

What can whole genome sequencing reveal about animal sociality?

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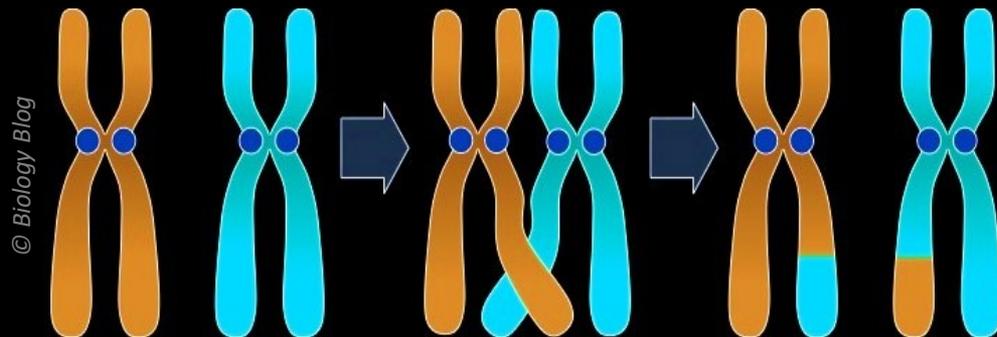
Evolution of sociality



- Difficult to understand evolution of sociality
- Kin selection theory predicts that individuals tend to bias their affiliative behaviours towards close relatives
- Challenging to accurately estimate dyadic relatedness

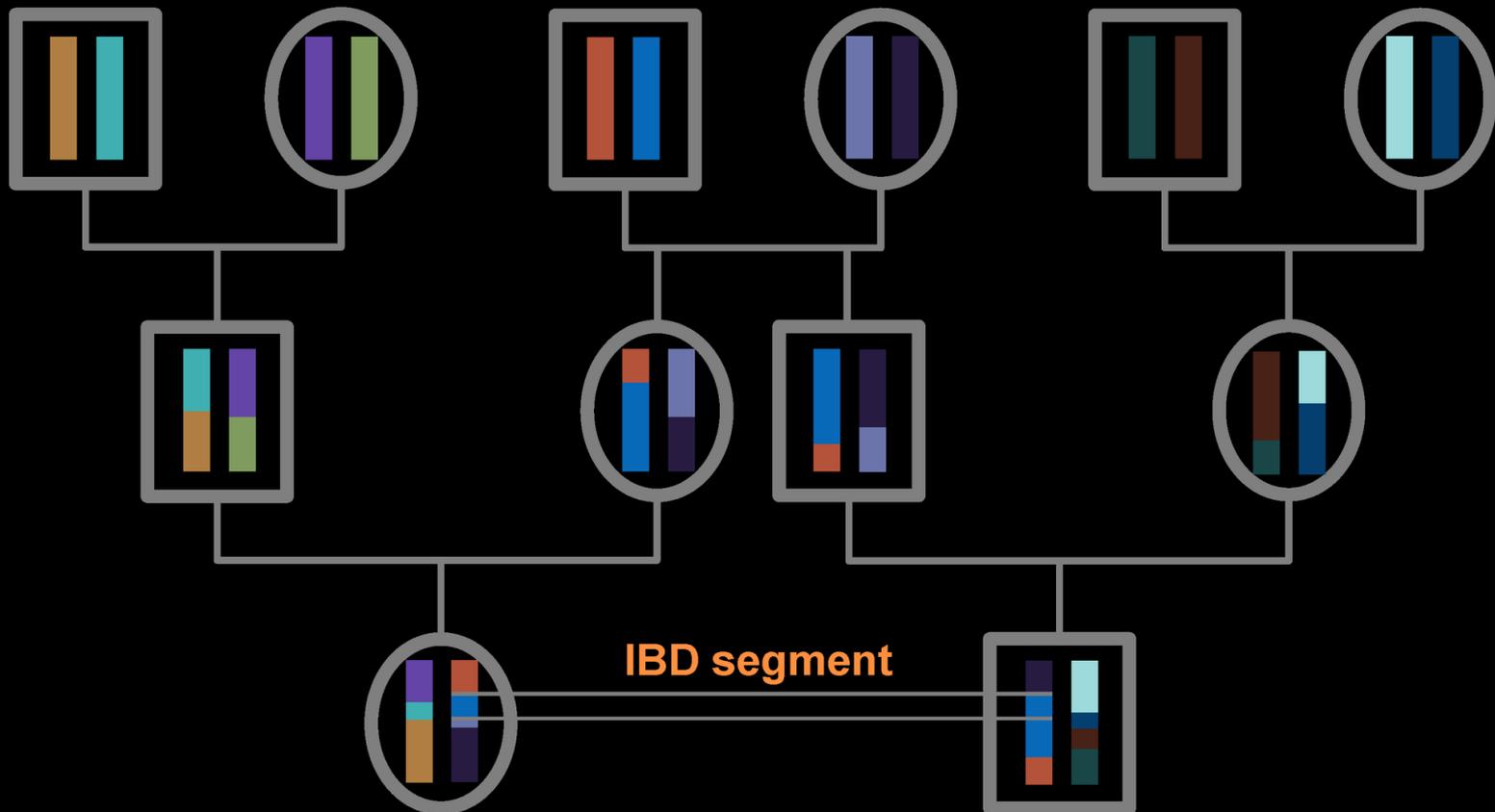
Kinship estimation

- Pedigree estimates probabilities of sharing alleles from common ancestors
- Pedigrees provide limited information
- Realized relatedness may strongly differ within categories
- Variation resulting from recombination events during meiosis



Realized relatedness

- Calculate length and number of DNA segments that are identical-by-descent (IBD) to assess realized relatedness



Macaca mulatta

- Multifemale, multimale groups consisting of kin and nonkin
- Female philopatry, male dispersal
- Extensive female family groups that hang out together continuously
- Females mate with different males in consecutive years
- Many maternal or paternal half-siblings, but full siblings rare



Study population

- Cayo Santiago, Puerto Rico
- 409 animals from India introduced in 1938
- Demographic data since 1956, genetic data since 1992
- Pedigree data limited to three generations



Whole genome sequencing

Sample preparation (n = 880)

Sample collection
(blood, tissue)



DNA extraction



Preparation for
sequencing

Whole genome sequencing

Sample preparation (n = 880)

Sample collection
(blood, tissue)



DNA extraction



Preparation for
sequencing

Sequencing

(PCR amplification)



Library preparation



Illumina sequencing
20x or 6x coverage

Whole genome sequencing

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DNA extraction



Preparation for
sequencing

Sequencing

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Library preparation



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Data processing

Mapping of
reads to
ref-genome



Variant calling
(SNPs)



Imputation of
missing variants



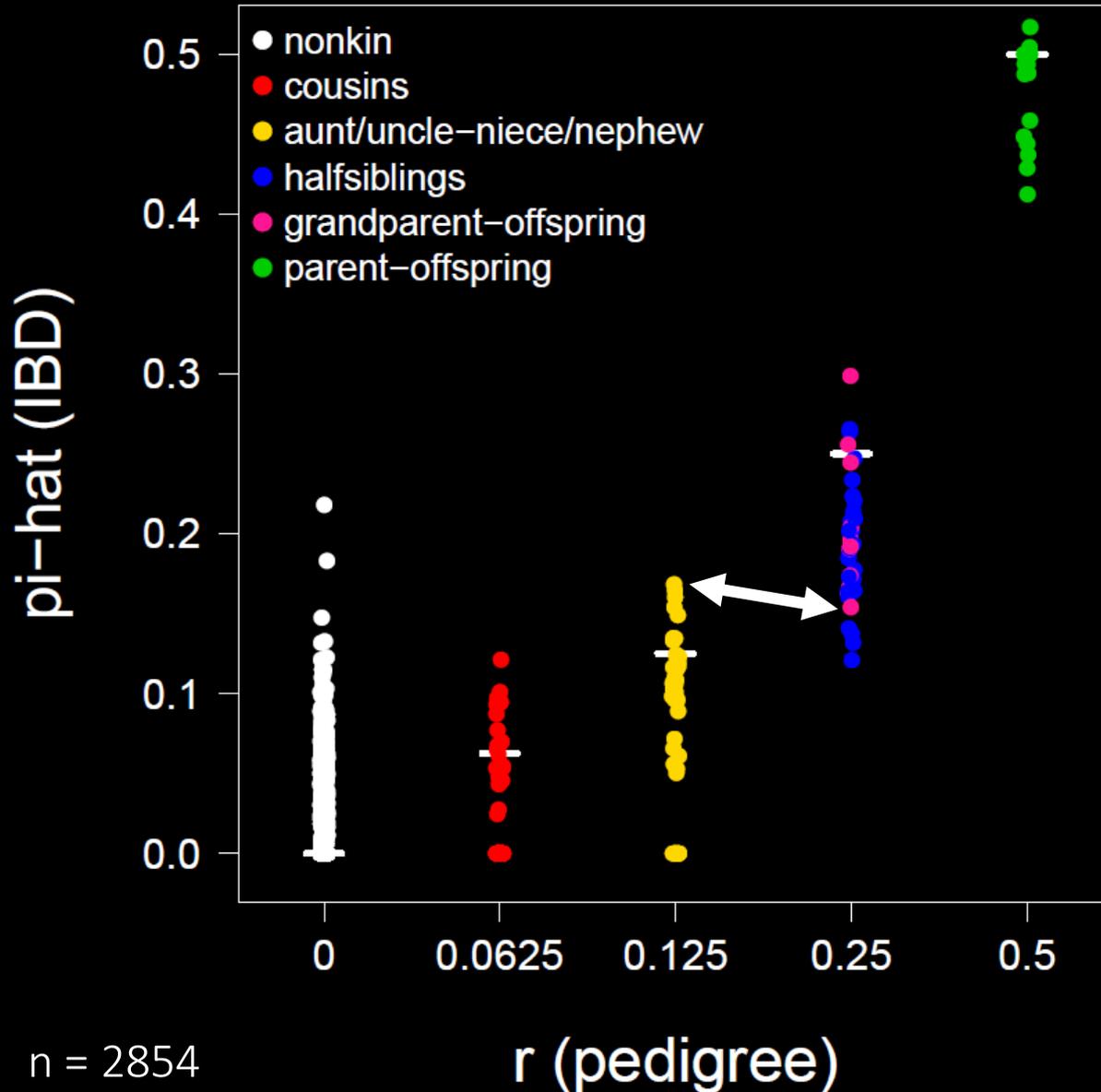
IBD calculation

1.

Quantify variation in IBD within and between kin classes using whole genome sequencing data (WGS)

- ongoing work -

1. IBD vs. pedigree



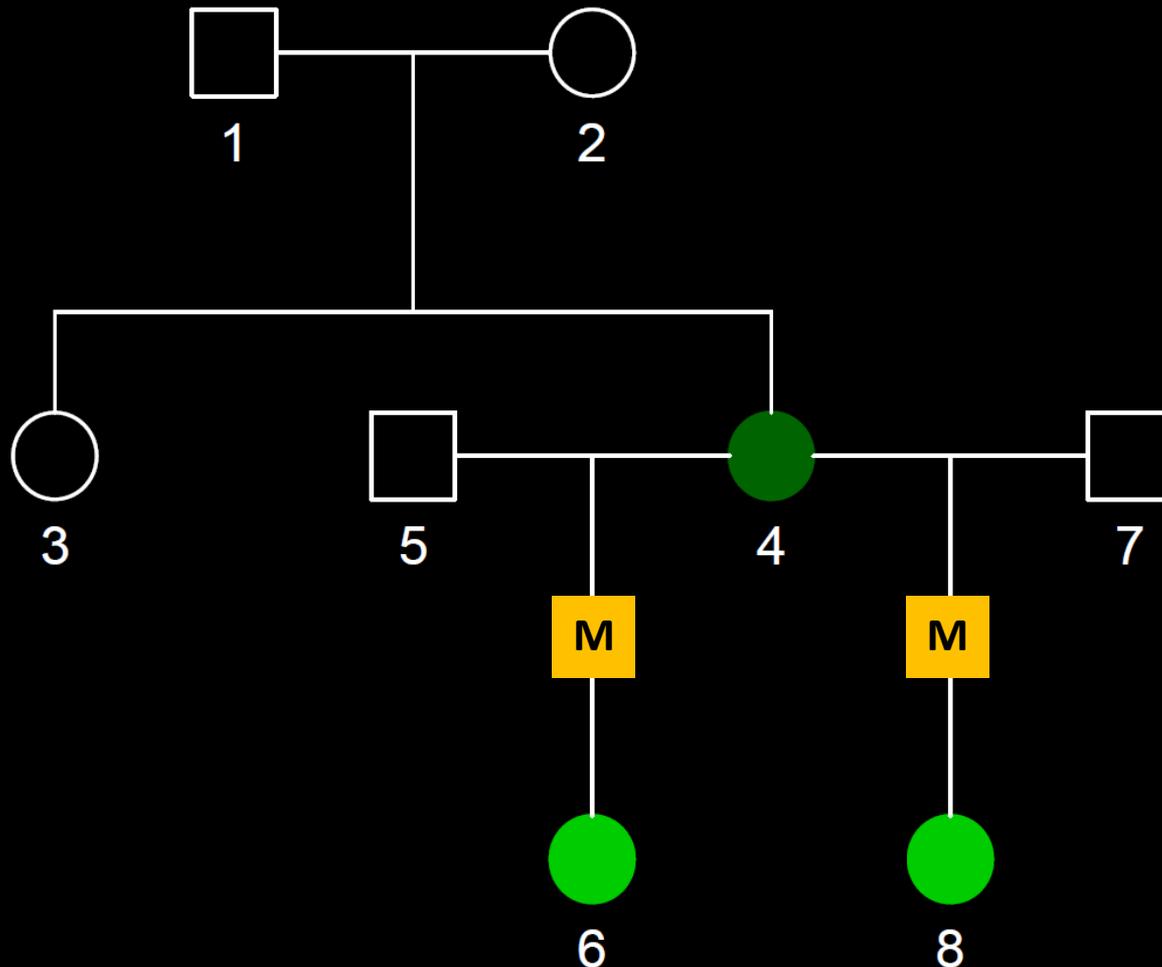
- High variability within kin classes
- Overlap between kin classes

→ relatedness is continuous!

1. IBD segments

half-siblings

aunt/uncle-niece/nephew

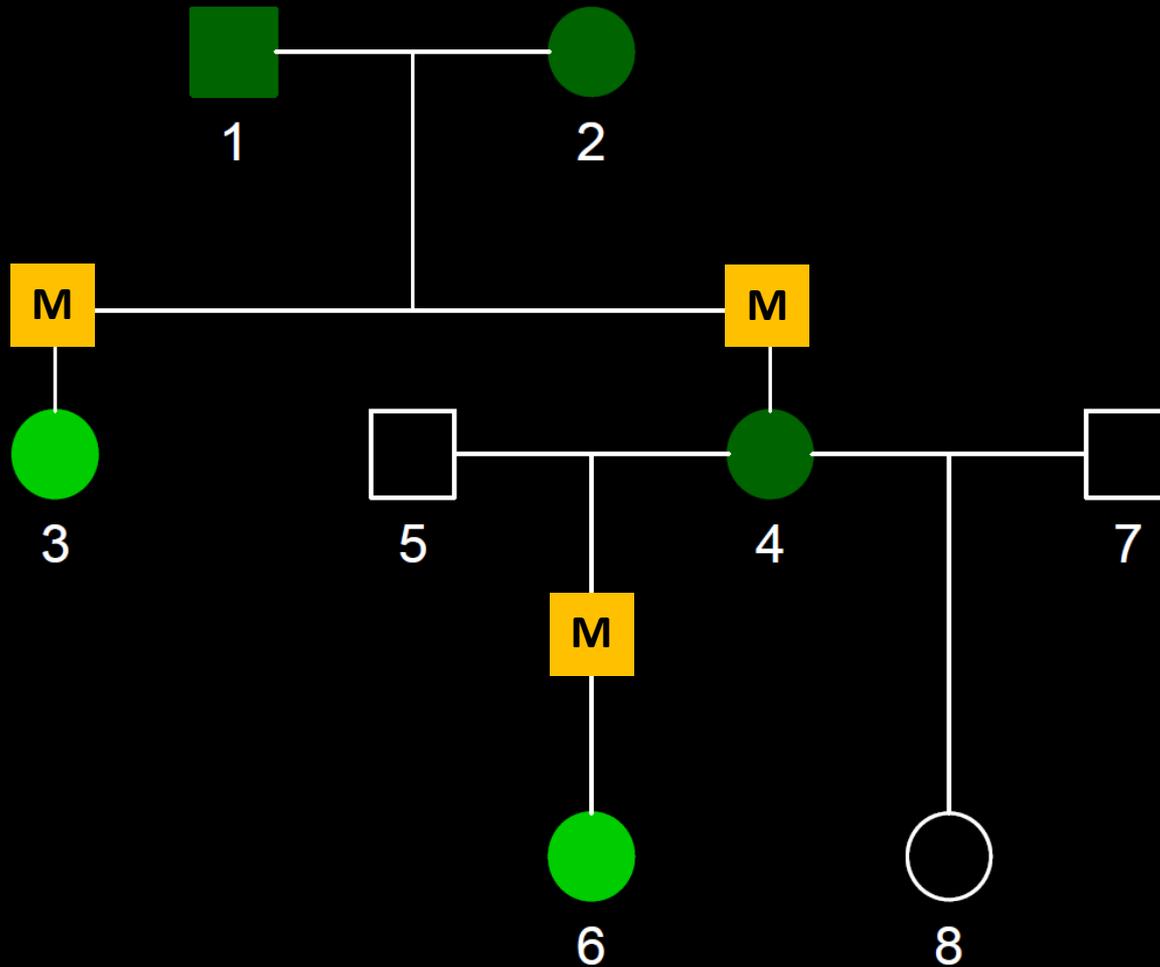


$r = 0.25$

1. IBD segments

half-siblings

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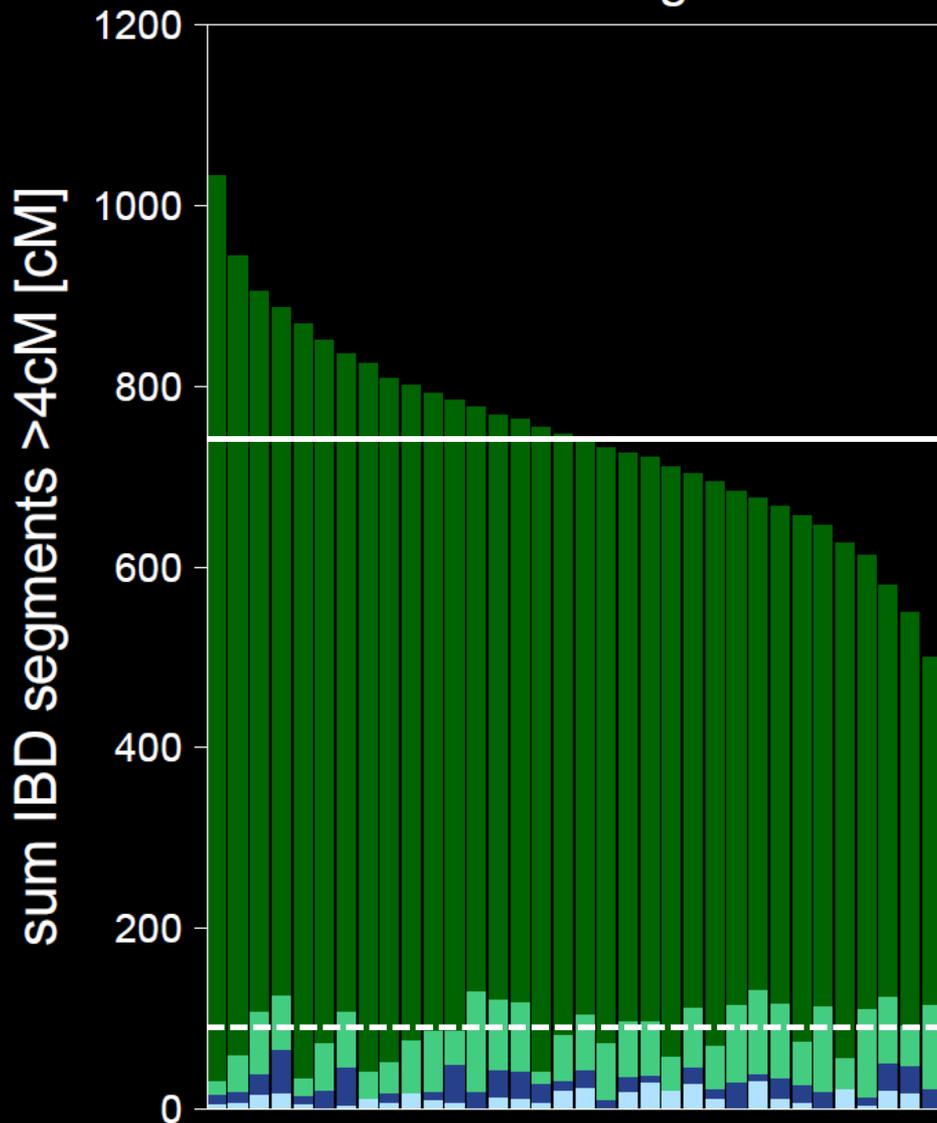


$r = 0.25$

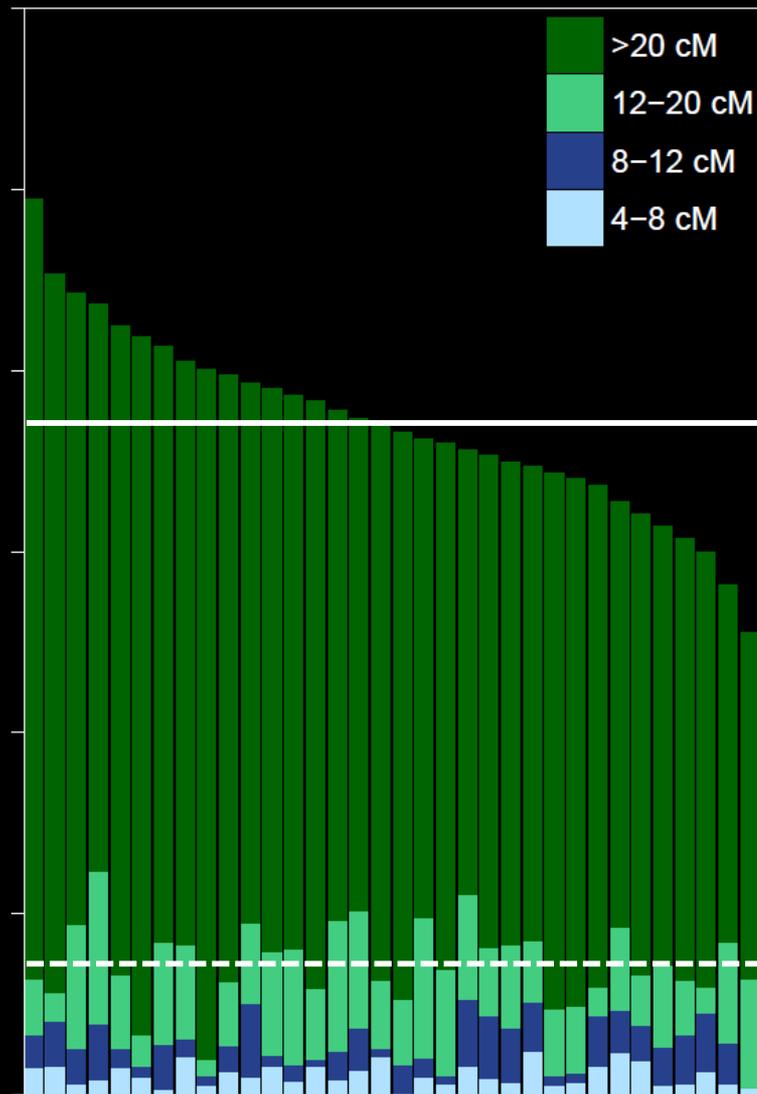
1.

IBD segments

half-siblings



aunt/uncle-niece/nephew



2.

Determine whether social preferences are predicted by gradient of IBD

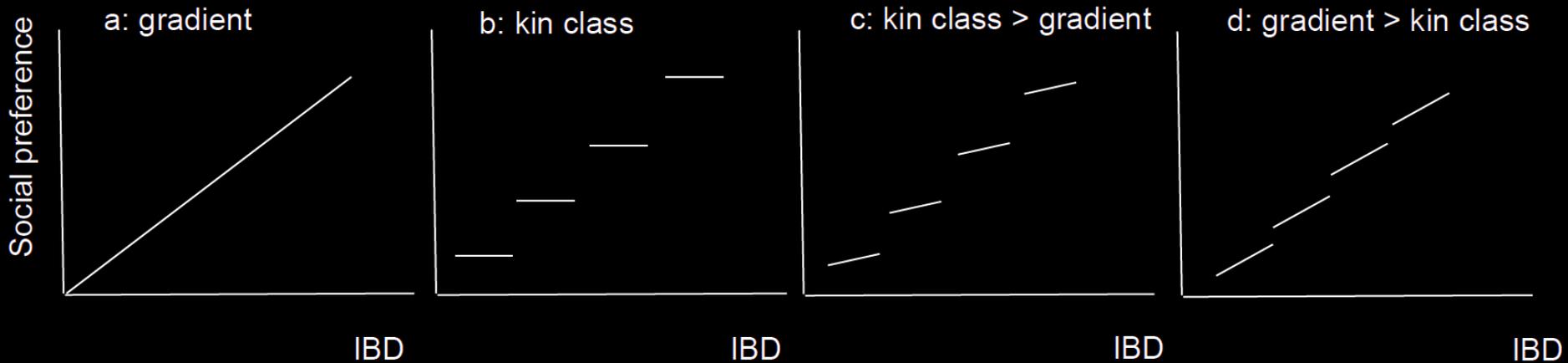
- future work -

2. Kin recognition and kin bias

- Kin recognition basis for kin bias to evolve
- Maternal kin use familiarity
- Paternal kin may use phenotype matching: similar behavioural and/or physical traits
- Previous studies: rates of social interactions between kin increases with increasing pedigree relatedness
- What does realized genetic variation contribute to kin recognition and kin bias?

2. Predictions

- Available data: social preference and perception of kin cues
- Amount of IBD shared will predict kin bias within and between kin classes



- Paternal kin will mainly follow gradient in IBD (a/d)
- Maternal kin are primarily influenced by social constrains (c)

Conclusion

- IBD based on WGS data reveals variation in relatedness within and between kin classes
- Novel way to understand role of relatedness in evolution of sociality in animals

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