2013 7.03 Exam 1
Review Sheet

Crosses, genotypes and phenotypes

- How to set up a test cross to test if an allele is dominant/recessive
  - in haploid organism (yeast)?
  - In diploid organism (drosophila, mice, etc.)?

Complementation Test

- How does it work in haploid organisms (yeast)?
- How does it work in diploid organisms (drosophila, mice, etc.)?
- What does a complementation test tell you about the mutations?
  - recessive or dominant.
  - in same gene or different genes.

Modes of inheritance in diploid organism (assuming genes unlinked)

- Autosomal/ X-linked; Dominant or recessive?
- Genotypic/ phenotypic pattern of inheritance of single gene with 2 alleles.
- Genotypic/ phenotypic pattern of inheritance of 2 genes, with 2 alleles per gene.
- How to use Chi-squared test to test mode of inheritance:
  high Chi-sq value → low p-value → observation is different from expected model of inheritance → reject expected model.
- Given a mode of inheritance and the phenotype/ genotype of a child, how to calculate P(mother carrier) using **Bayes' Theorem**, and thereby calculate P(next child is affected).

Genetic linkage in experimental diploid organisms (drosophila, mice, etc.)

- For two linked genes (or two nearby mutations in the same gene), how can a crossover event happen between them in meiosis?
- How to calculate genetic distance (cM) between 2 linked genes (or 2 nearby mutations in the same gene)
  - in a 2 factor cross
  - in a 3 factor cross

  by setting up appropriate crosses and identifying recombinant/parental F2 progeny.
- Genetic distance = physical distance X recombination rate

Genetic linkage in haploid organism (yeast) - Tetrad analysis

- In sporulation, a 2n yeast undergoes DNA replication and meiosis to form a tetrad, each with 4 gametes/ spores (1n).
- Identify PD, NPD, TT from given genotype/ phenotype of a tetrad.
- Determine if 2 genes are linked or unlinked based on observed PD, NPD, TT.
  If unlinked, PD:NPD:TT = 1:1:4
- If linked, how to calculate genetic distance using PD, NPD, TT.

Genetic linkage in human

- How to calculate LOD score for a given pedigree
  - if phase is known?
  - if phase in unknown?
  - if marker (SSR) and trait is completely linked ($\theta = 0$)?
  - if marker (SSR) and trait is loosely linked ($\theta > 0$)?