Welcome to OEB 253r Spring 2023!

Go to Files for pdfs of the readings.

Schedule:

Week 1 - Jan 23 John Wakeley (Leffler et al, 2012)

Week 2 - Jan 30 Julius Tabin (DeWitt et al, 2021)

Week 3 - Feb 06 Artur Rego-Costa (Aggarwala and Voight, 2016)

Week 4 - Feb 13 Christina Steinecke (Brown and Kelly, 2020)

Feb 20 NO MEETING (Presidents' Day)

Week 5 - Feb 27 Cheshta Bhatia (Seplyarskiy et al, 2021)

Week 6 - Mar 06 Ian Hughes (Baumdicker et al, 2012)

Mar 13 NO MEETING (Spring Break)

Week 7 - Mar 20 Peyton Jones (Hodgkinson and Eyre-Walker, 2011)

Week 8 - Mar 27 Shuzhe Guan (Bergeron et al, 2023)

Week 9 - Apr 03 Lily Wang (de Manuel, Wu and Przeworski, 2022)

Apr 10 NO MEETING (John away)

Week 10 - Apr 17 Berk Alpay (Hopf et al, 2017)

Week 11 - Apr 24 Galen Tiong (Waldvogel and Pfenninger, 2021)

Some possible readings (* already discussed):

* Aggarwala and Voight (2016) An expanded sequence context model broadly explains variability in polymorphism levels across the human genome. Nature Genetics, 48(4):349â€“355. doi: 10.1038/ng.3511

* Bergeron et al (2023) Evolution of the germline mutation rate across vertebrates. Nature 615:285 doi: 10.1038/s41586-023-05752-y

* Brown and Kelly (2020) Severe inbreeding depression is predicted by the â€œrare allele loadâ€ in Mimulus guttatus. Evolution, 74: 587â€“596. doi: 10.1111/evo.13876

Carlson et al (2018) Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. Nature Communications, 9(1):3753. doi: 10.1038/s41467-018-05936-5

* de Manuel, Wu and Przeworski (2022) A paternal bias in germline mutation is widespread in amniotes and can arise independently of cell division numbers. eLife 11:e80008. doi: 10.7554/eLife.80008

* DeWitt et al (2021) Nonparametric coalescent inference of mutation spectrum history and demography. Proceedings of the National Academy of Sciences, 118(21):e2013798118. doi: 10.1073/pnas.2013798118

Harpak, Bhaskar and Pritchard (2016) Mutation rate variation is a primary determinant of the distribution of allele frequencies in humans. PLoS Genetics, 12:e1006489. doi: 10.1371/journal.pgen.1006489

Harris and Pritchard (2017) Rapid evolution of the human mutation spectrum. eLife, 6:e24284. doi:

10.7554/eLife.24284

* Hodgkinson and Eyre-Walker (2011) Variation in the mutation rate across mammalian genomes. Nature Reviews Genetics, 12(11):756â€“766. doi: 10.1038/nrg3098

* Hopf et al (2017) Mutation effects predicted from sequence co-variation. Nature Biotechnology, 35(2):128. doi:10.1038/nbt.3769

* Leffler et al (2012) Revisiting an old riddle: What determines genetic diversity levels within species? PLOS Biology, 10(9):1â€“9. doi: 10.1371/journal.pbio.1001388

Matsen and Ralph (2022) Enabling inference for context-dependent models of mutation by bounding the propagation of dependency. Journal of Computational Biology, 29(8):802-824. doi: 10.1089/cmb.2021.0644

* Seplyarskiy et al (2021) Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 373(6558):1030â€“1035. doi: 10.1126/science.aba7408

Seplyarskiy et al (2022) A mutation rate model at the basepair resolution identifies the mutagenic effect of Polymerase III transcription. bioRxiv. doi: 10.1101/2022.08.20.504670

* Waldvogel and Pfenninger (2021) Temperature dependence of spontaneous mutation rates. Genome Research 31:1582-1589. doi:10.1101/gr.275168.120