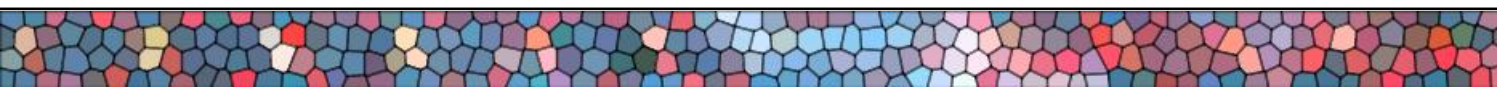
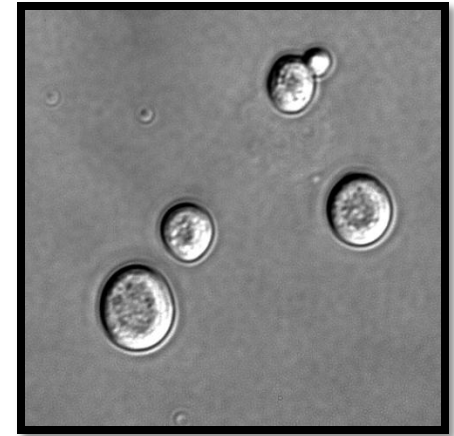


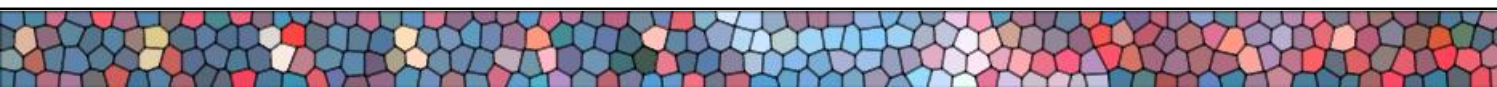
Experimental Design

- *S. cerevisiae* (2 strains)
 - Oak (o_*)
 - Wine (w_*)
- Skewed Read counts
 - 454
 - Oak = 453,722 (Roche 454)
 - Wine = 213,232 (students)
 - Illumina
 - 1 full run (CSHL staff) + 2 small runs (students)



Experimental Design: Questions

- Biological Question: **Where do SNPs occur between the two strains?**
- Bioinformatics Question: **How do the respective technologies affect your SNP finding results?**
 - 454
 - Illumina
 - Co-assembly

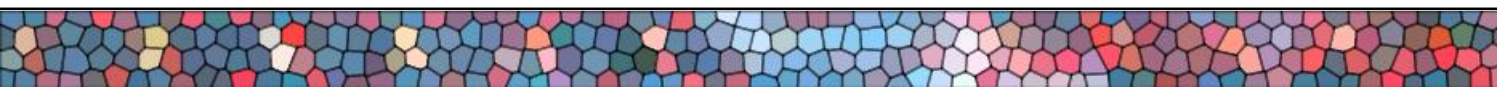


Experimental Design: Questions

- Biological/Bioinformatics Question: In the middle of chromosome 12 we see a huge pileup of reads, but Michael said that MOSAIK prevents a pileups due to repetitive regions.

What's going on here?

- Is this a biological event?
- Is this a bug in MOSAIK?



Experimental Design: Tools

