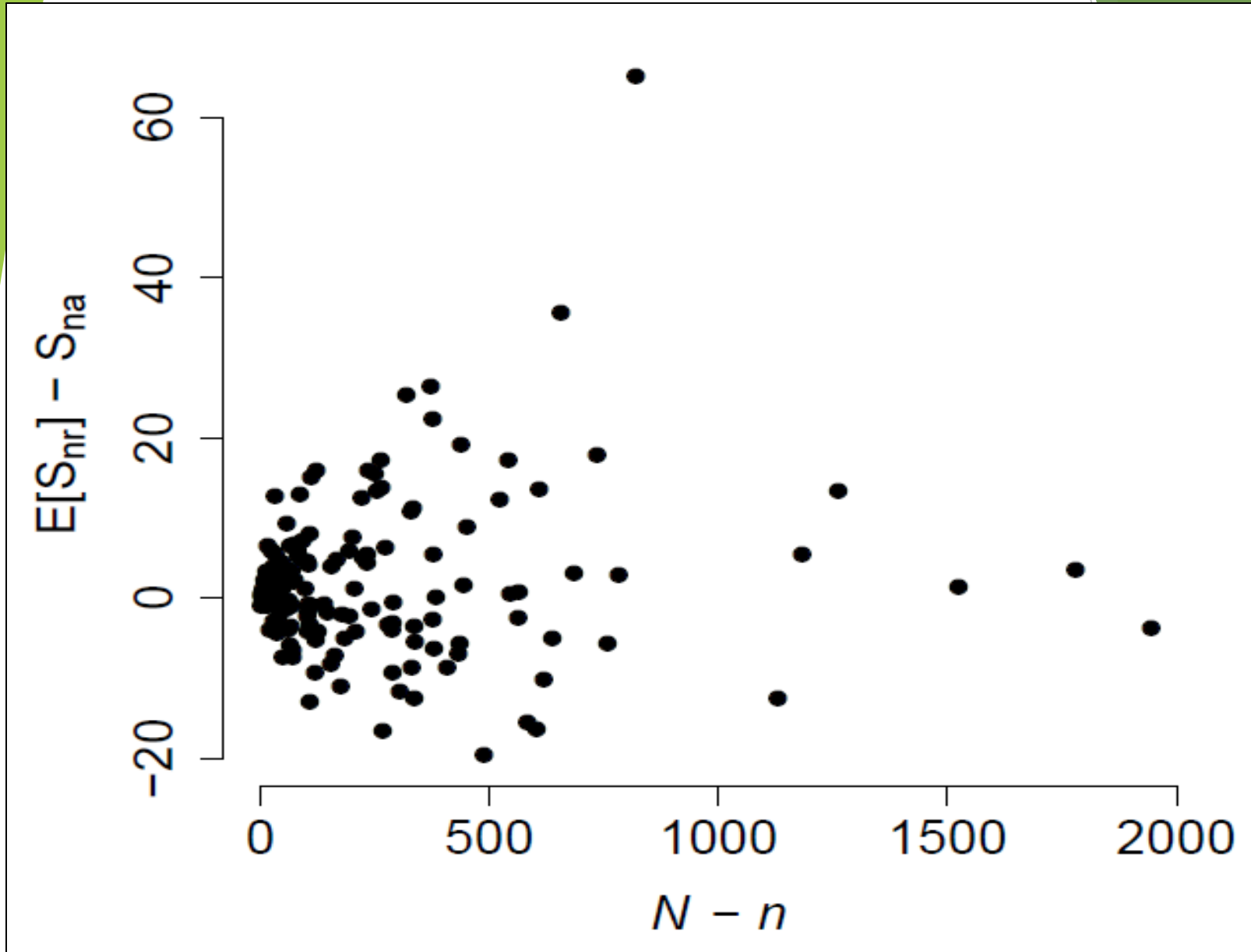
Results of testing prediction 1



Prediction 2

The relationship between $[S_{n.r}] - S_{n.a}$ and $N - n$ is positive

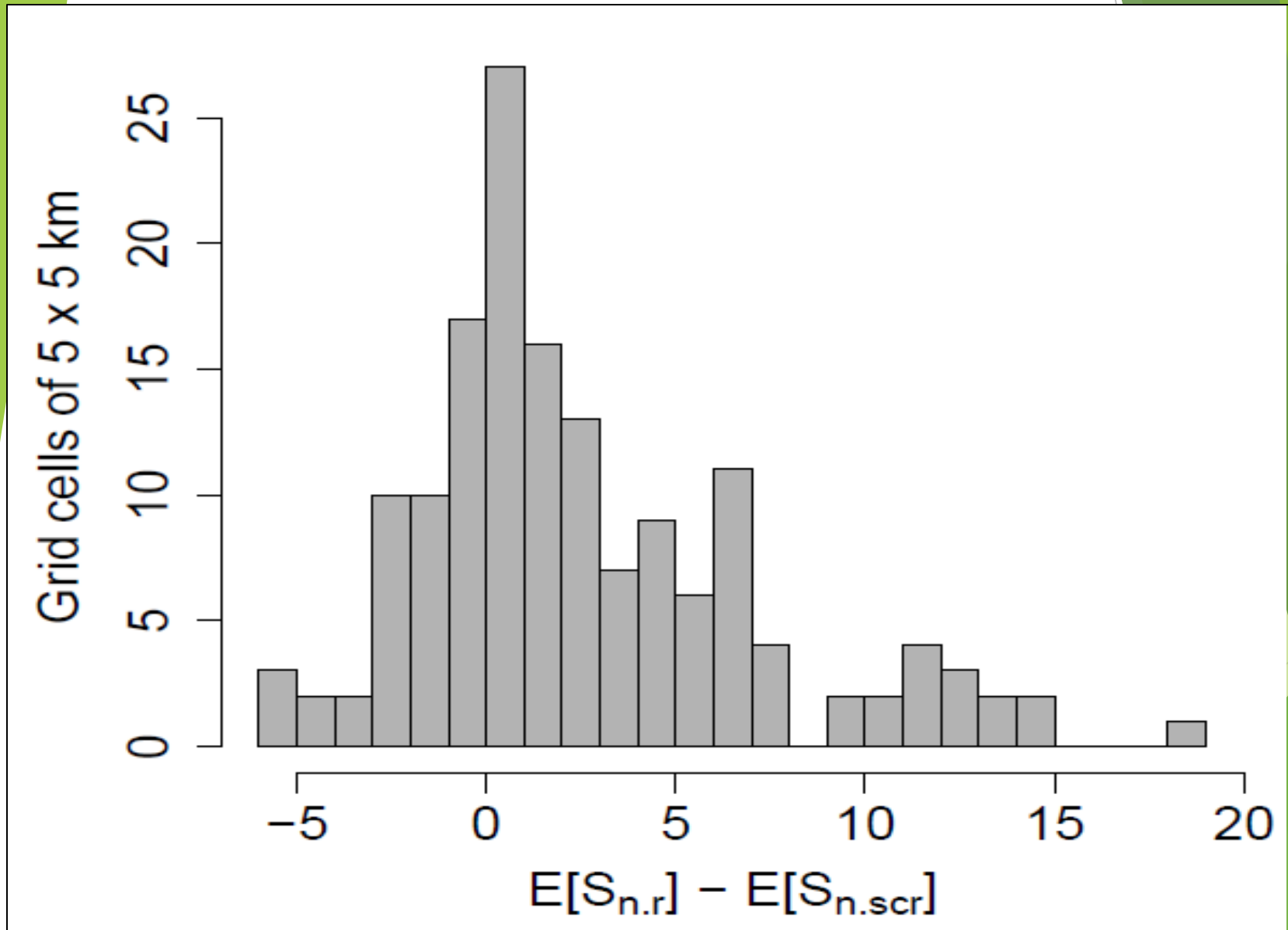
Results of testing prediction 2



Prediction 3

$$E[S_{n.r}] - E[S_{n.scr}] > 0$$

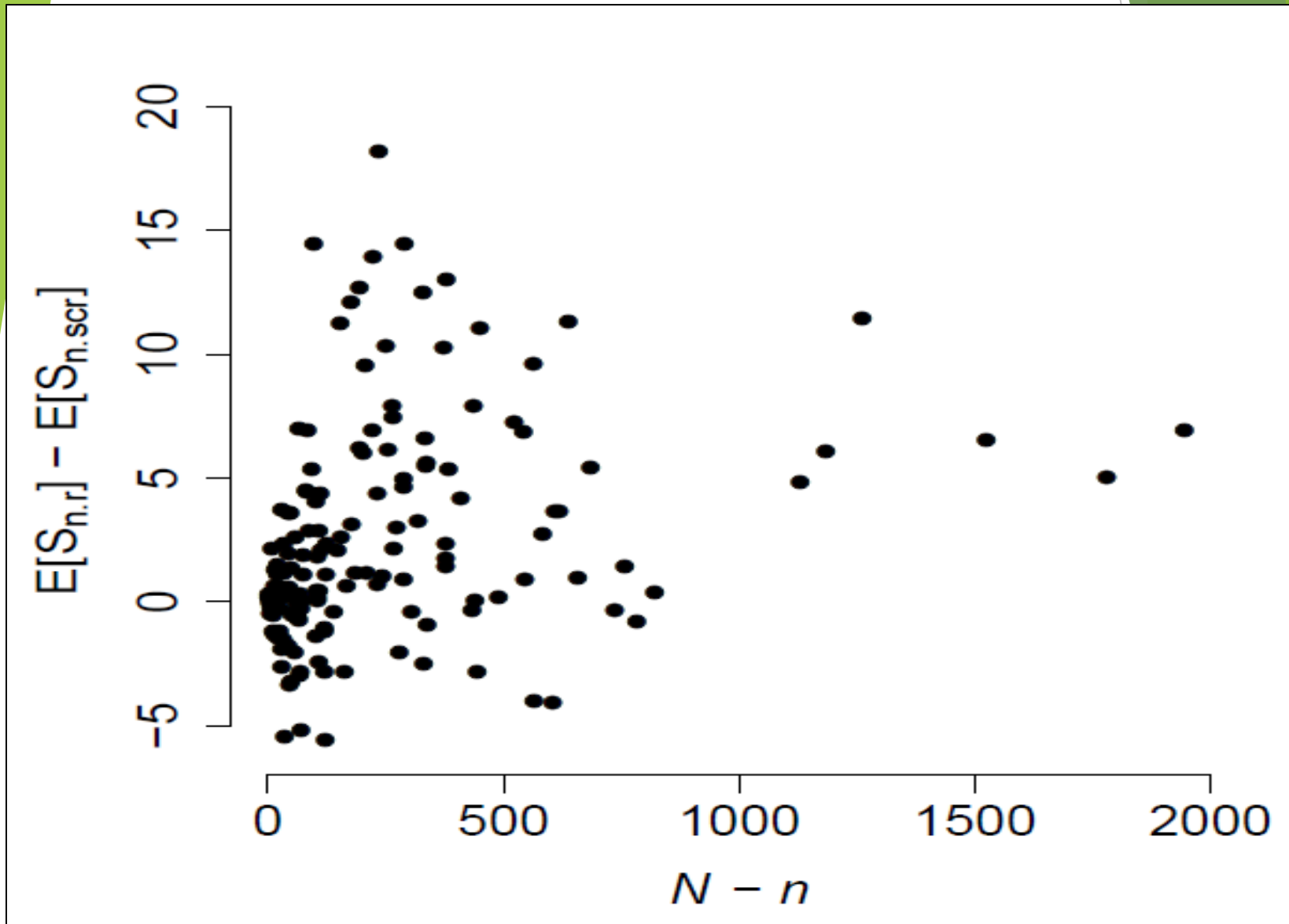
Results of testing prediction 3



Prediction 4

The relationship between $E[S_{n.r}] - E[S_{n.scr}]$
and $N - n$ is positive

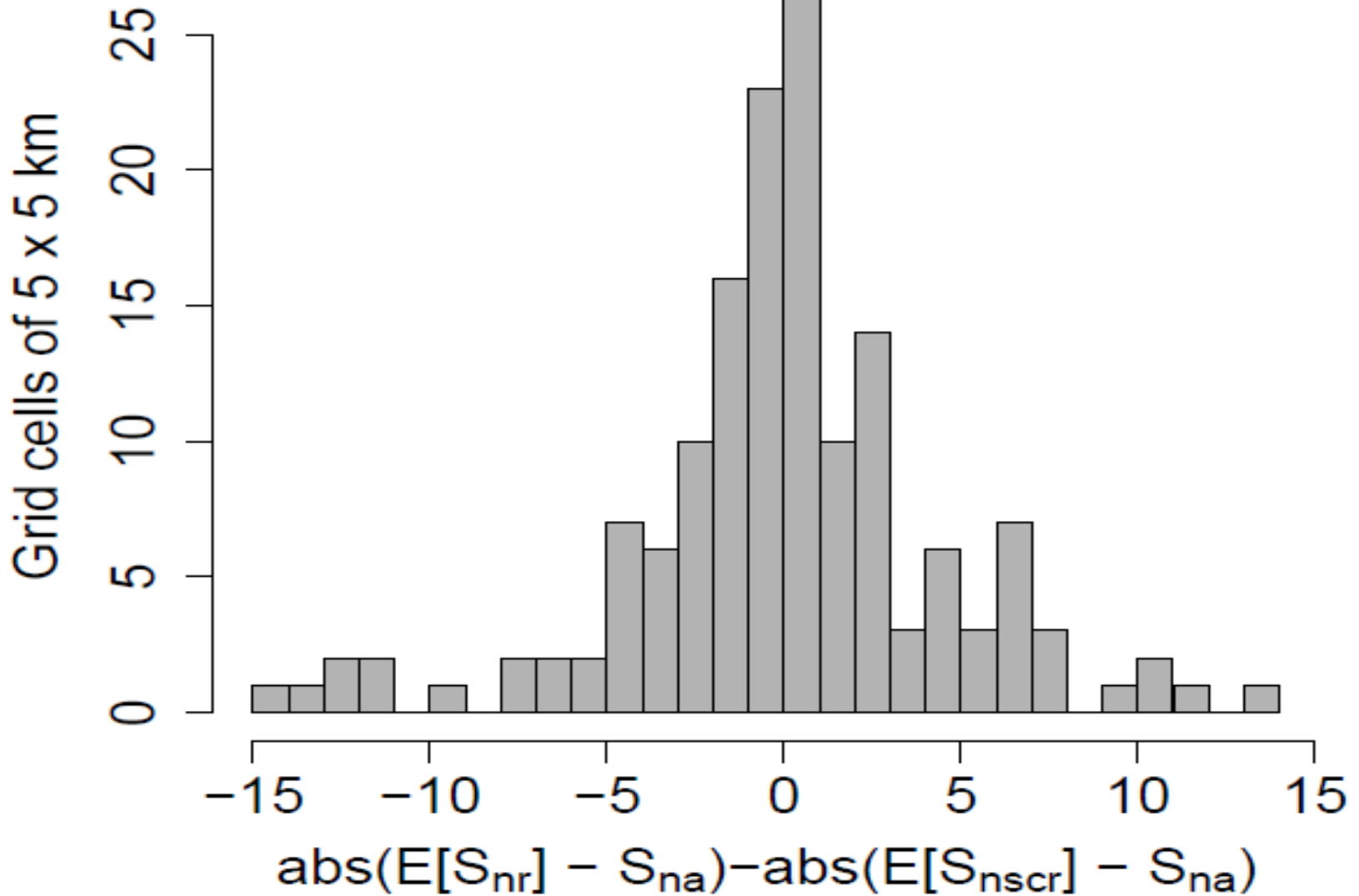
Results of testing prediction 4



Prediction 5

$$| E[S_{n.scr}] - S_{n.a} | - | E[S_{n.scr}] - S_{n.a} | > 0$$

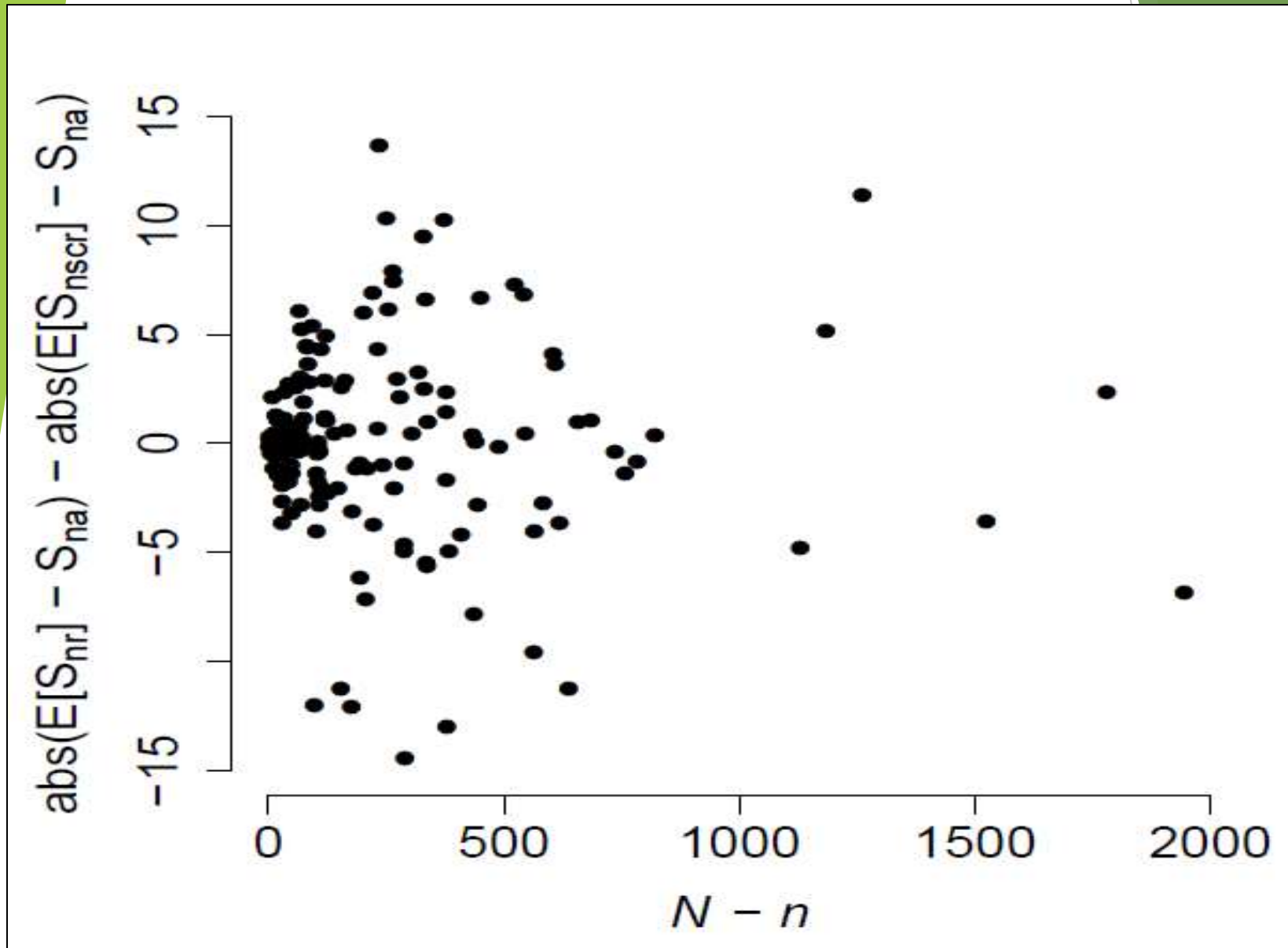
Results of testing prediction 5



Prediction 6

The $| E[S_{n.scr}] - S_{n.a} |$ and $N - n$ is a relationship between positive.

Results of testing prediction 6



Conclusions

The hypothesis was not empirically supported. Broad-scale species richness estimates based on spatially-constrained rarefaction do not seem to be less biased than those based on individual-based rarefaction

Acknowledgements

REU program, Missouri Botanical Garden, Warren
Douglas Stevens & Iván Jiménez

