

PRIMATES, PSMC, AND PAPER QUESTIONS – A PEERLESS PILGRIMAGE –



AARHUS
UNIVERSITY
DEPARTMENT OF MOLECULAR BIOLOGY AND GENETICS

EVOLUTIONARY THINKING 2023
WEEK 45

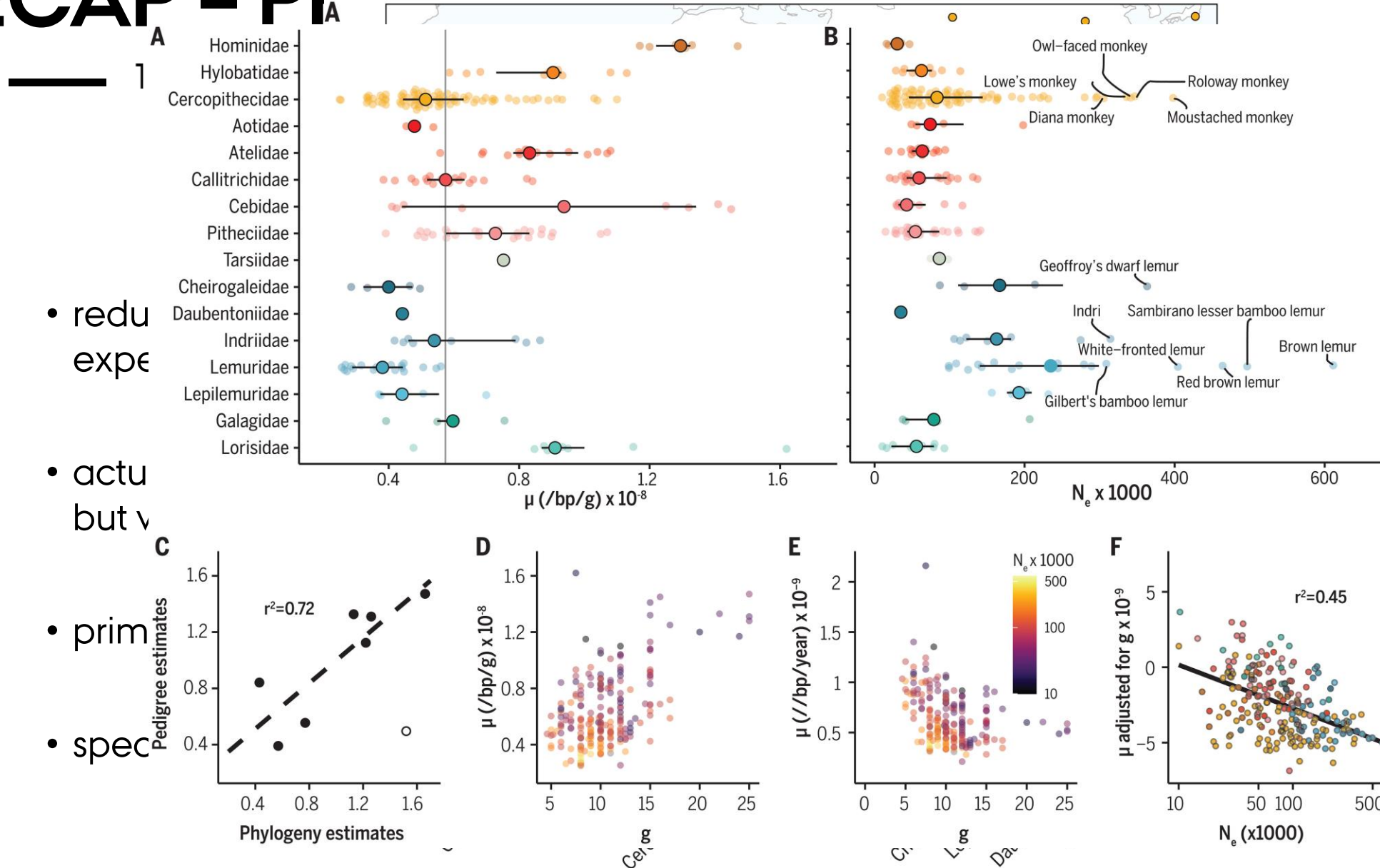
CALIN PANTEA
PHD STUDENT



TODAY'S OVERVIEW

- Lecture recap (brief) – until 12:25
- PSMC (will not show up in the R exercise this Friday) – until 12:35
- Missense variant paper – questions – until 13:35, with a break at 13:00
 - + discussion 13:35 to 13:50
- Menti quiz for the recap

RECAP – PRIMATE DIVERSITY 1



from 233

LON ID SHIVAKUMARA MANU ID

Affiliations

on size

tygosity,

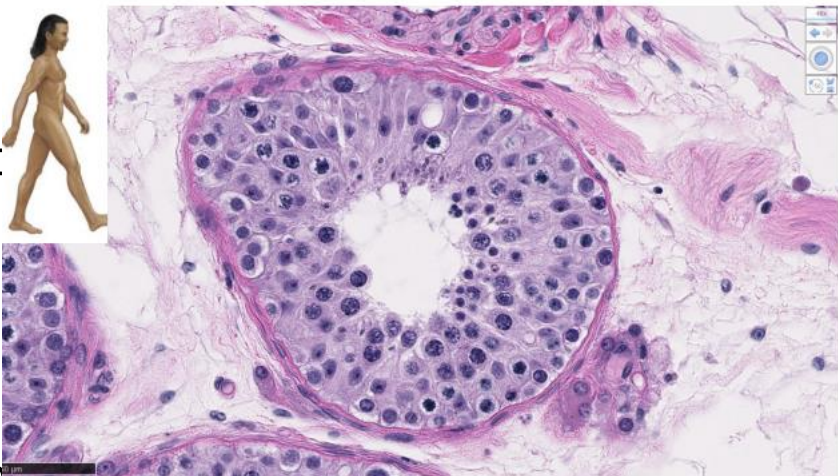
sity



RECAP – PRIMATE DIVERSITY 2

12:15-12:25

• fast



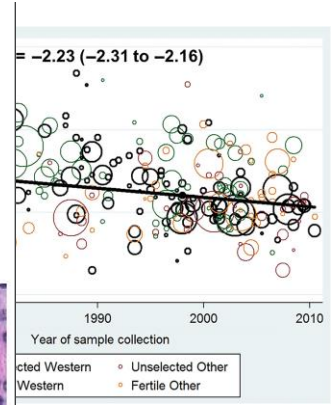
• prim



• SWE



Prepared by Sofia Boeg-Winge

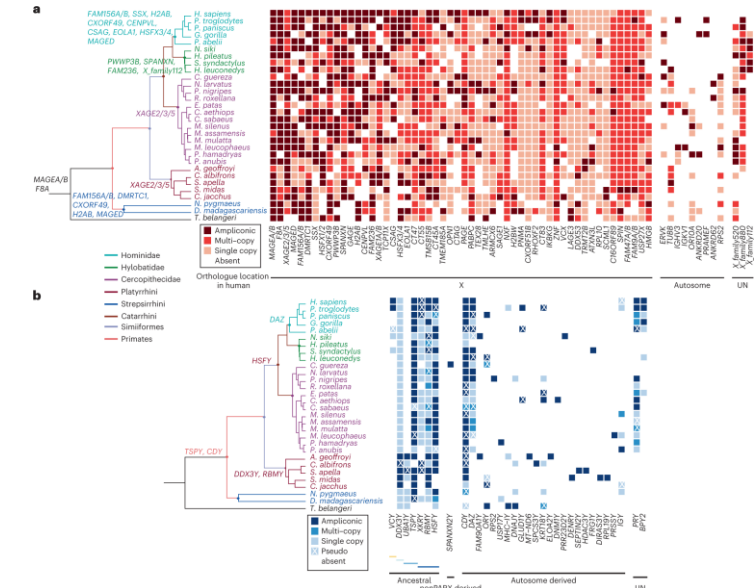
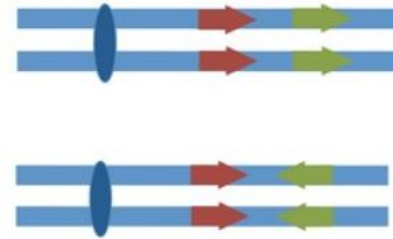
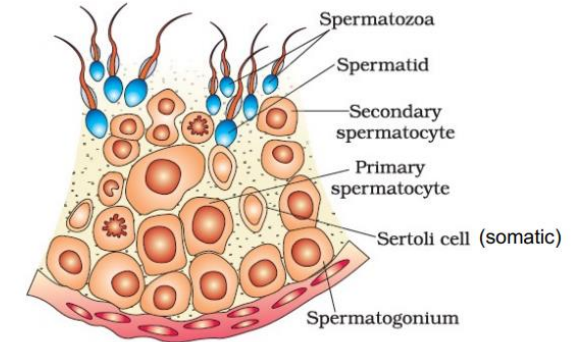
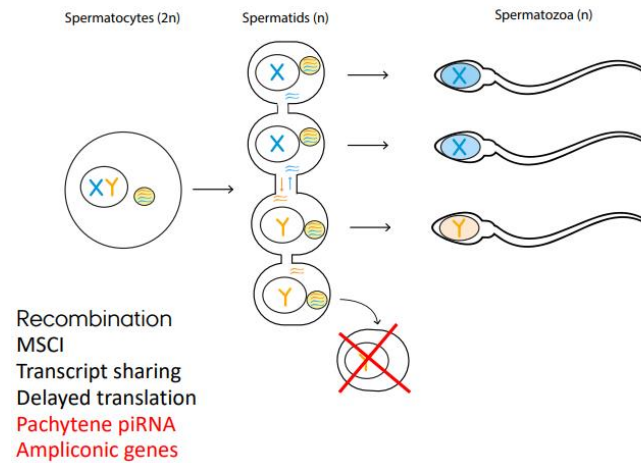


DS

RECAP – PRIMATE DIVERSITY 2

12:15-12:25

- meiotic drive
- may underlie primate testis evolution
- ampliconic genes might be involved
- strong selective sweeps on primate X amplicons



RECAP – PRIMATE DIVERSITY

— 12:15-12:25

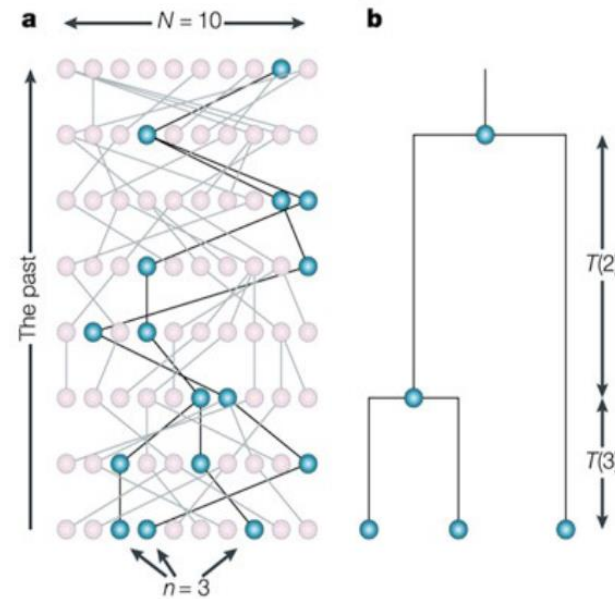
- Reduction in diversity around genes differs among great ape species and correlates with their estimated population size
- Background selection or constant rate of sweeps in different species does not explain this population size effect
- Larger populations have more strong sweeps
- This will be the case if the rate of adaptive evolution by strong sweeps is mutation limited
- Molecular sexual antagonism during gametogenesis can lead to very fast speciation
- Not observed in primates...yet. But we have very nice evidence from other species
- Ampliconic gene families are good candidates as the vehicle for such dramatic effects



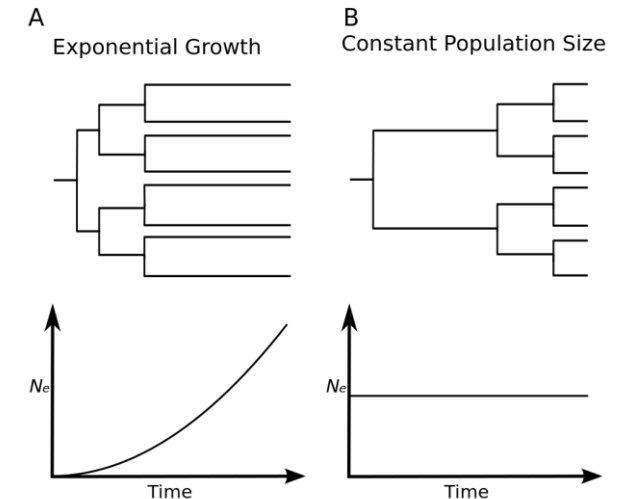
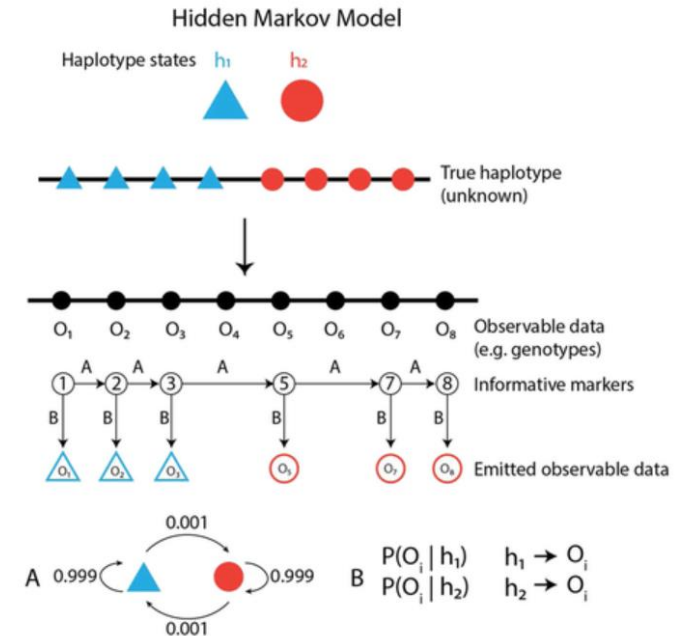
HMM, COALESCENT, AND N_e

12:25-12:35

- HMM to model the coalescent
- N_e estimation from coalescent
- what would we need to look at N_e history in a diploid individual?



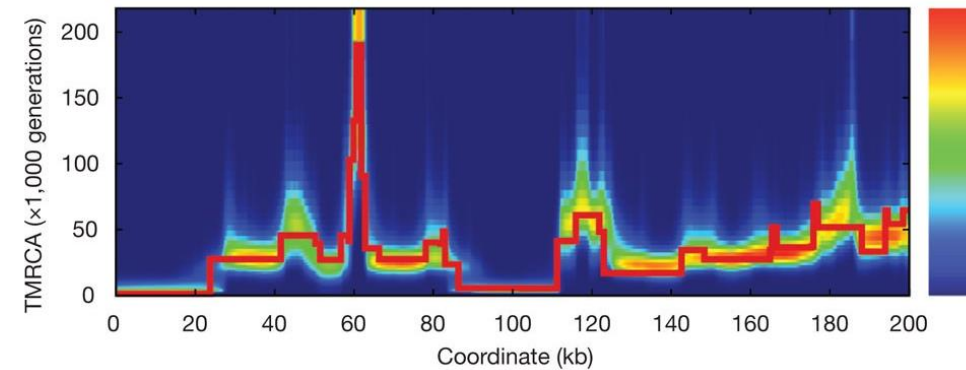
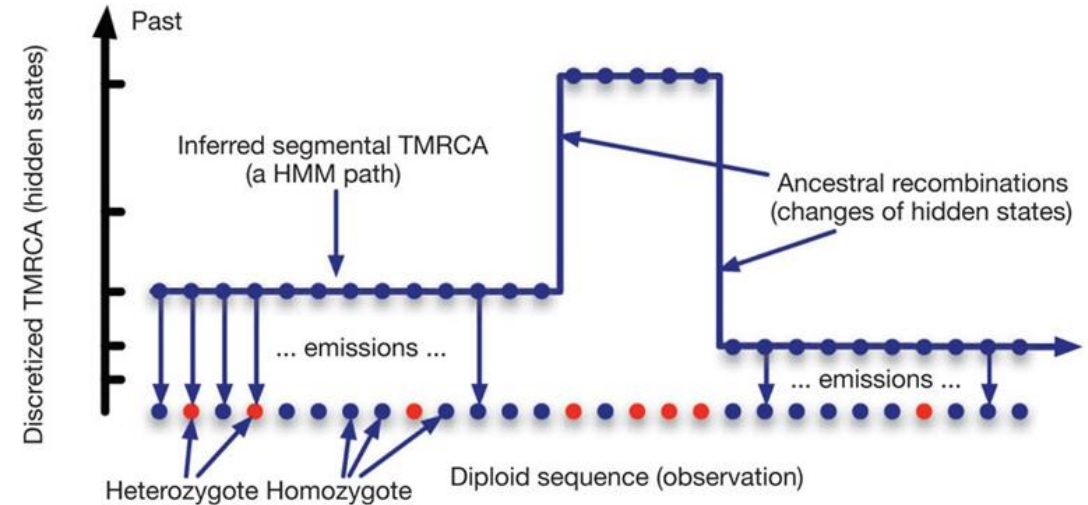
$$E[t_{MRCA}] = \sum_{k=2}^n E[t_k] = \sum_{k=2}^n \frac{2}{k(k-1)} \quad (3.12)$$



PSMC-HMM

12:25-12:35

- Pairwise sequentially markovian coalescent (PSMC): a HMM approach to estimating N_e
- TMRCA distribution across genome by local distribution of binned heterozygous sites
- considers changes in hidden states due to recombination

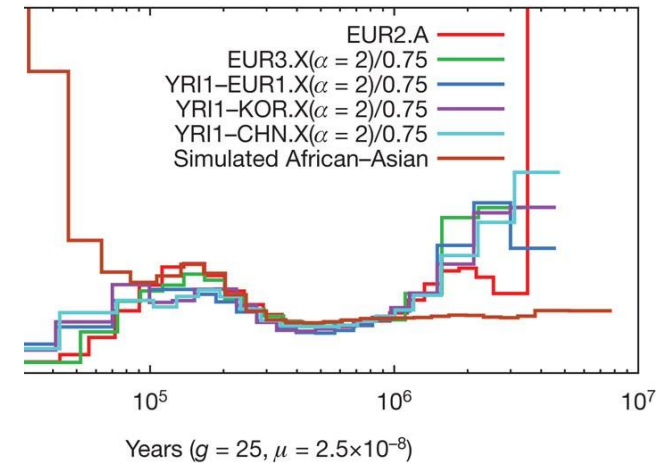
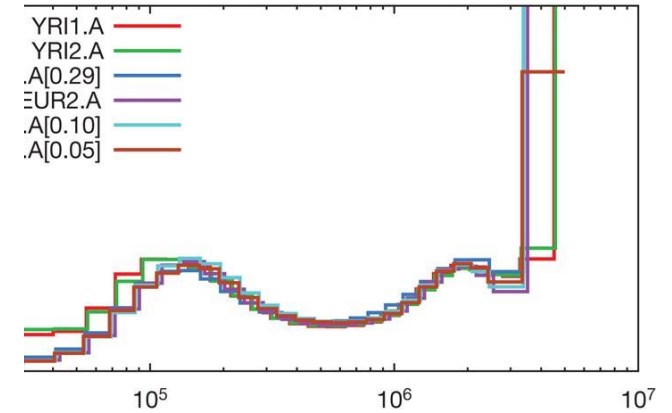
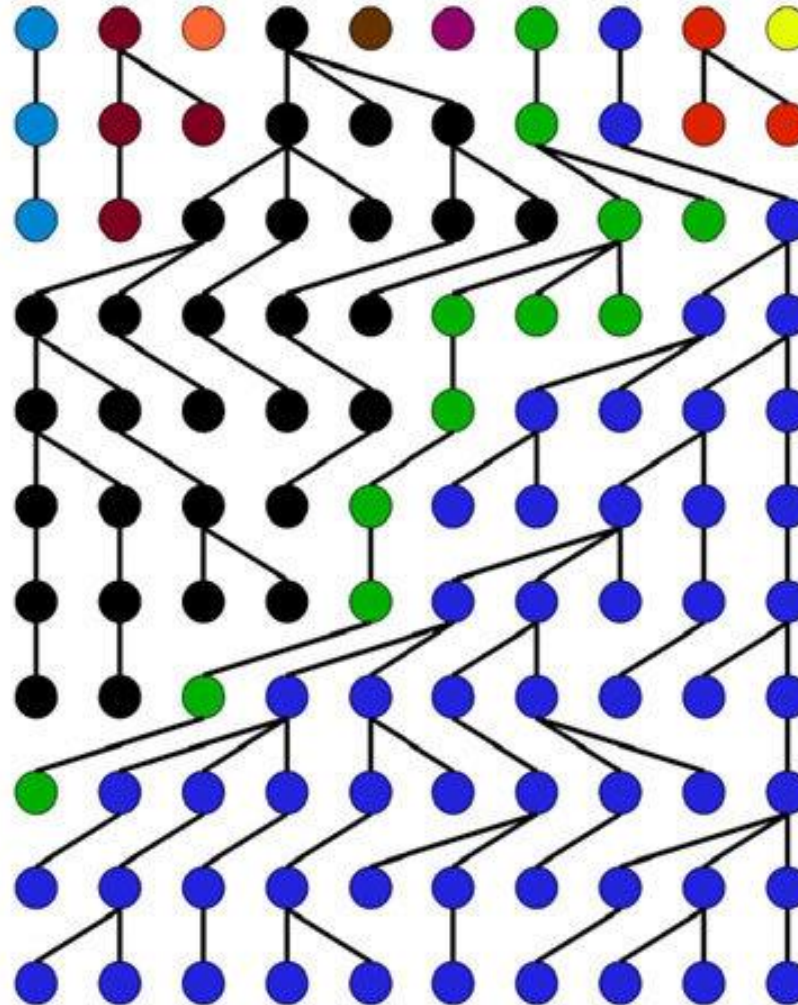


PSMC-HMM

— 12:25-12:35

- model N_e with respect to time
- interpretation of population history
- N_e estimation at very ancient times

why?



PSMC – PROS AND CONS

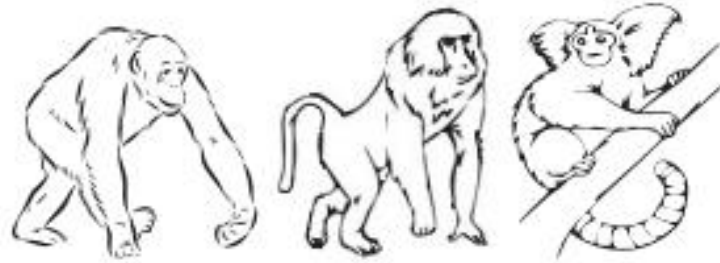
— 12:25-12:35

- N_e inference based on single, unphased genome sequence
- N_e trends throughout its history
- very poor estimates of recent and very ancient N_e due to reduced info on coalescence
- easily confounded by ILS and population dynamics
- only capable of single-genome N_e inference
 - but newer PSMC-based models take these into account



PAPER QUESTIONS

— 12:35-13:00 and 13:15-13:35

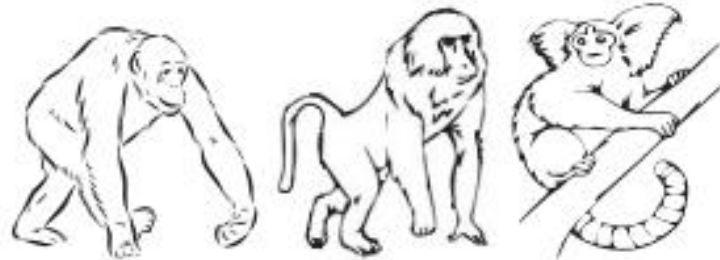


BREAK – UNTIL 13:15



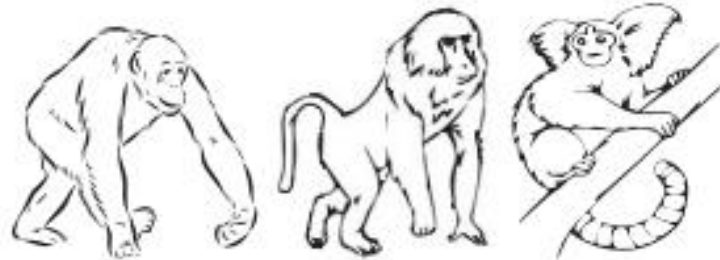
PAPER QUESTIONS

— 12:35-13:00 and 13:15-13:35



PAPER DISCUSSION

— 13:35-13:50



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MENTI QUIZ

— 13:50-14:00

Instructions

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