Exploring the statistical nature of independent chromosome segments

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Chromosome segments in a formula for accuracy approximation

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N = number of animals with phenotypes

M_e = number of independent chromosome segments

Number of independent segments 1k-20k

$$r = \sqrt{\frac{Nh^2}{Nh^2 + M_e}}$$

Daetwyler et al., 2008

Chromosome segments in APY

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Breeding values → $\mathbf{u} = \mathbf{Ts}$ ← M_e chromosome segments

Choose any N_e animals called "founder": $\mathbf{u}_f$

$\mathbf{s} = \mathbf{Q}\mathbf{u}_f + \boldsymbol{\varepsilon}_f$ Segments as a linear function of N_e founder animals

$\mathbf{u}_n = \mathbf{T}_n\mathbf{s} = \mathbf{P}_{nf}\mathbf{u}_f + \boldsymbol{\varepsilon}_n$ Non-founder animals as linear functions of founder animals

Accuracy of APY algorithm high when $M_e = 4N_eL$
(Stam, 1980; Pocrnic et. al, 2016)

What are the chromosome segments physically?

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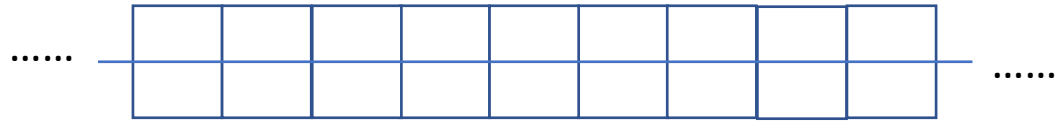
Hypothesis 1: equal size blocks

Average segment size 1/4M
With L=10, 40 segments per animal
$4N_eL$ equal size independent segments

Hypothesis 2: equal size haplotypes



Average haplotype size 1/2M
With L=10, 20 haplotypes per animal
$2N_eL$ equal size independent haplotypes

Materials and Methods: Data

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- QMSim (Sargolzaei & Schenkel, 2009)
  - Ten generations: 2,000 animals each
  - One polygenic trait, $h^2 = 0.3$
  - $N_e = 20$
  - Last 3 generations genotyped
    - L = 10 M, 50k SNP, 1,660 QTL

Models and Computations

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$$\mathbf{y} = \mathbf{1}'\mu + \mathbf{Z_s}\boldsymbol{s} + \boldsymbol{e}$$

- Validation:

  $cor(\mathbf{TBV}, \mathbf{Z_s}\hat{\boldsymbol{s}})$

  $cor(\mathbf{TBV}, \mathbf{GEBV})$

- GEBV computed using GBLUP in BLUPF90 software suite
- $\hat{\boldsymbol{s}}$ and $\mathbf{Z_s}\hat{\boldsymbol{s}}$ computed using in-house software written in Fortran

Results

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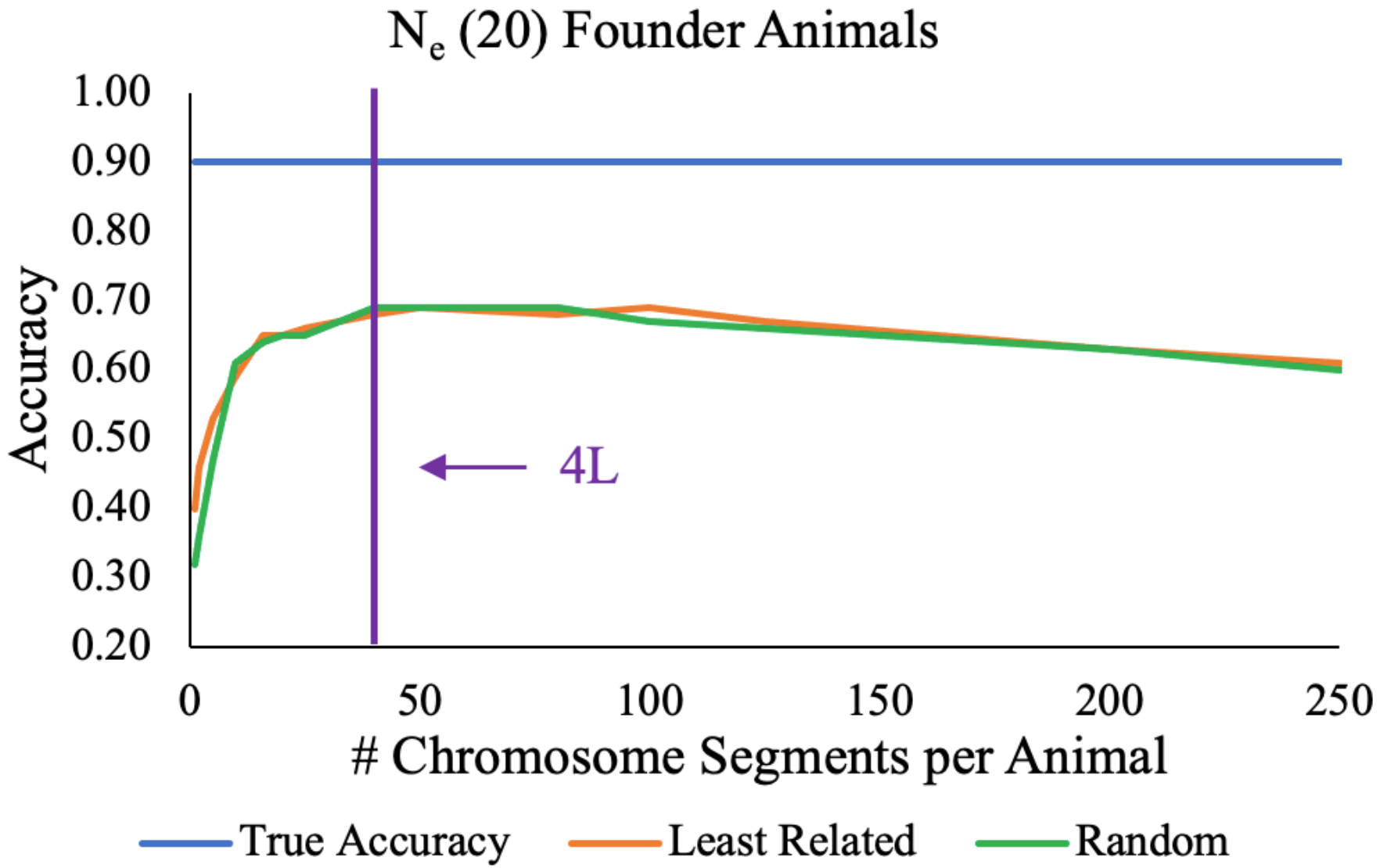

Results

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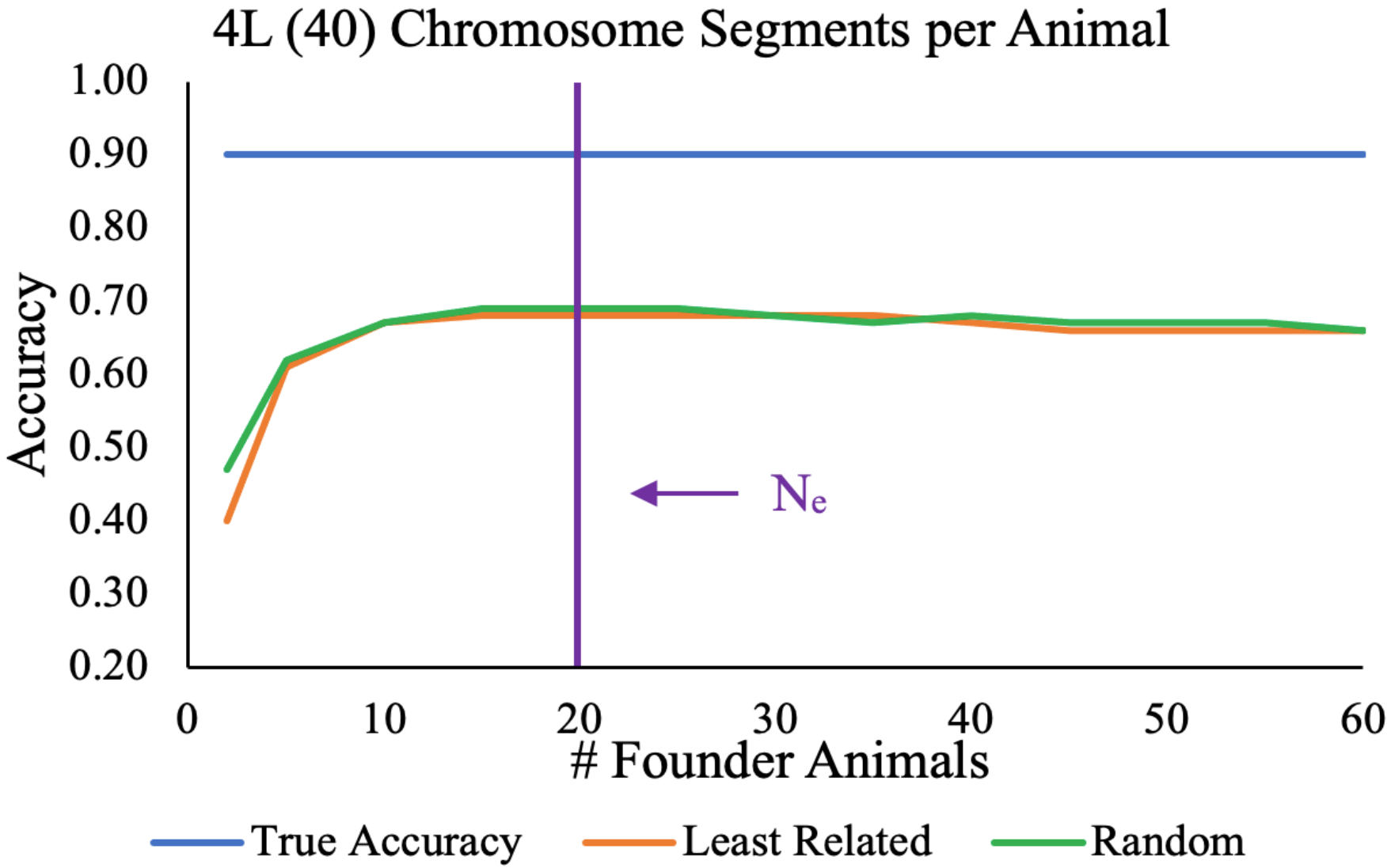

Why accuracies are not as high as GBLUP?

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- Wrong hypothesis
- Used pseudo-founders, not founders
- Used most similar segment of pseudo-founders, not a combination

Thank You!

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