Universität Zürich[UZH]
Department of General Linguistics

# Areal diachronies

Balthasar Bickel

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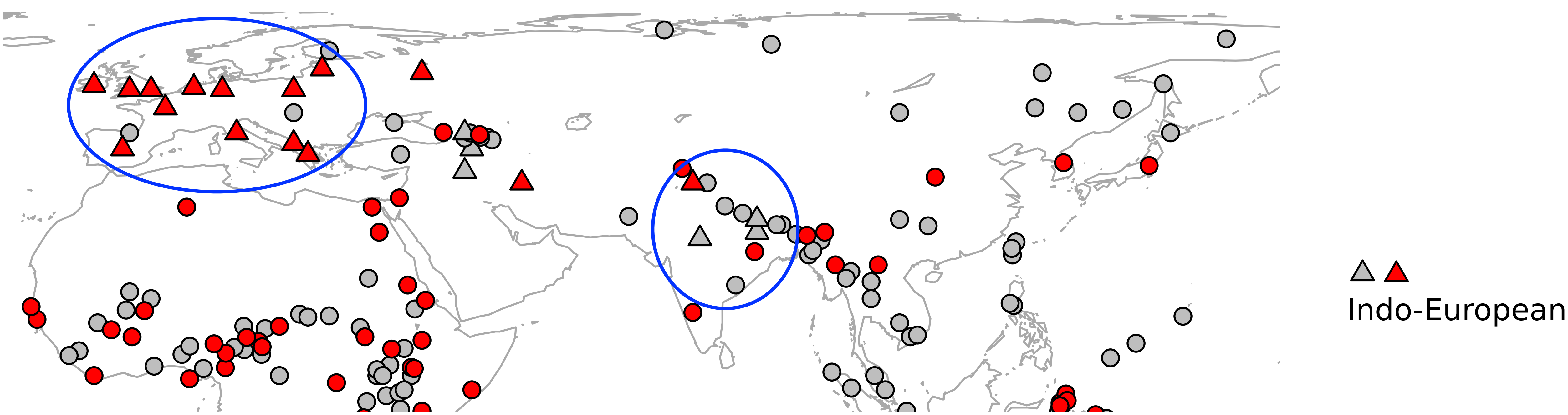
- they take place over time → need methods for estimating the diachronic process that led to areas
- they can involve innovation ***and*** retention alike

for example, gender systems tend to cluster areally not by innovation but by retention (Nichols 2003): pronominal gender (Siewierska 2005)



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- But let's estimate diachronic trends, nevertheless!
- And do so without neglecting isolates and small families!

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    - languages may prefer to innovate X more inside than outside an area
  - The synchronic result is the same: we have bias towards X in the end.

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on *demonstrably related*
languages:

| | | | |
|---|---|---|---|
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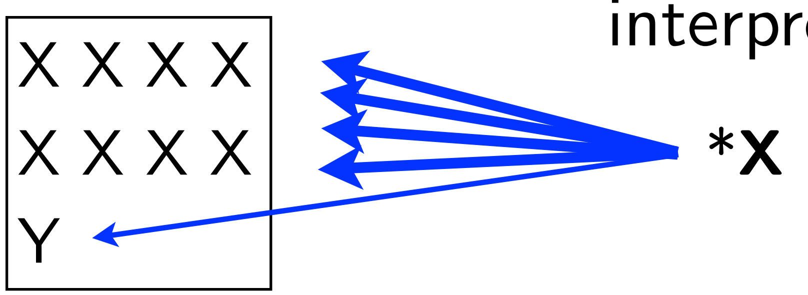

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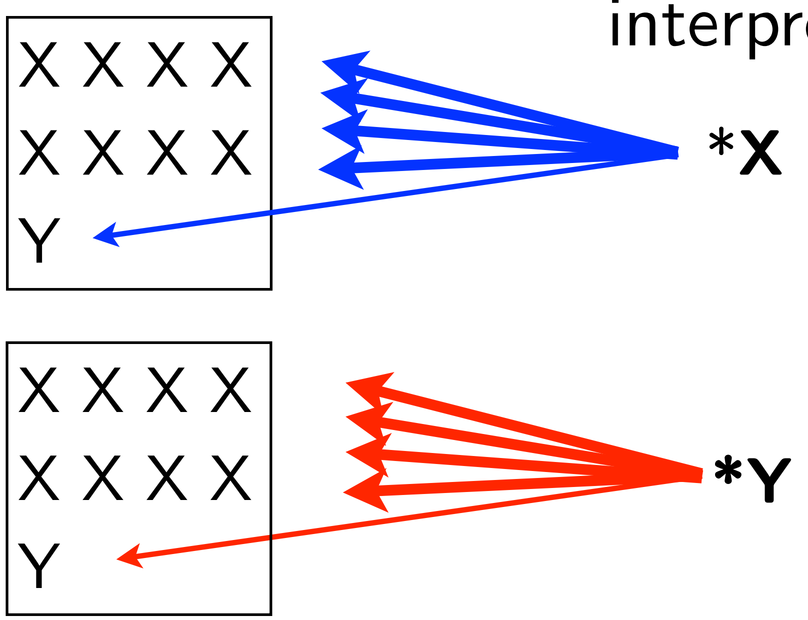

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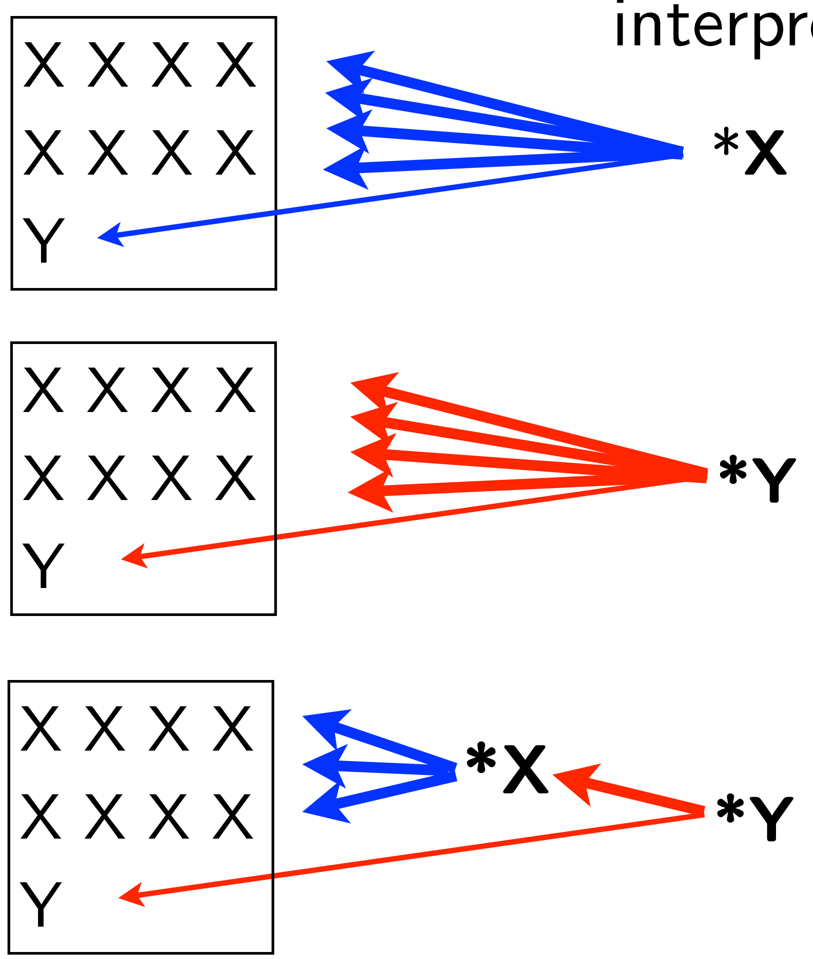

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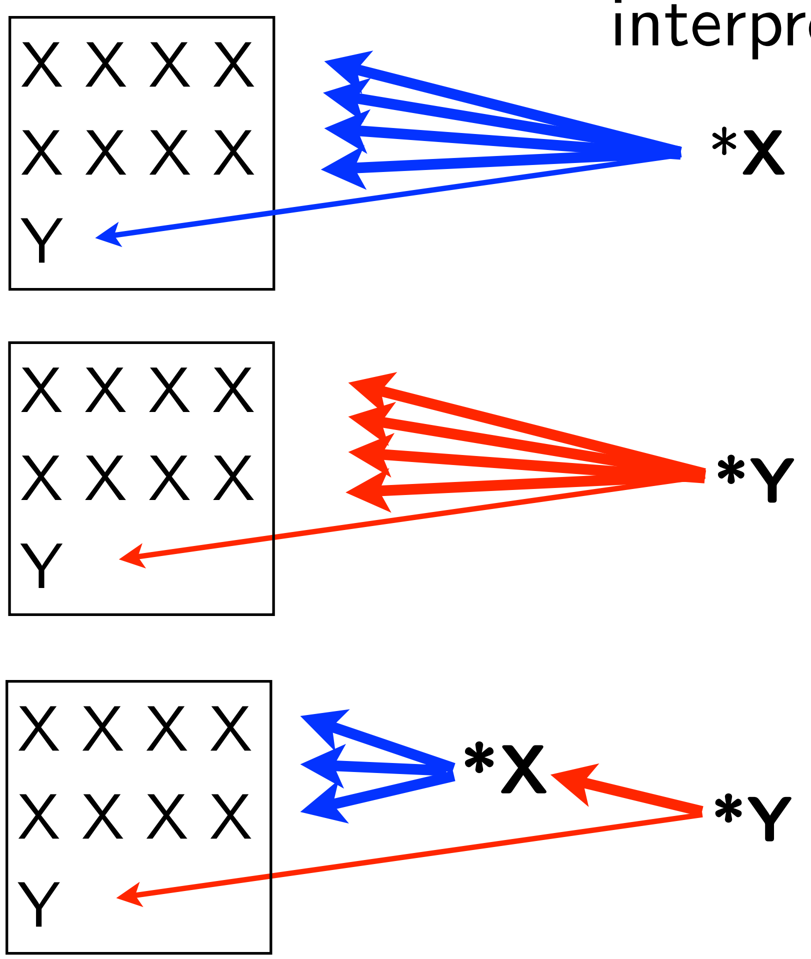

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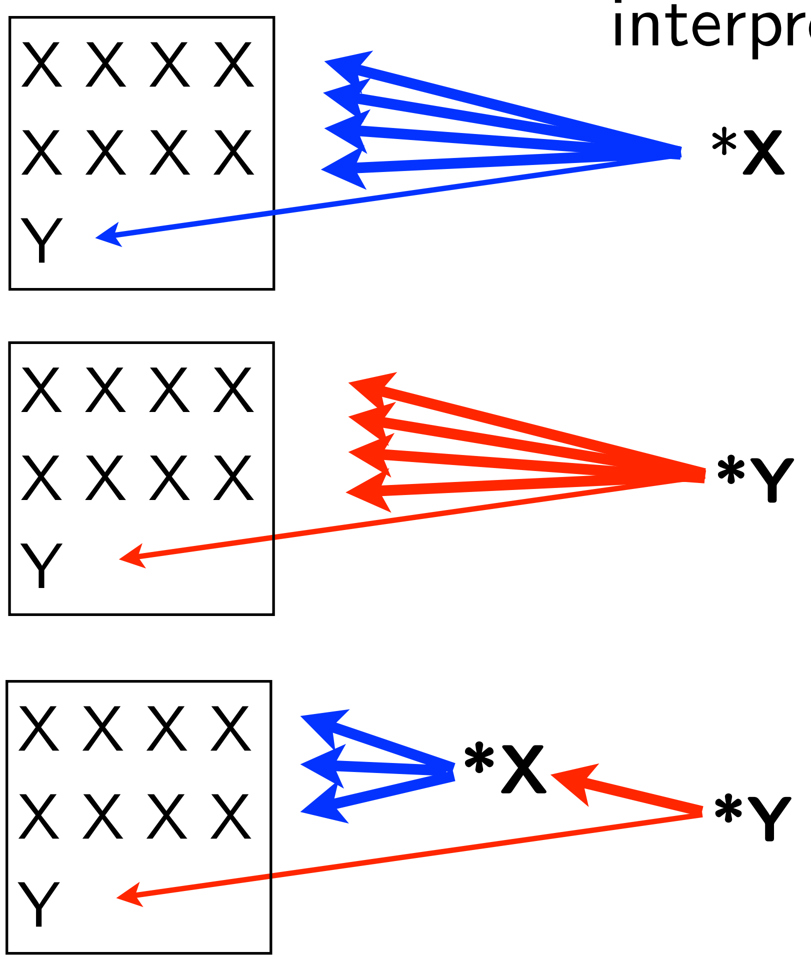


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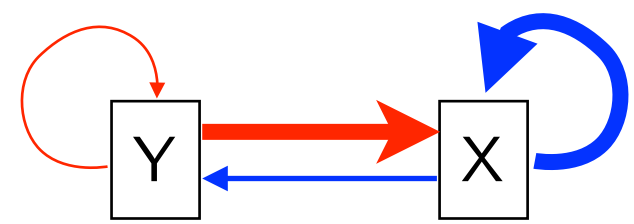

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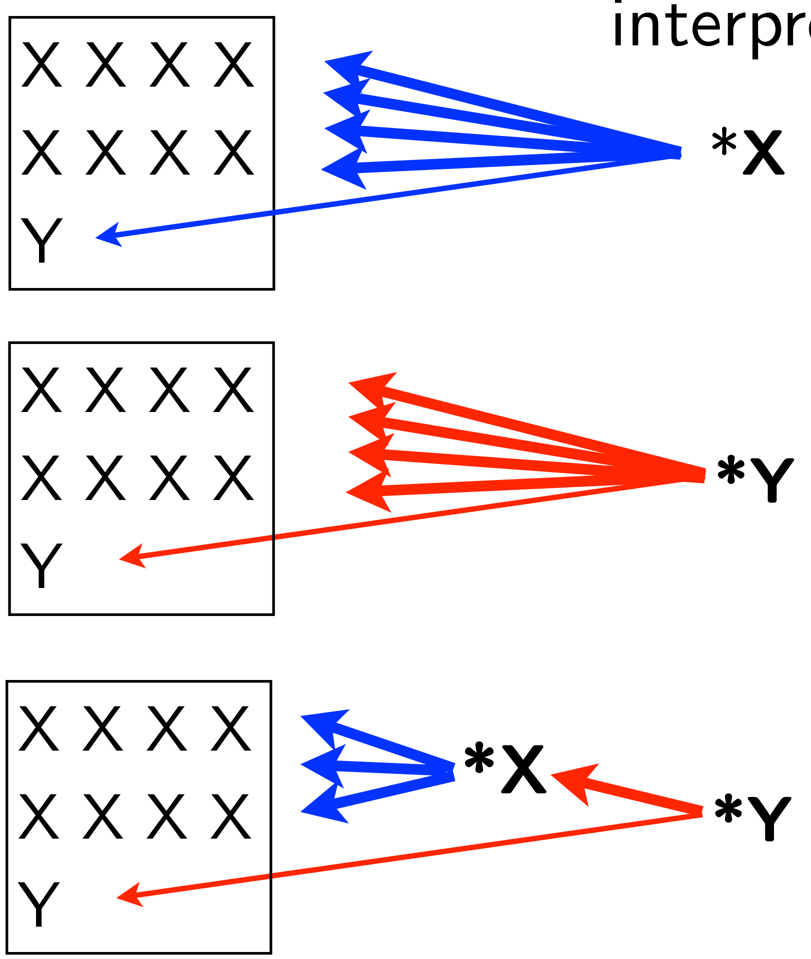


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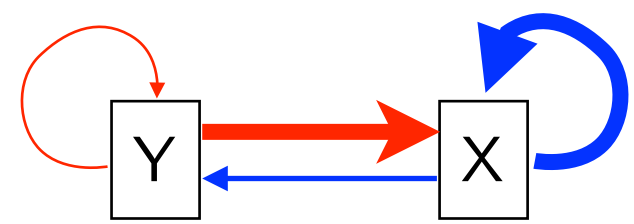


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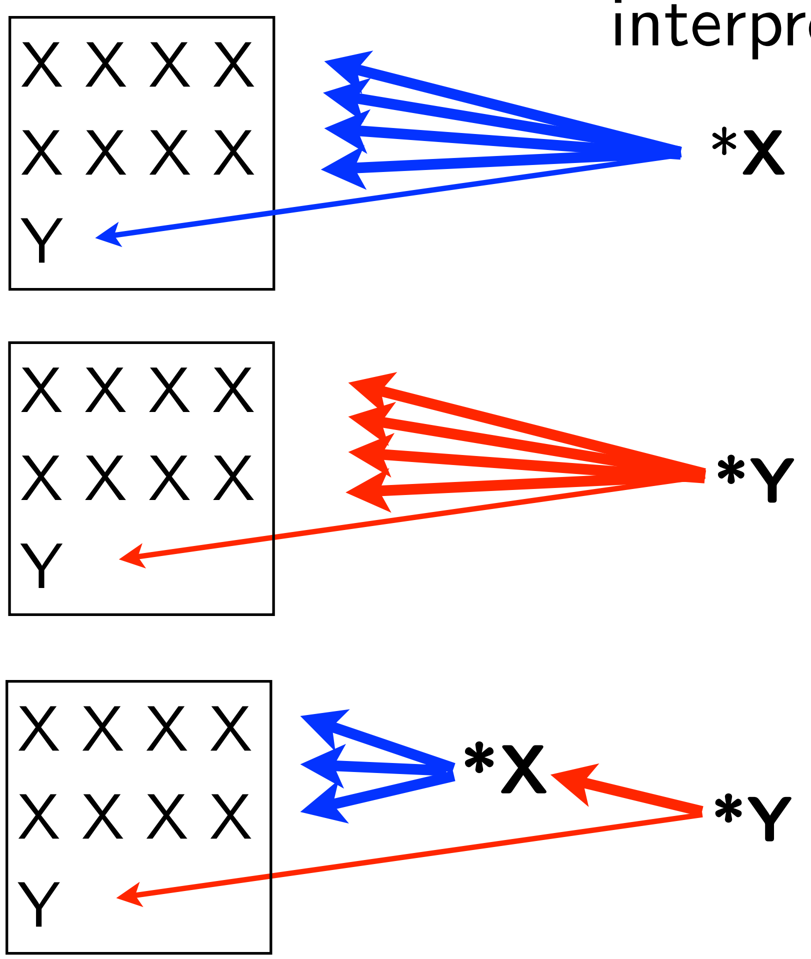


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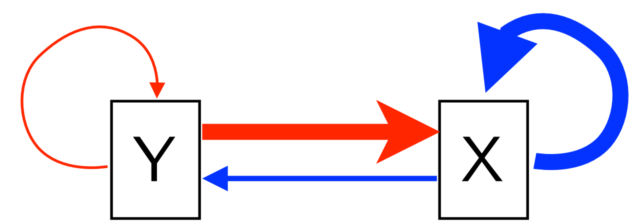


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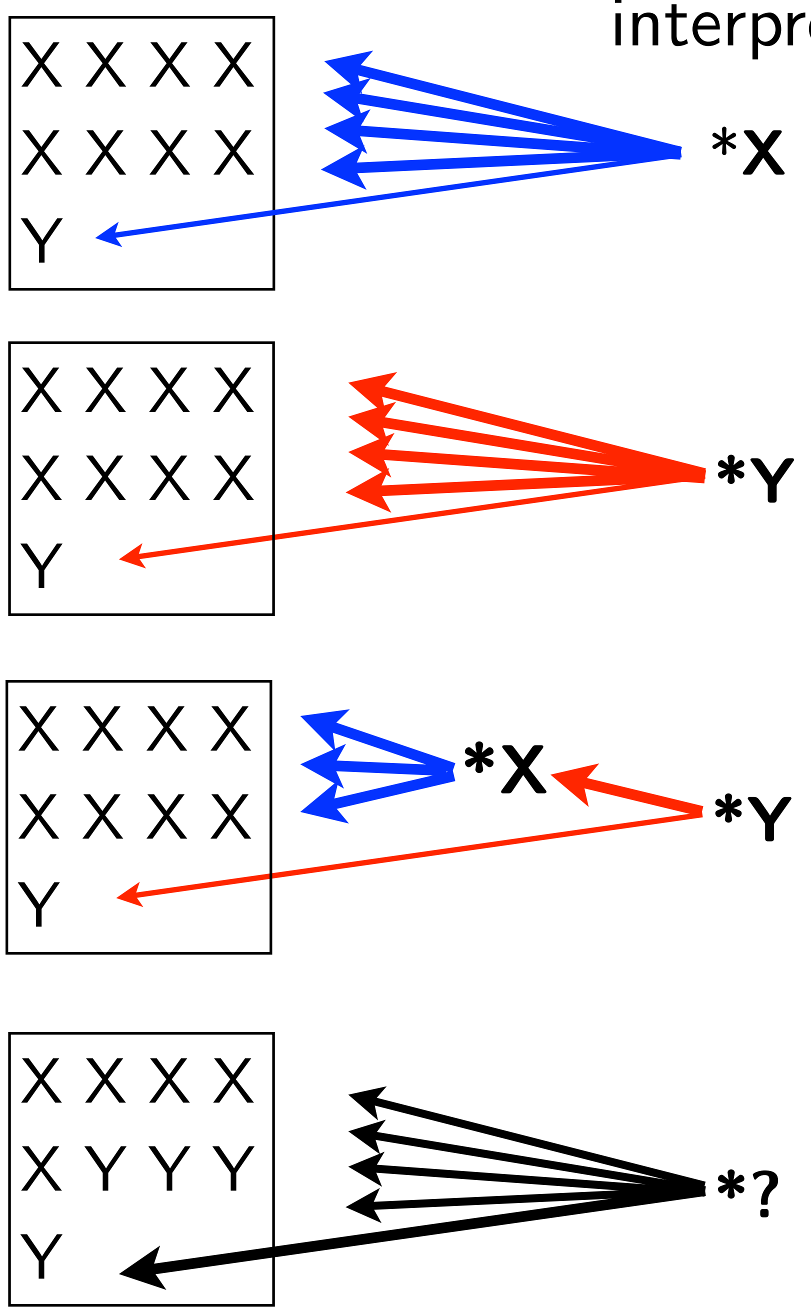


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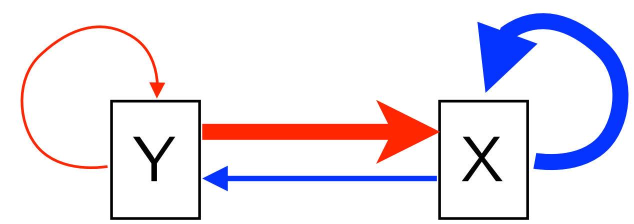


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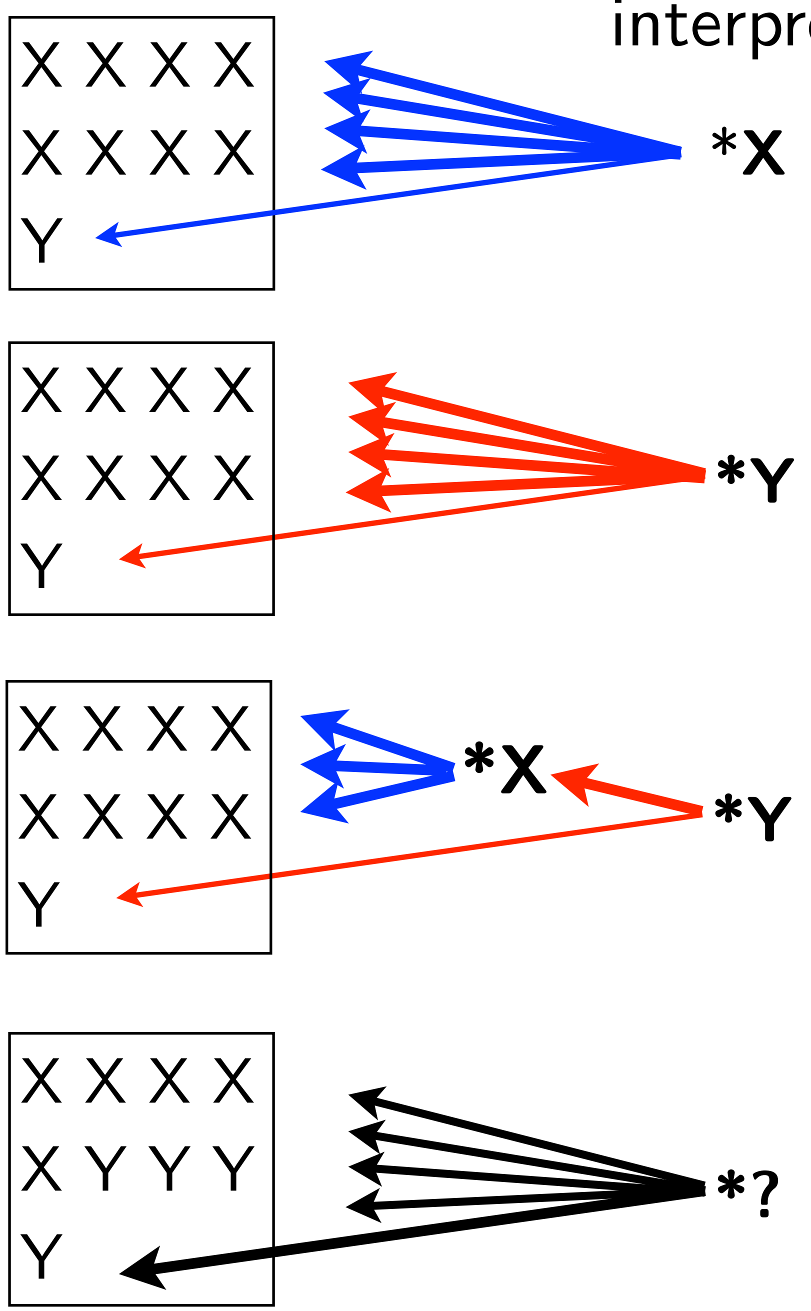


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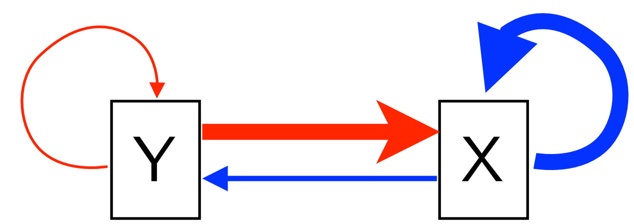


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$Pr(Y>X) \approx Pr(X>Y)$

(“no bias”, “diverse”)

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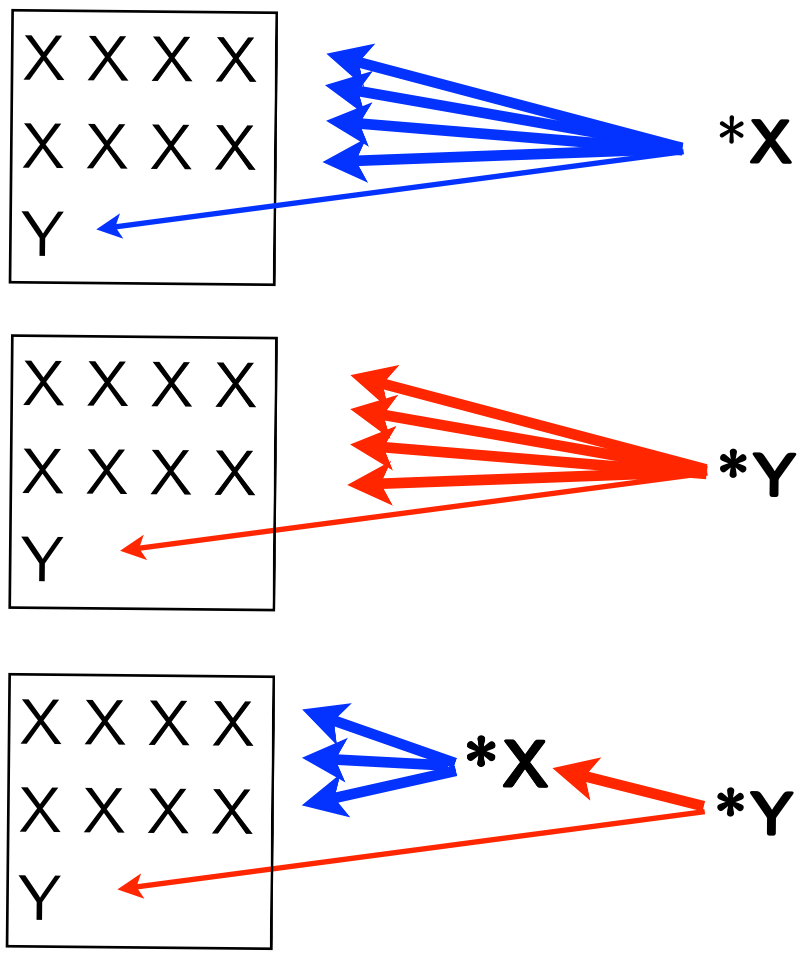


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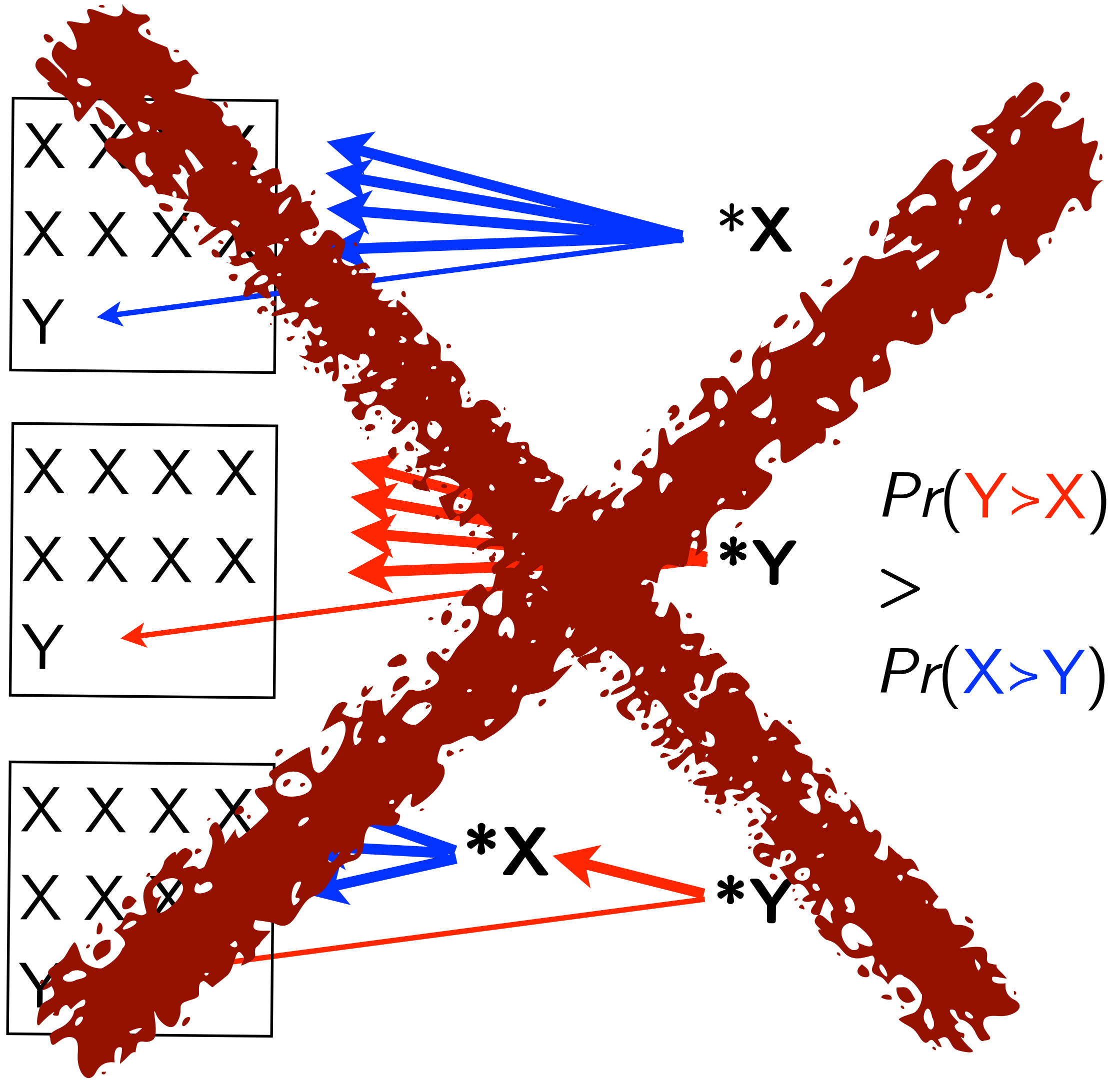

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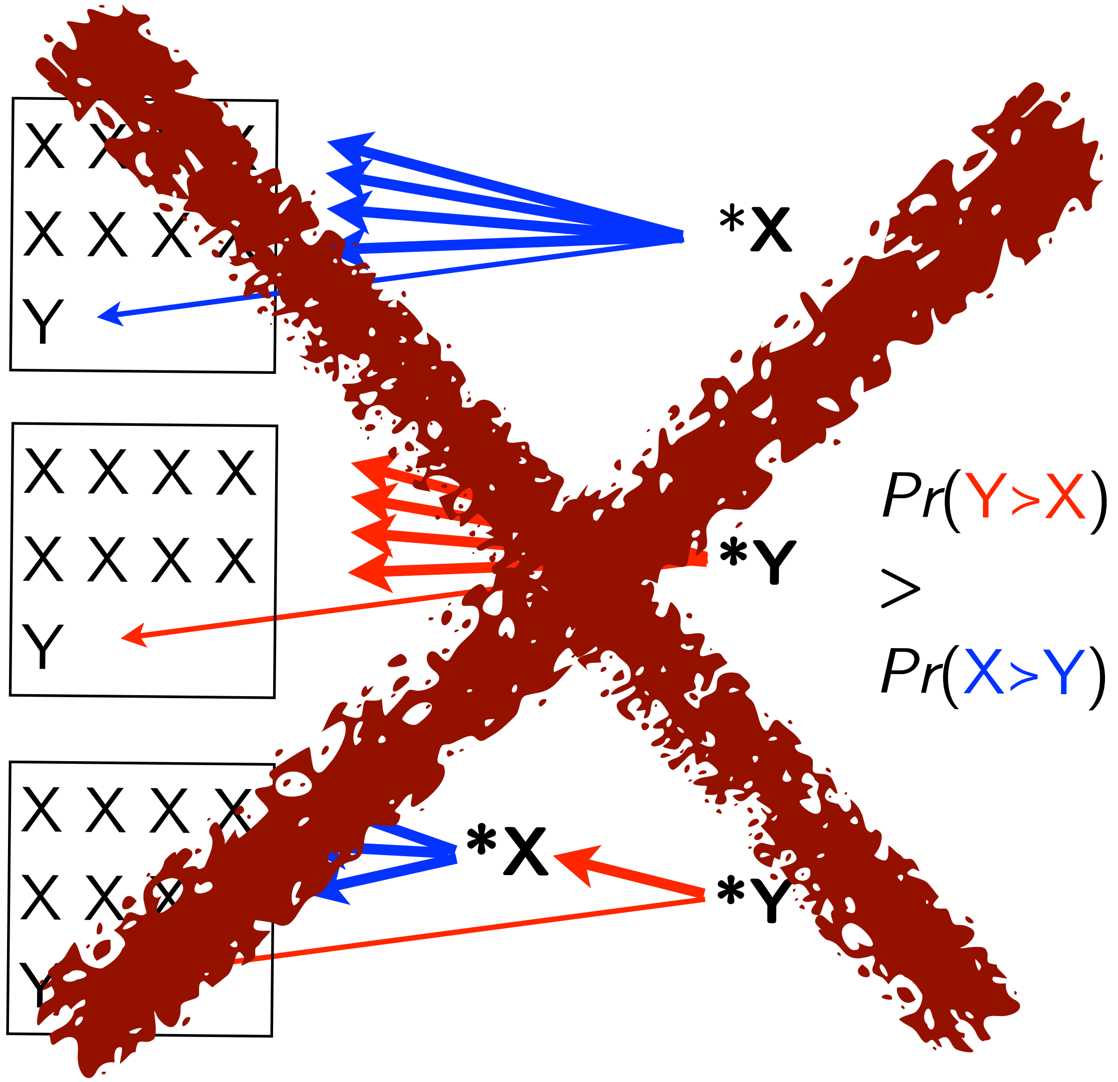


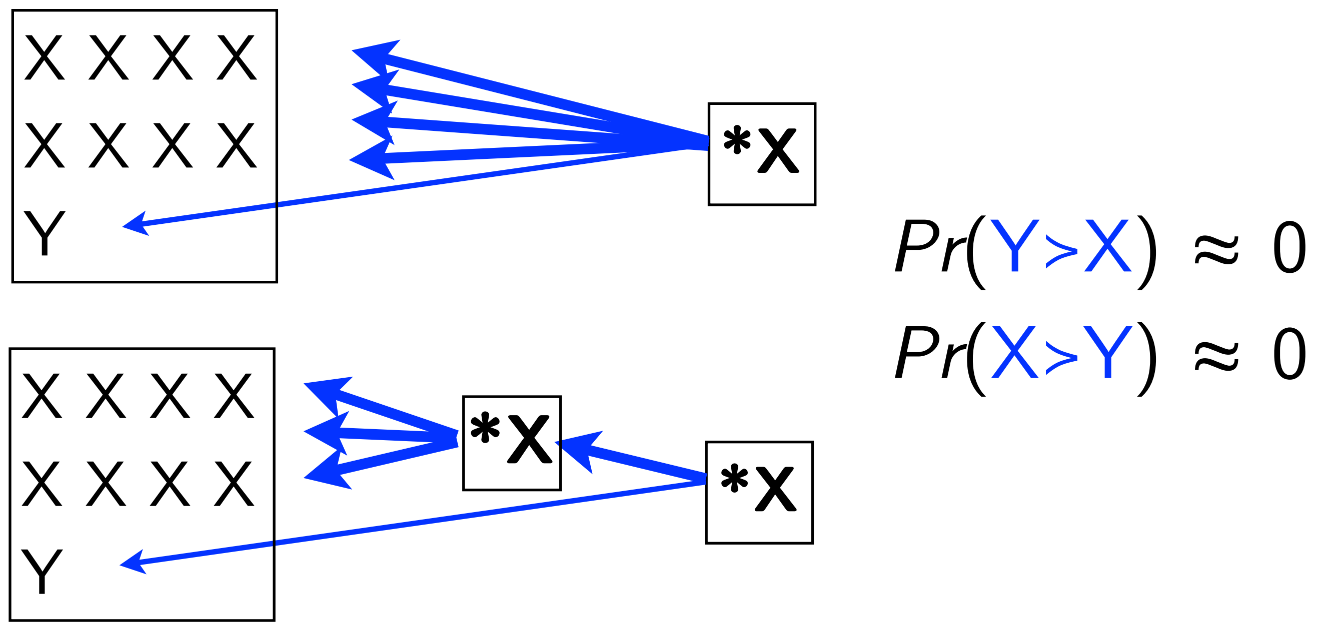

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  - all attempts to "control for genealogical relatedness" by building families into statistical models as control factors (e.g. Bickel et al. 2008, Jaeger et al. 2011)
- But typological variables are not remotely as stable as would be required for this ...

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- Pr(Y>X) ≈ Pr(X>Y) ≈ 0 means that changes are extremely unlikely within short time intervals such as those of known families
- Is this so? Given a set of variables, how many of them show changes within known families?

# Is $Pr$(Y>X) ≈ $Pr$(X>Y) ≈ 0 (extreme stability) plausible?

- The minimum number of attested changes $C$ for a variable $V$ with $k$ attested types (“levels”, “choices”) in a family $F$ is

  $\min(C_F) = k_F - 1$

  A family: A A A A A B B B A A, so $k_F = 2$
  Minimum change scenarios:
  *A > B in one branch, the rest stays, *or*
  *B > A in one branch, the rest stays

  Another family: A A C A A B B B A A, so $k_F = 3$
  Minimum change scenarios:
  *A → B in $F_1$, *A → C in $F_2$, A stays in $F_3$ or
  *B → A in $F_1$, *B → C in $F_2$, B stays in $F_3$, or
  *C → A in $F_1$, *C → B in $F_2$, C stays in $F_3$

  That’s the logical minima. (There can always be many more!)

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- Minimum opportunities for change min($O_F$) = $(k_V\text{-}1) \cdot N(\text{families})$ where $k_V$ is the number of types defined by a variable (what's possible), e.g. $k$=2, $N$=50 families: 50 opportunities for $V$ to change at least once
  $k$=3, $N$=50 families: 100 opportunities for $V$ to change at least once

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- NB: since we only look at minima, this underestimates the number of unexpected changes, i.e. it favors small $\pi$!
- Compute the proportion of variables for which min($C_F$) is expected, given the assumption of a specific value of $\pi$ between 0 and 1

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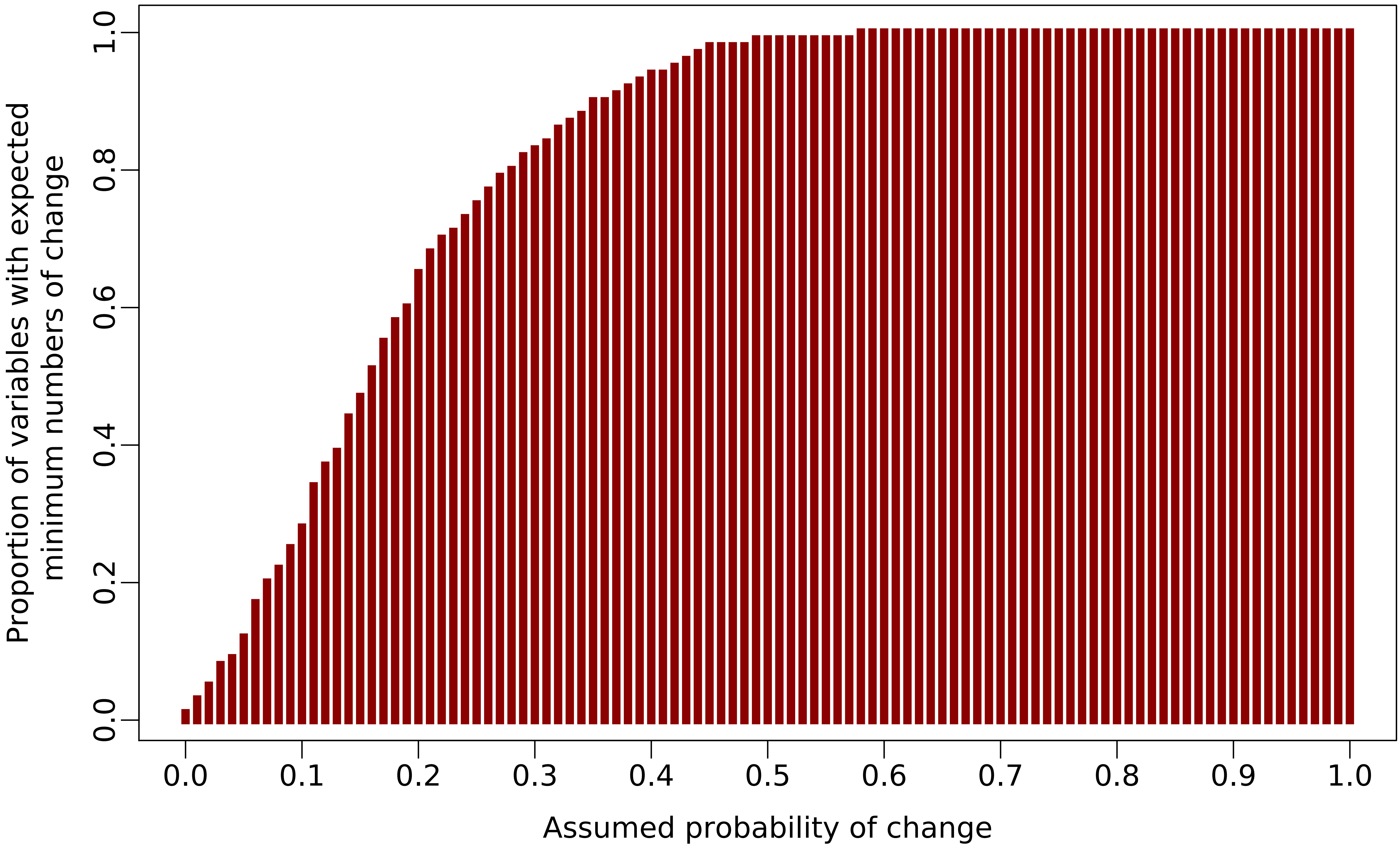


448 variables from WALS and AUTOTYP

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- Some of the variables with $\min(C_F)$ expected under $\pi = .01$:

| Variable (and data source) | Changes $N_{min}$ | Opportunities $N_{min}$ | Entropy $\hat{H}$ | Ratio of values |
|---|---|---|---|---|
| Interrog./decl. distinction (Dryer, 2005a) | 1 | 89 | 0.01 | 841:1 |
| Indep. subject pronouns (Daniel, 2005) | 0 | 31 | 0.07 | 258:2 |
| Tonal case (autotyp and Dryer, 2005b) | 3 | 91 | 0.07 | 698:6 |
| Stem flexivity condit. by NEG (autotyp) | 0 | 40 | 0.12 | 141:1:1 |
| ‘Have’-perfect (Dahl & Velupillai, 2005) | 1 | 15 | 0.35 | 101:7 |
| Co-exponent type of NEG (autotyp) | 4 | 234 | 0.60 | 185:5:3:1:1:1:1:1:1:1 |

- This is typical: $\pi \leq .10$ suggest **rara vs. universalia** distributions, not extreme stability

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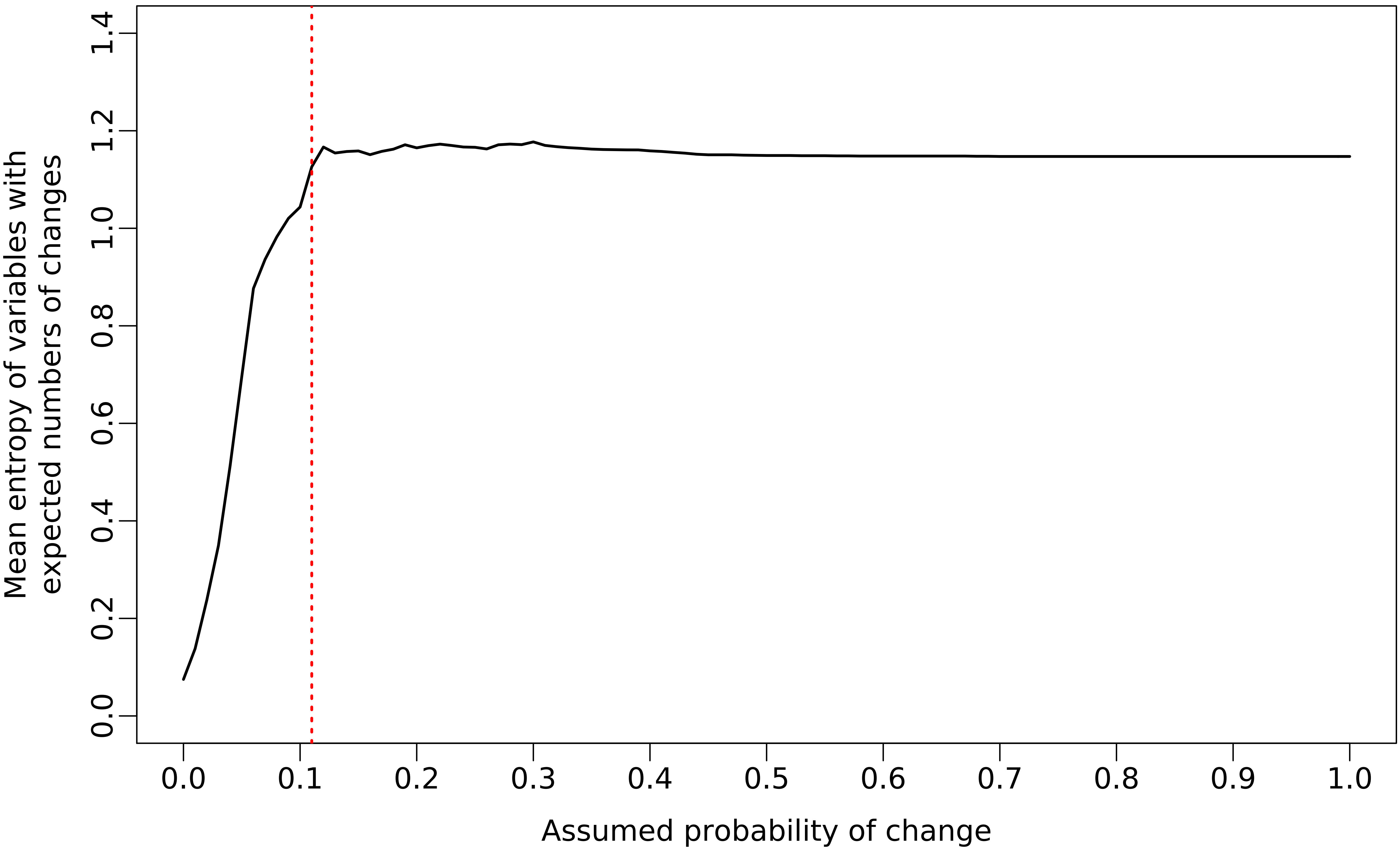


Bickel in press ("Distributional biases in language families"), in Fs. Nichols

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- So, the key assumption behind the Family Bias Method — synchronic biases reflect directional trends in diachrony — is justified by exclusion of the alternatives: (i) deny the synchronic bias; (ii) assume extreme stability
- But how to implement the Family Bias Method?

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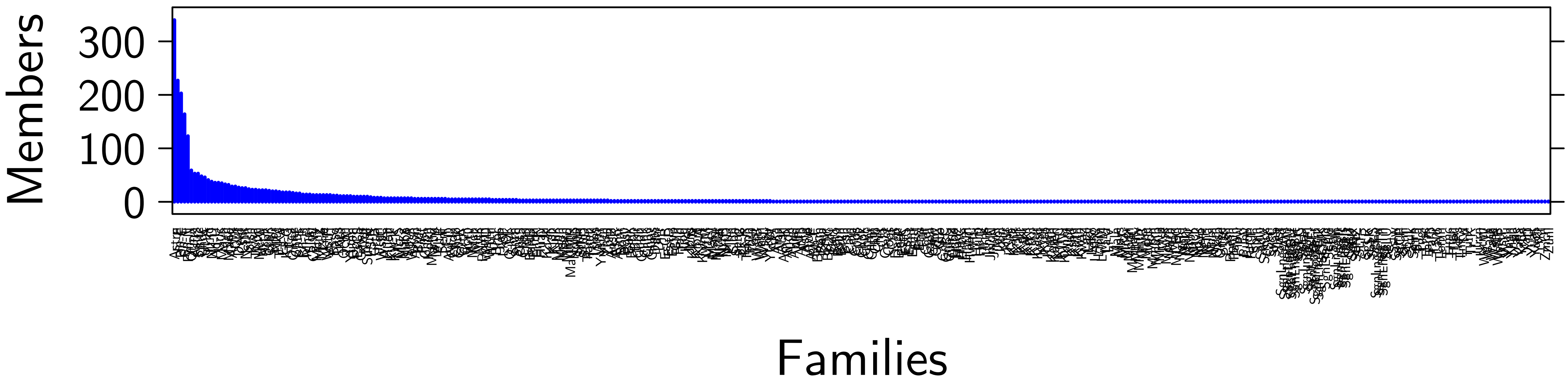
3. A way of dealing with small families and isolates:



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  - binomial tests for binomial variables, and then generalize to multinomial designs (currently the only option we have fully implemented)

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## Detecting diachronic biases

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    at `http://www.uzh.ch/spw/software`
  - estimate likelihoods of synchronic distributions given diachronic biases (work in progress)
- Justification of the binomial test approach by computer simulation (joint work with Taras Zakharko)

## Justification of binomial tests for detecting diachronic biases

Simulation of a discrete-time Markov process, where language varieties can (within steps of ca. 100 years $\sim$ 3 generations)

- give birth: Poisson process with **birth rate $\boldsymbol{\lambda}$** within [.7, .9]

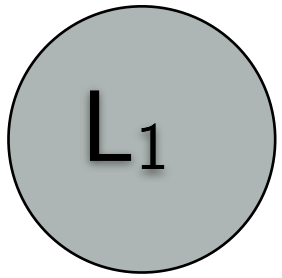
  meaning that it takes 1 or 2 steps (100-200 years, 3-6 generation) for a new language variety to get established, *on average*

- die or stay live: Bernoulli process with **survival prob. $\boldsymbol{\pi}$** within [.1, .2]

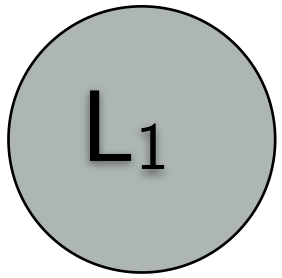
  meaning that most varieties die after 1 or 2 steps (100-200 years), *on average*

(for simplicity, $\lambda$ and $\pi$ are assumed to be constant within one simulation)

A proto-language, $t = 0$



**Step 1 (about 100y or 3 generations)**

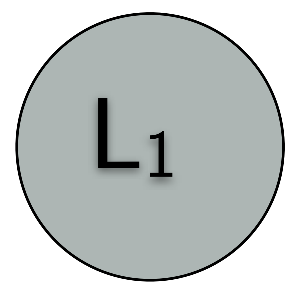


# Simulating birth and survival: an example

**Step 1 (about 100y or 3 generations)**

$\texttt{rpois}(.8) \;= 1$

$\texttt{rbinom}(.1) = 1$



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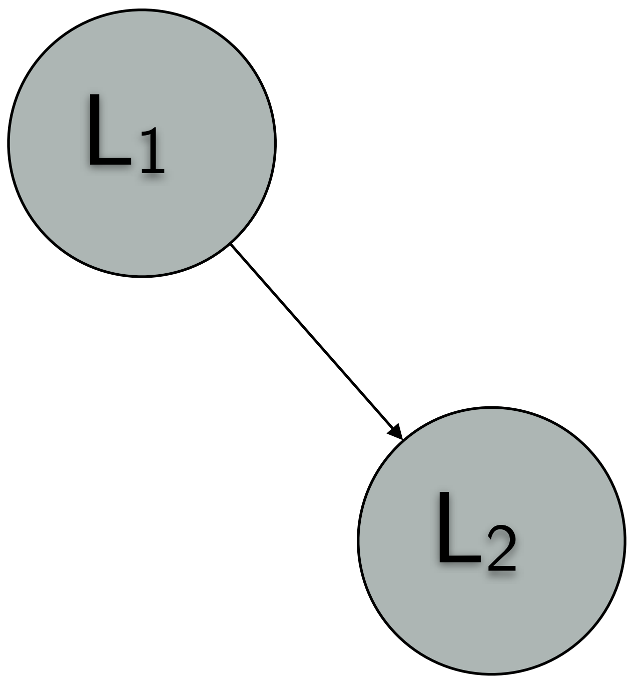

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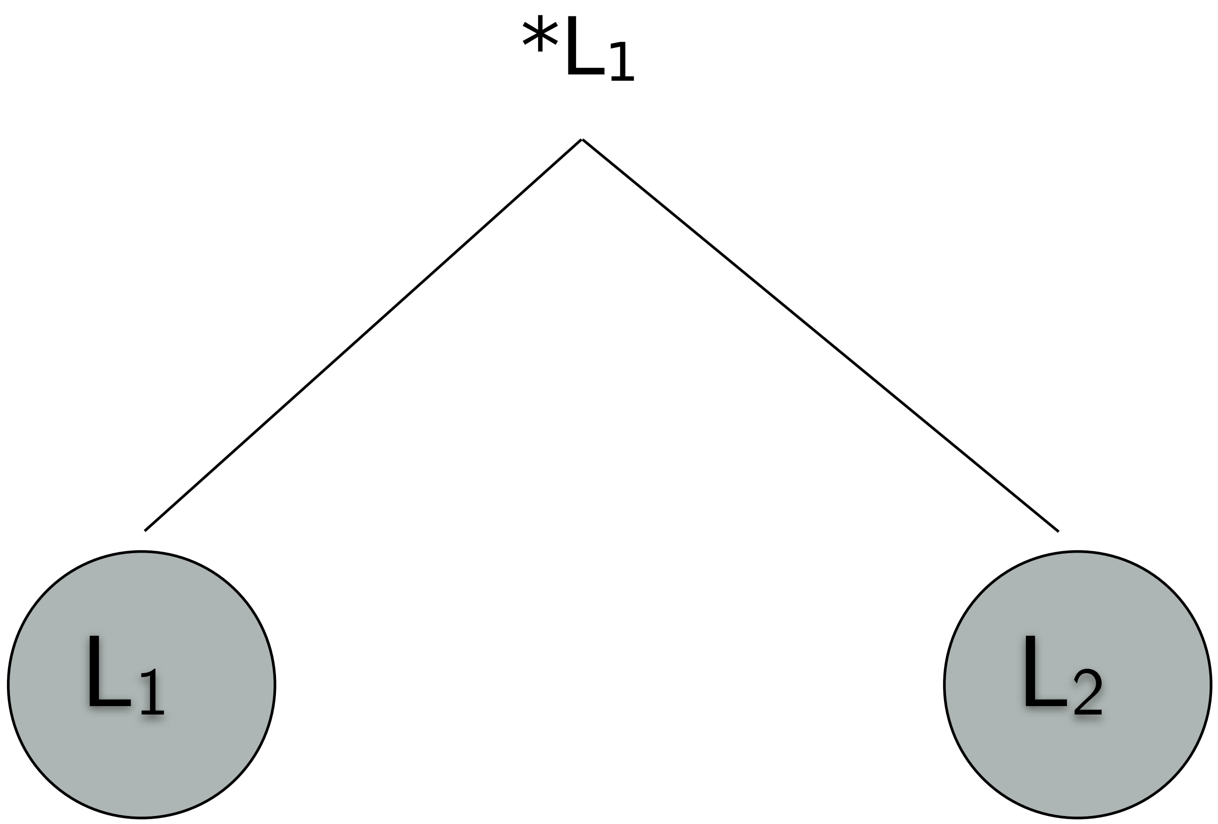


(conservative variety of $L_1$, no or negligible changes)

(innovative variety of $L_1$, coexisting with it)

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$\texttt{rpois}(.8) = 0$ $\quad$ $\texttt{rpois}(.8) = 2$

$\texttt{rbinom}(.1) = 0$ $\quad$ $\texttt{rbinom}(.1) = 0$

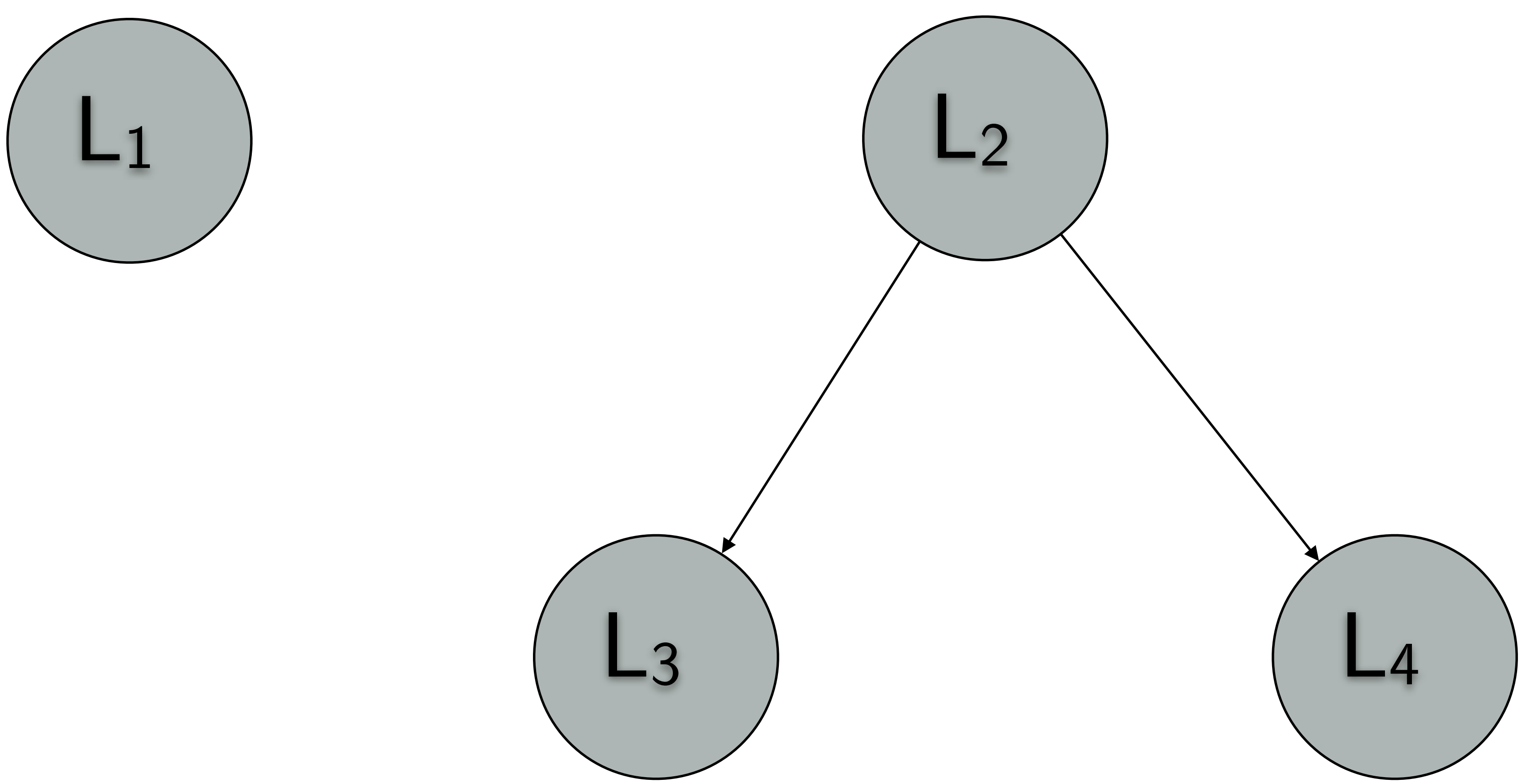
**Step 2 (another 100y or 3 generations)**

$\texttt{rpois}(.8) = 0$

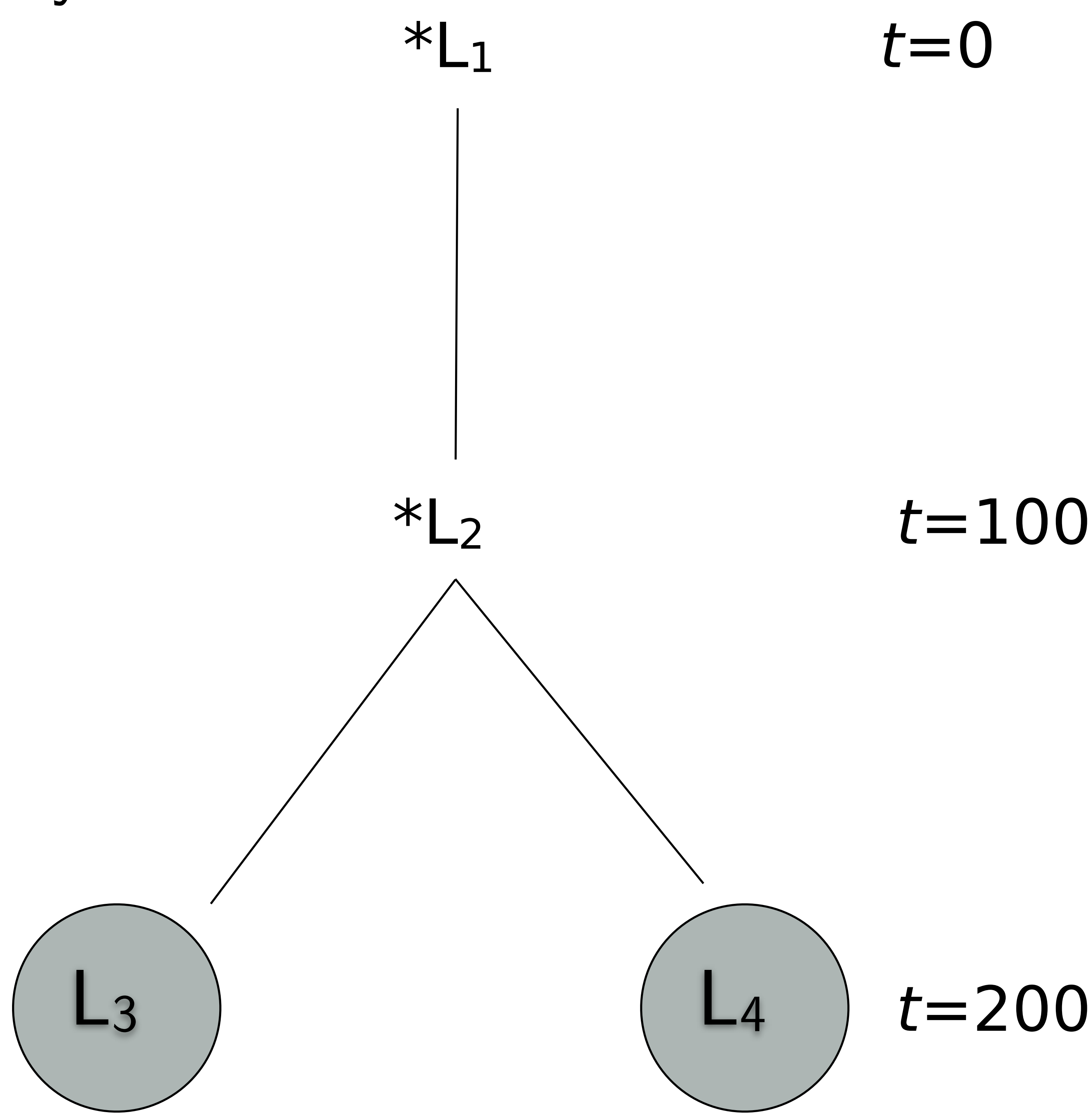
$\texttt{rbinom}(.1) = 0$

$\texttt{rpois}(.8) = 2$

$\texttt{rbinom}(.1) = 0$

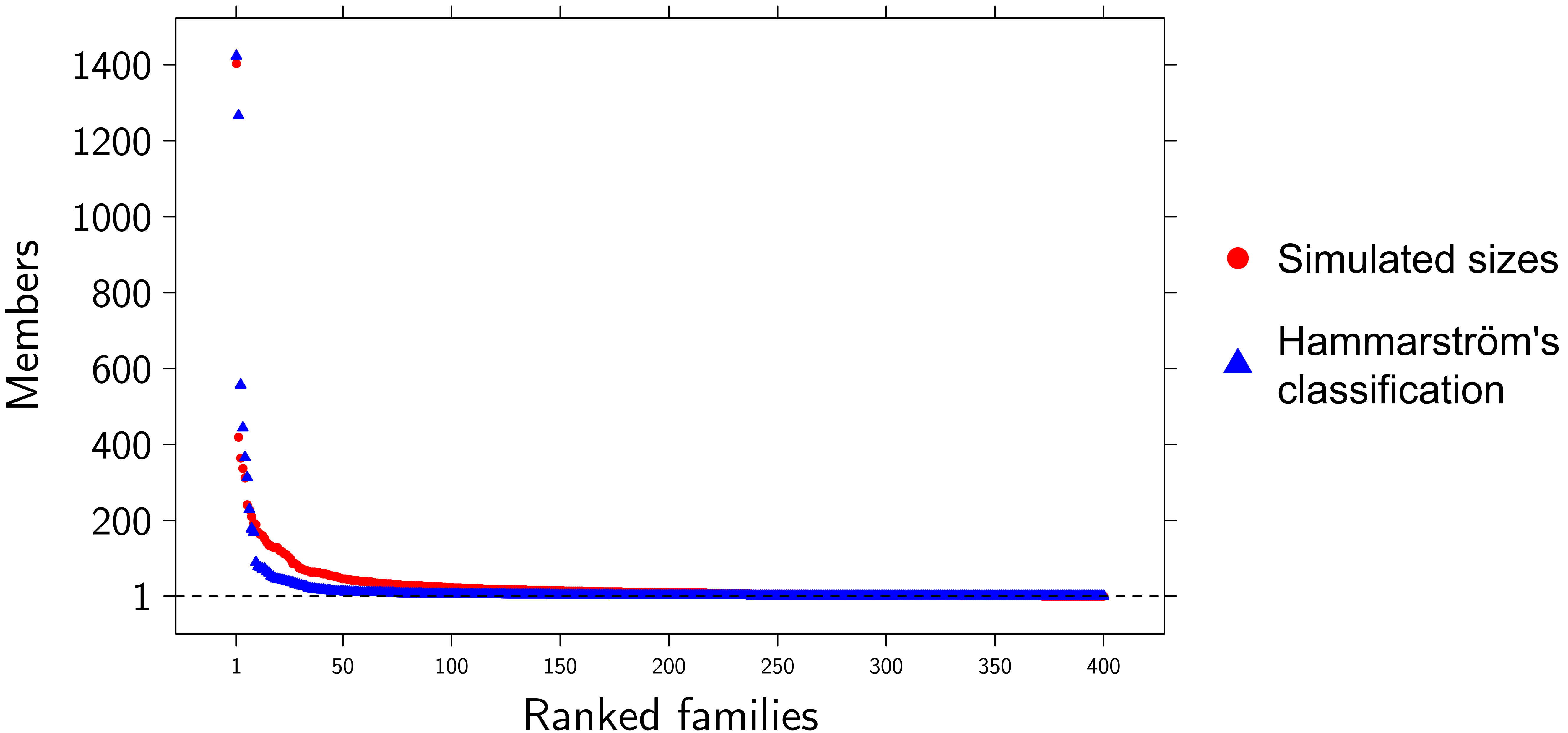


Result after two steps, $t = 200$y



# Simulating birth and survival: reality check

400 simulated families with randomly chosen birth rates $\lambda$ between [.7,.8] and survival probabilities $\pi$ between [.1,.2], running randomly between 30 and 50 steps, i.e. 3'000 - 5'000y:



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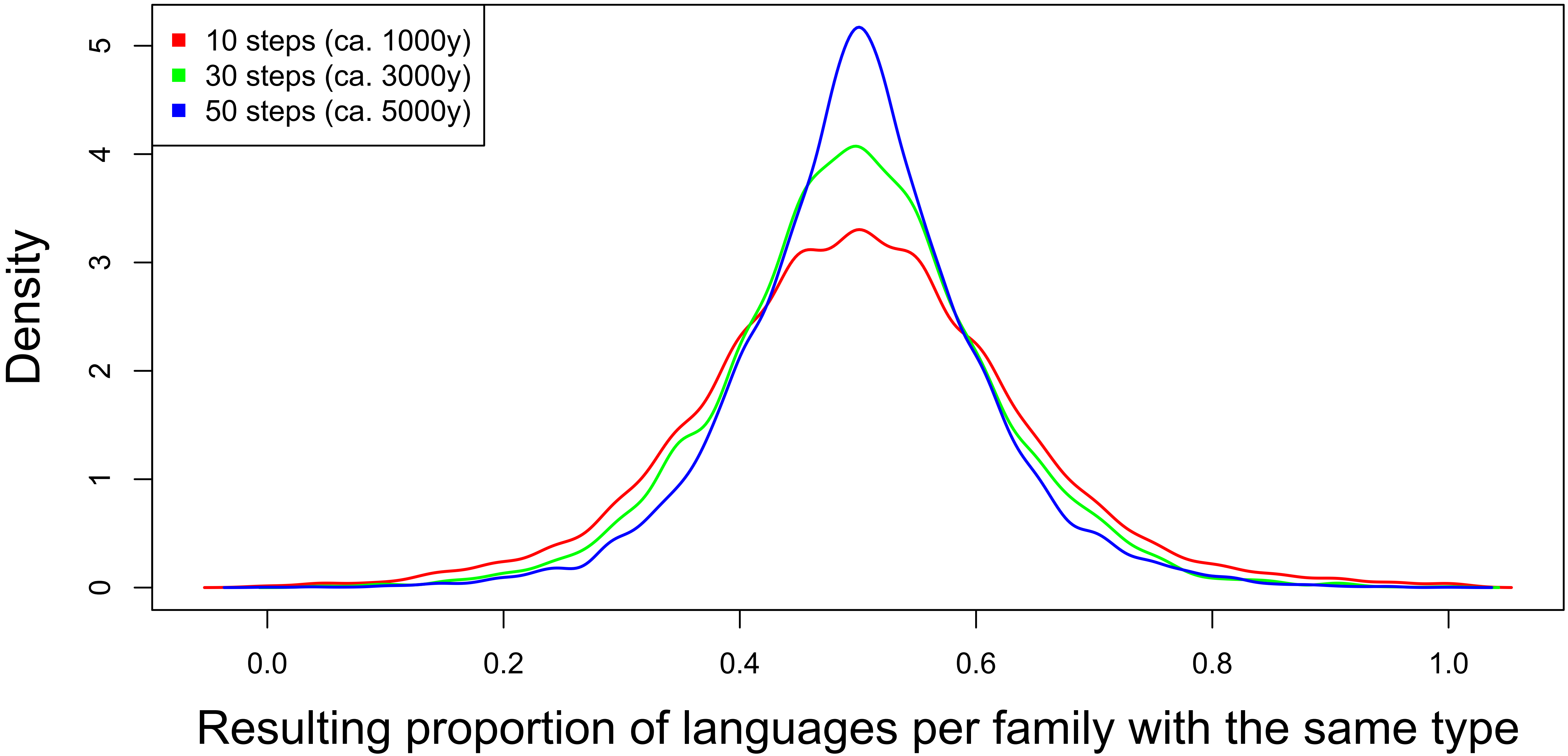
- and examine the resulting distribution in families that have at least 20 survivors in the simulations (10k runs)

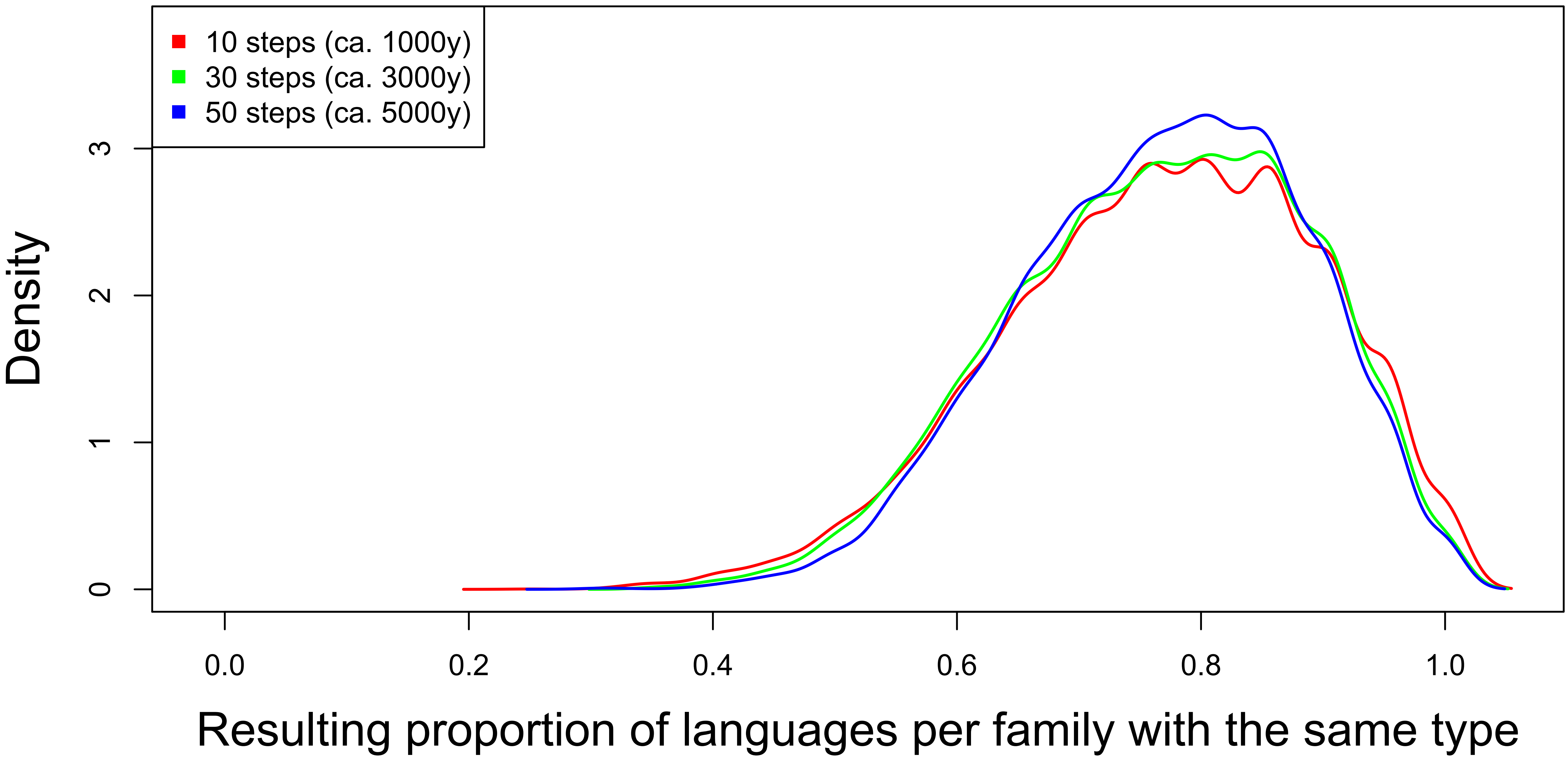
# Simulating change in this model

- without bias, |Pr(Y>X) - Pr(X>Y)| ≤ .05



# Simulating change in this model

- with a bias, |Pr(Y>X) - Pr(X>Y)| ≥ .25



- The clear shift in the probability mass suggests that an exact binomial test (with a 10% rejection level) is a reasonable bias test (families with at least 20 members, 10k simulations):

| | no bias detected | bias detected |
|---|---|---|
| family has no bias | 0.87 | 0.13 |
| family has bias | 0.19 | 0.81 |

False positives

False negatives

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  - the proportion of biased vs. diverse large families
- Various techniques for extrapolation. One technique:

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   E.g. families with biases towards possessive classes (176 families, 274 languages)

| | Pr(bias) |
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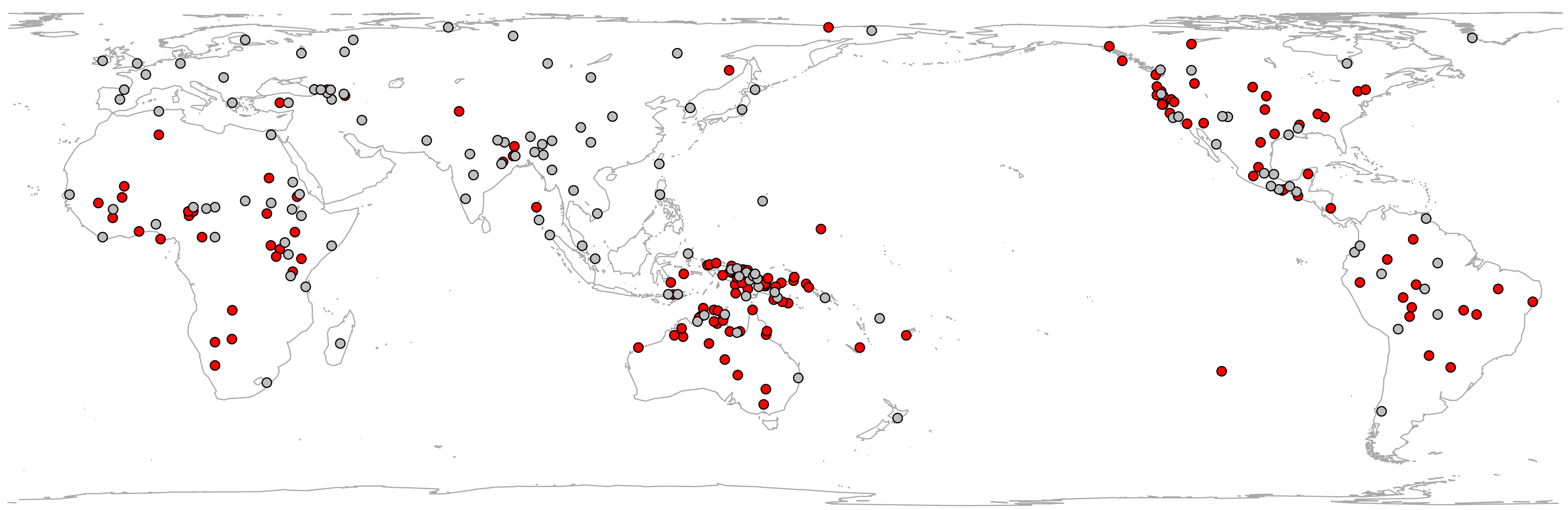
| Eurasia | 0.67 |
| Other | 0.40 |



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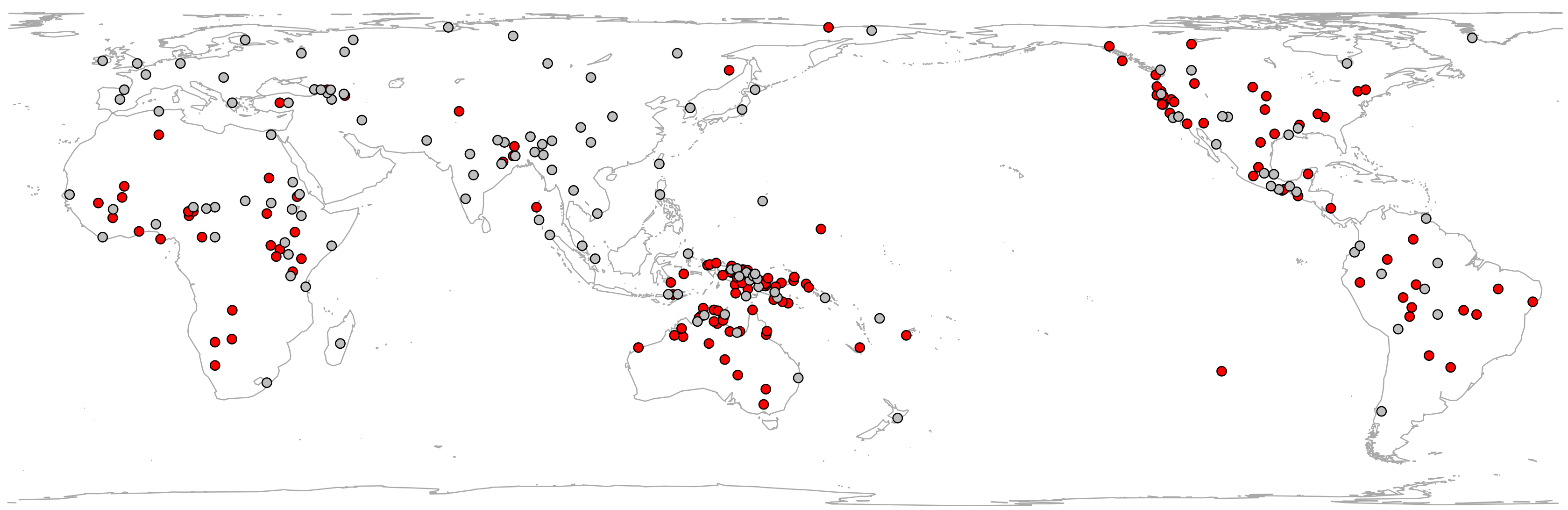

→ Randomly take *Pr(bias)* small families and declare them has being the sole survivors of larger families with a bias, and 1-Pr(bias) as being the sole survivors of larger families without a bias

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- with 1-Pr(type is representative), i.e. pick the only available or a random alternative type as the "real" direction of the bias

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$\rightarrow$ Therefore, we can take the mean of a set of random assignments, e.g. the mean of 2,000 extrapolations

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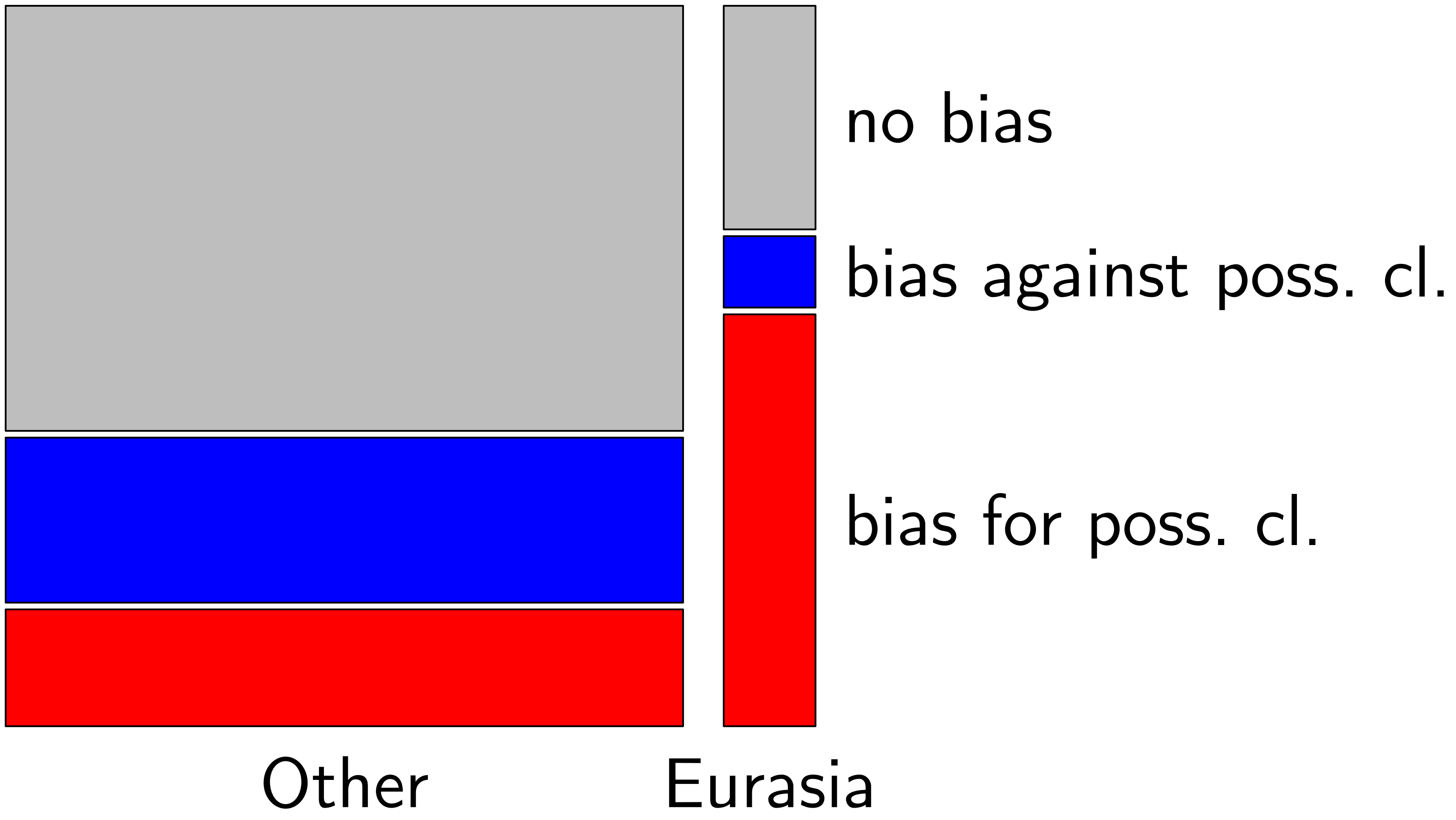

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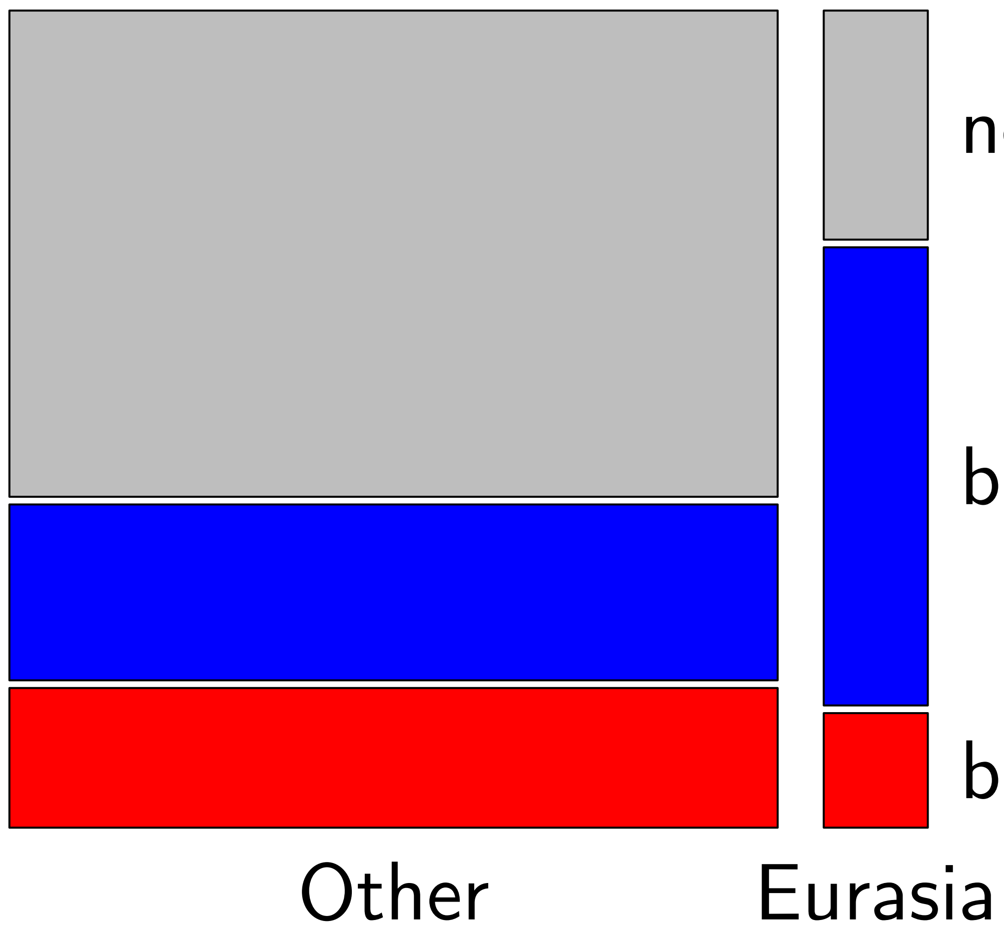

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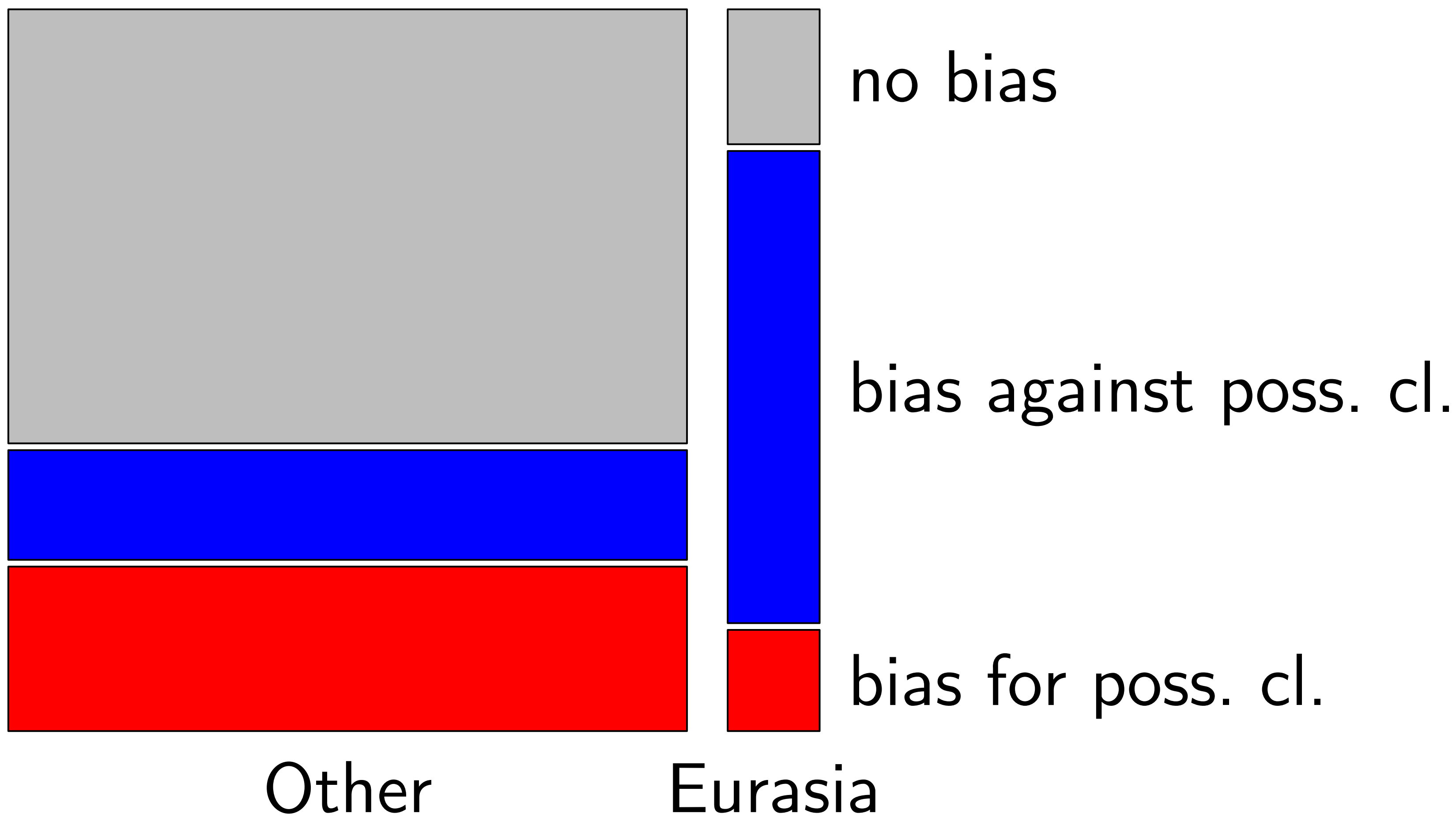

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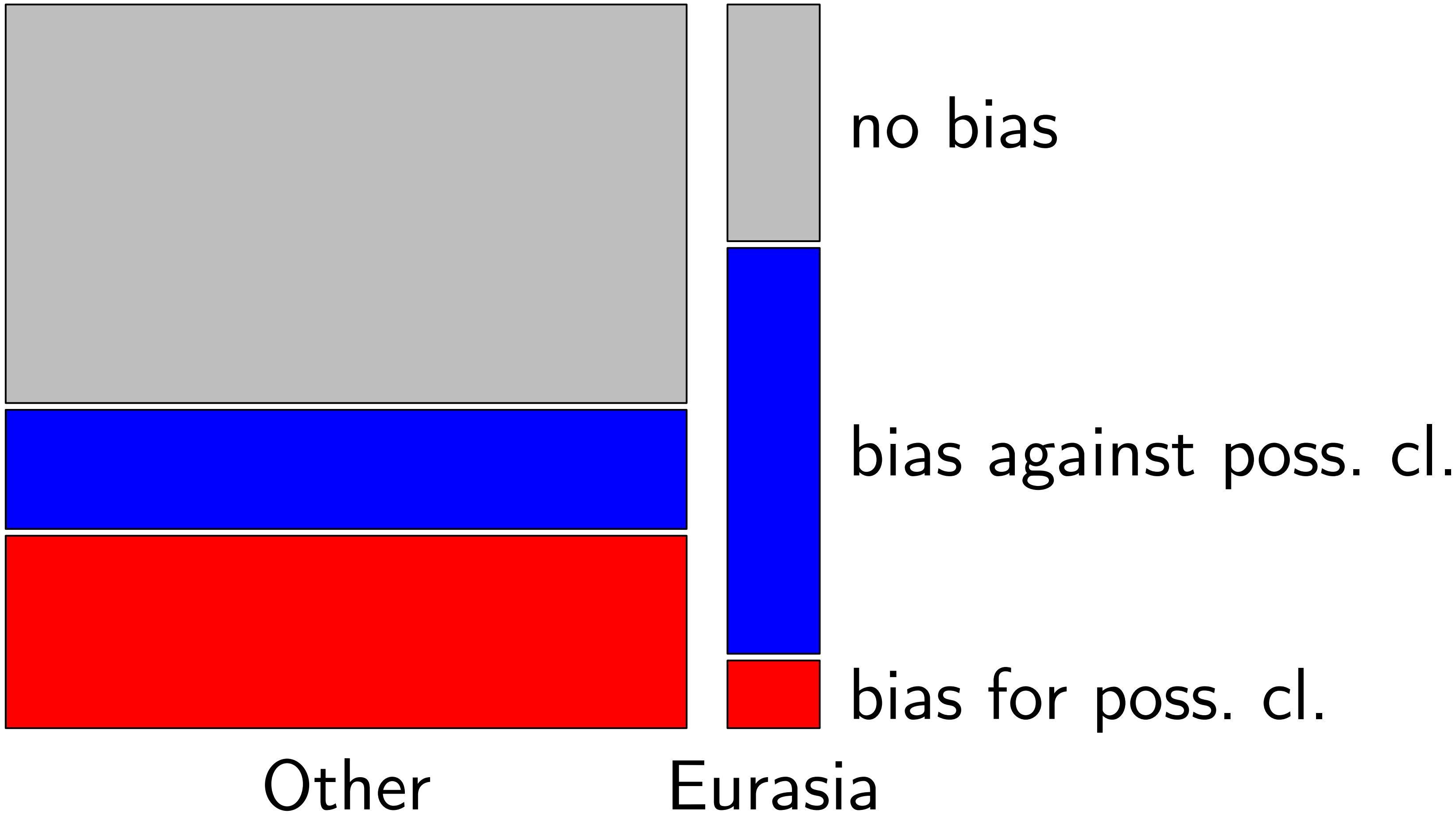

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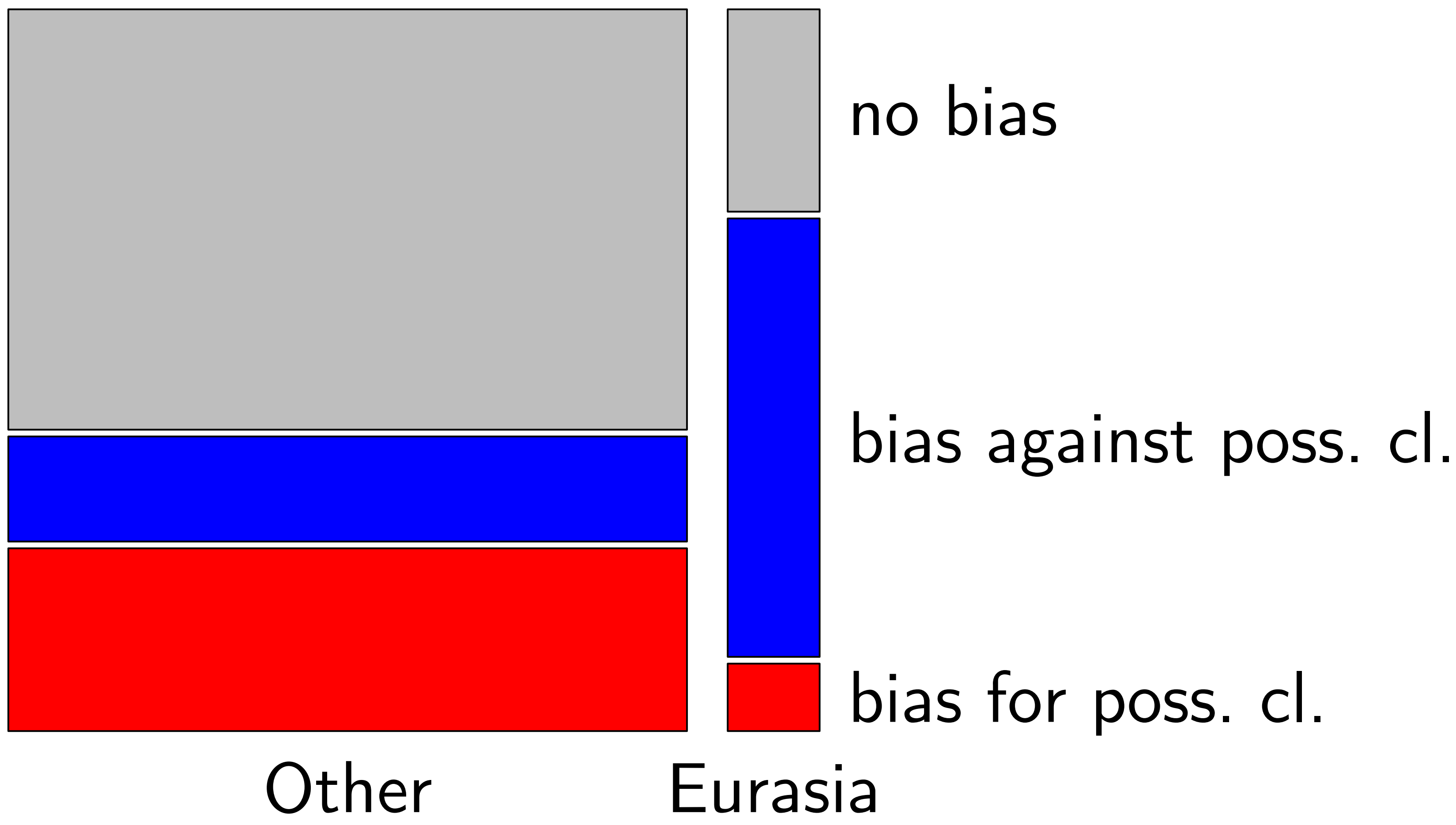

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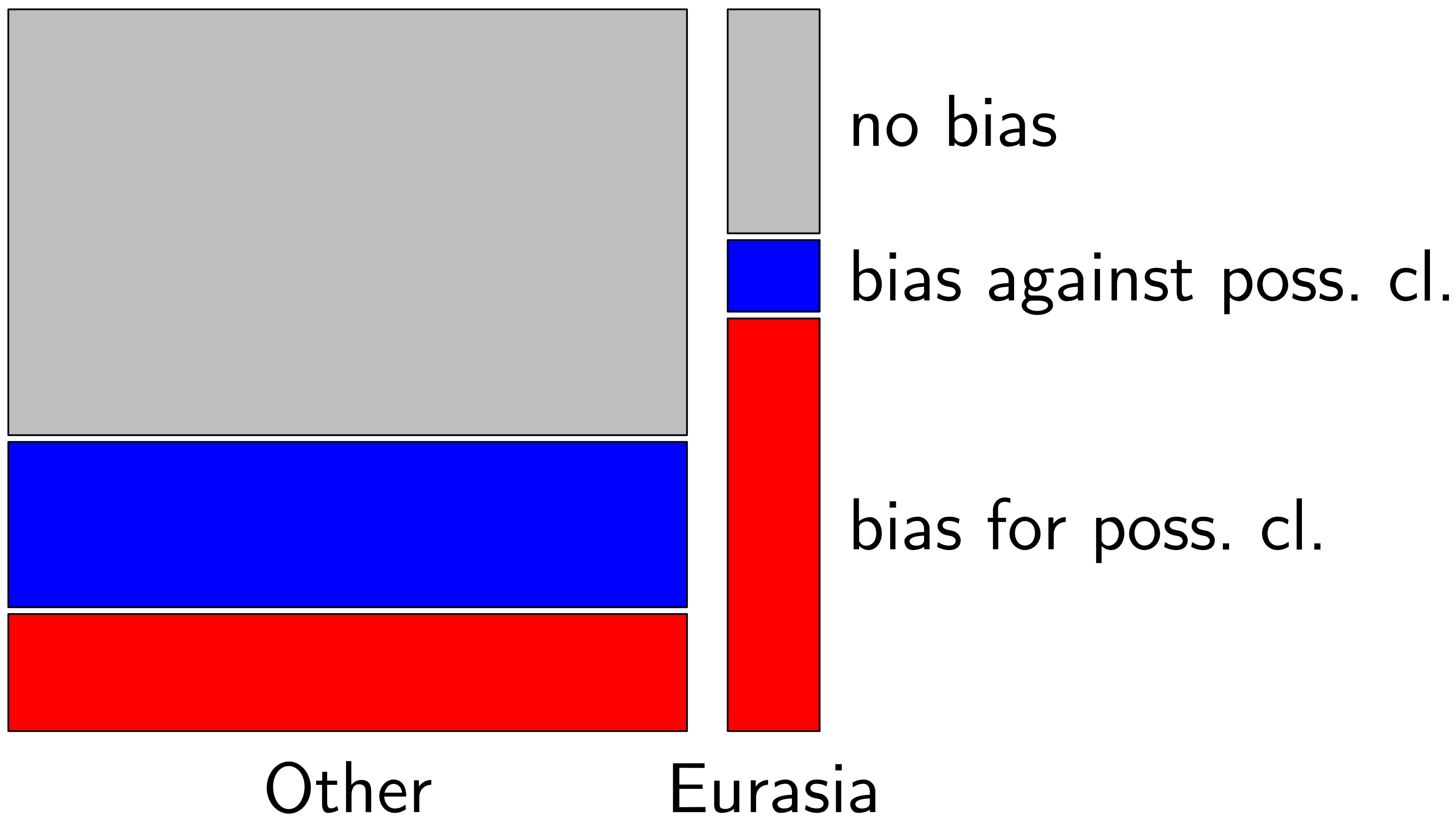

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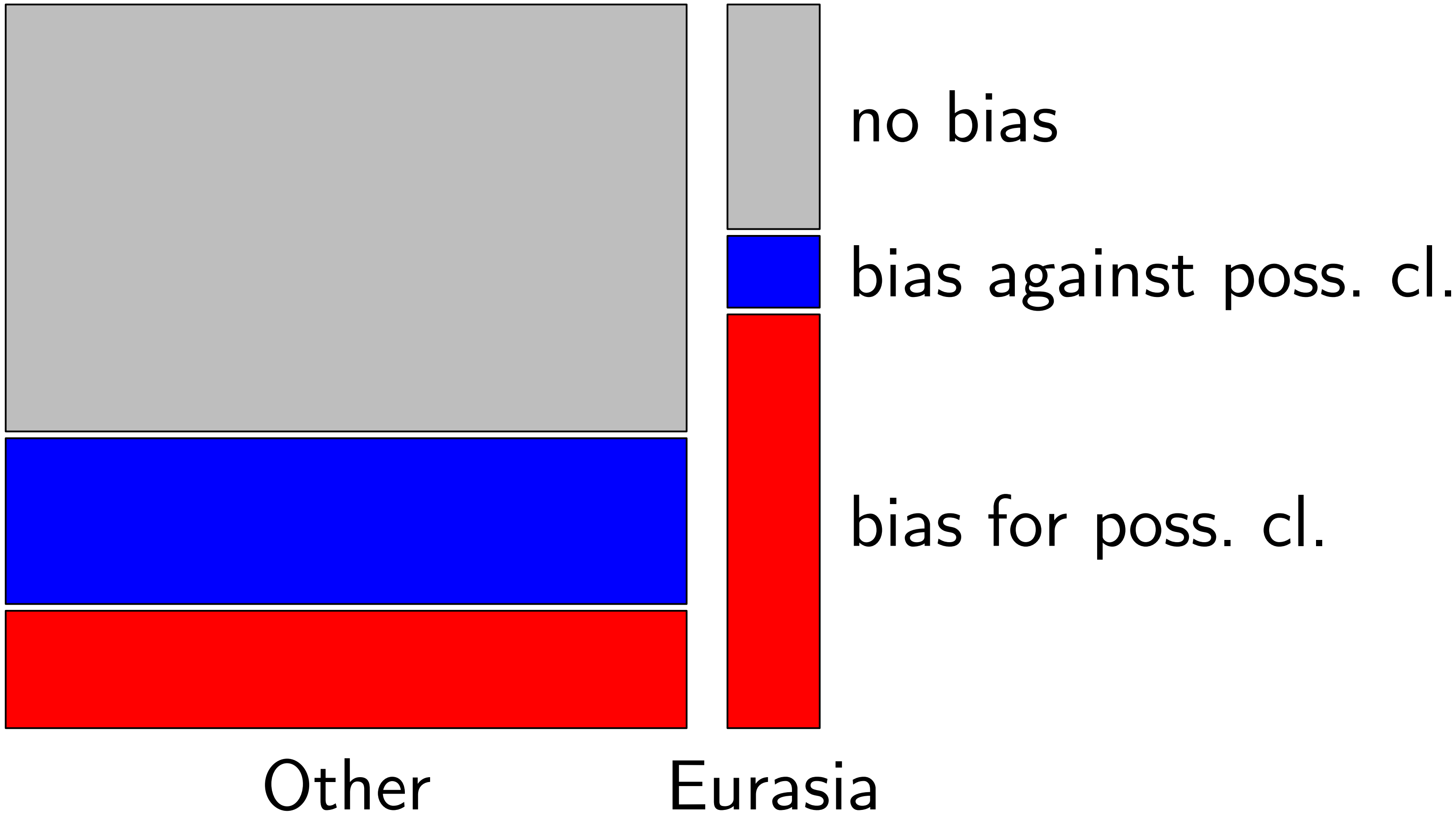


BIAS DIRECTION × AREA: $p = .006$ (Fisher Exact test)

DIVERSITY × AREA: $p = .03$ (Fisher Exact test)

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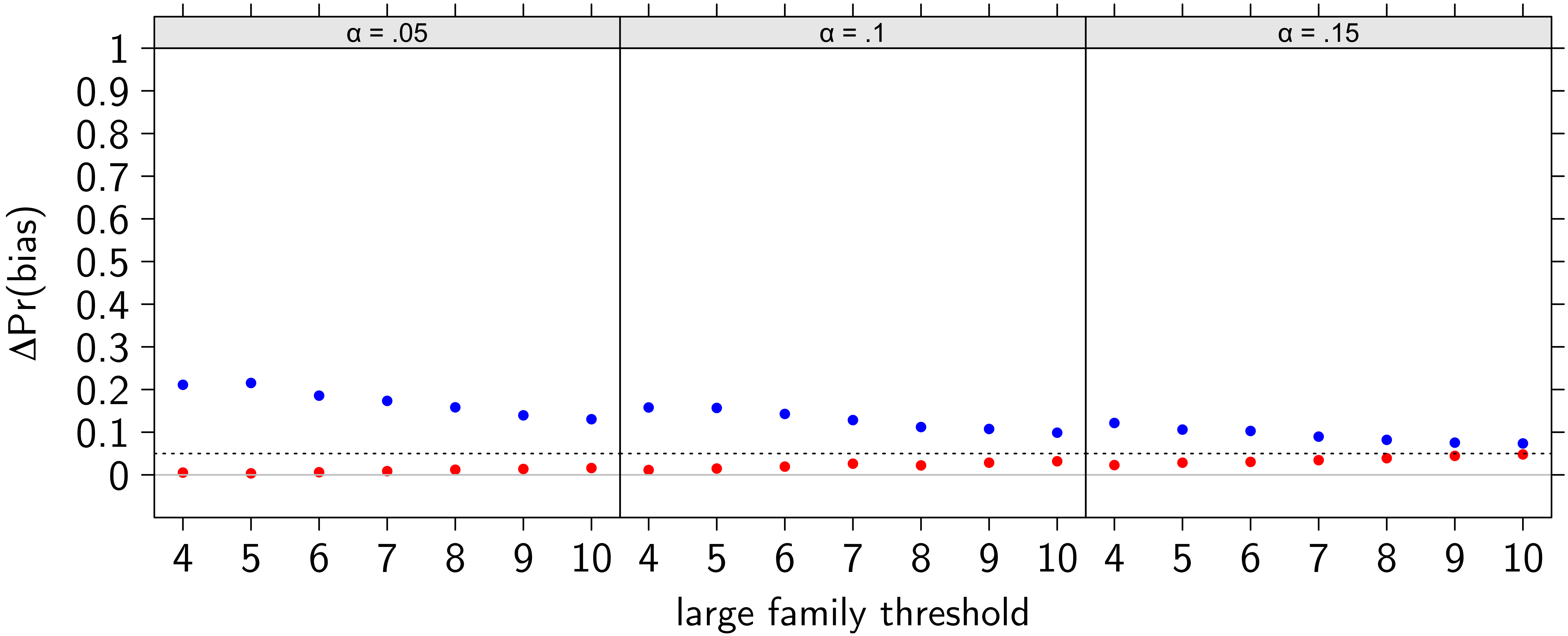
  - rejection levels of the binomial test that evaluates the presence of a biase

- ΔPr(bias): Absolute difference between Pr(bias) built into the simulation and what is estimated from the results by the Family Bias Method:

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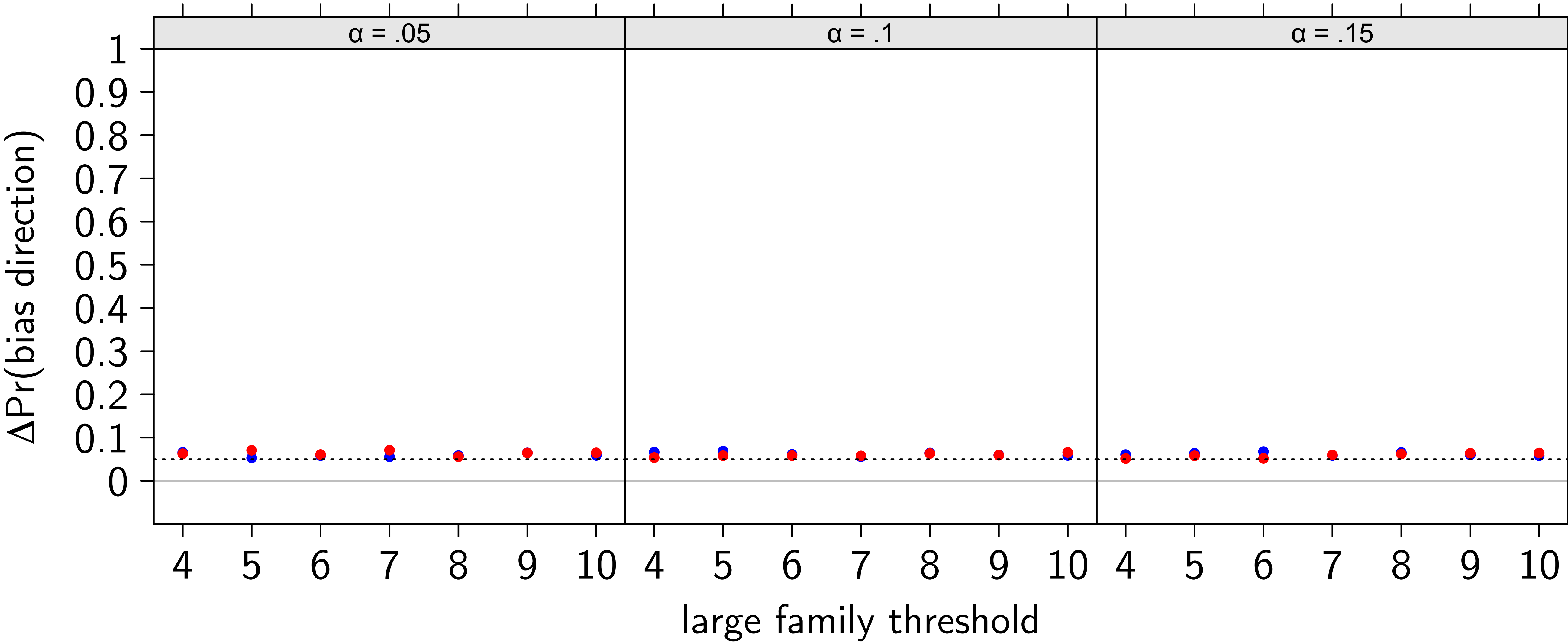


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