7.03 Spring 2011
PSet 1 Solutions

1. a) Plate strains on lawn of Mat a and Mat α on (strains 1-10) -Ura or -Lys-Ura or (strains 11-20) -Leu or -Leu-Lys
If yeast colonies grow on Mat a, then the strain must be Mat α (and vice versa).

Therefore, strains 1-10 are Mat a and strains 11-20 are Mat α

b) Plate strains 1-10 with MAT a wt (wild type) and strains 11-20 with MAT a wt on YPD 37°C medium. Thus, only strain 8 is dominant, as there is no growth of yeast colonies when mated with wt. The rest of the strains (1-7, 9-20) are recessive.

c) Plate strains 1-10 and MATA wt with strains 11-20 and MAT α wt on YPD 37°C medium. The following results appear with "+" indicating growth and "-" indicating no growth of colonies. Can also plate on minimal at 37 degrees. Both ways will get you the same answer.

MAT α strains

Mat a strains	11	12	13	14	15	16	17	18	19	20	wt
1	+	+	+	+	+	+	+	+	+	+	+
2	+	+	+	+	-	+	+	-	+	-	+
3	+	+	+	+	+	+	-	+	+	+	+
4	+	+	+	+	-	+	+	-	+	-	+
5	+	+	+	+	+	+	-	+	+	+	+
6	-	+	-	+	+	+	+	+	+	+	+
7	+	+	+	+	+	-	+	+	-	+	+
8	-	-	-	-	-	-	-	-	-	-	-
9	-	+	-	+	+	-	+	+	-	+	+
10	-	+	-	+	+	+	+	+	+	+	+
wt	+	+	+	+	+	+	+	+	+	+	+

"+" means complementation (different genes) and "-" means no complementation (same genes). Thus, the groups are as follows:

Group I: 1
Group II: 2, 4, 15, 18, 20
Group III: 3, 5, 17
Group IV: 6, 10, 11, 13, (9)
Group V: 7, 16, 19, (9)

9 is a double mutant since it can be placed in 2 complementation groups. 8 cannot be placed in a group since it is dominant. 12 and 14 could define either one or two additional groups (same mating type, so we cannot mate to test complementation).

1 d) The minimum number of genes is 6: (1, 8?), (2, 4, 15, 18, 20, 8?), (3, 5, 17, 8?), (6, 10, 11, 13, 9, 8?), (7, 16, 19, 9, 8?), (12, 14, 8?).

The maximum number of genes is 8: (1), (2, 4, 15, 18, 20), (3, 5, 17), (6, 10, 11, 13, 9), (7, 16, 19, 9), (8), (12), (14)

2 a) Mate strains 1-6 with MATα wt on min + FOA media. No growth results for strains 1, 2, 4-6, but growth with strain 3. Thus, strains 1, 2, 4-6 are recessive and strain 3 is dominant.

Mate strains 7-12 with MATa wt on min + FOA media. No growth is seen for strains 7-11, but growth is seen for 12. Thus, strains 7-11 are recessive and strain 12 is dominant.

b) Mate strains 1-6 and MATa wt with strains 7-12 and MATα wt on Min + FOA media. "+" = no complementation (same gene). "−" means complementation (different genes). REMEMBER, we are dealing with a "resistance" phenotype.

Matα strains

Mata strains	7	8	9	10	11	12	wt
1	−	+	−	+	−	+	−
2	+	−	−	−	+	+	−
3	+	+	+	+	+	+	+
4	−	−	+	−	−	+	−
5	+	−	−	−	+	+	−
6	−	−	+	−	−	+	−
wt	−	−	−	−	−	+	−

Group I: 1, 8, 10

Group II: 2, 5, 7, 11

Group III: 4, 6, 9

3 and 12 cannot be placed since they're dominant alleles.

c) Min. number of genes is 3: (1, 8, 10, 3?, 12?), (2, 5, 7, 11, 3?, 12?), (4, 6, 9, 3?, 12?)
Max number of genes is 5: (1, 8, 10), (2, 5, 7, 11), (4, 6, 9), (3), (12)

3 a) Cross #1 to analyze mutant 1

mutant 1 wingless ♂ $\frac{mut1}{?}$ × wild type winged ♀ $\frac{+}{+}$

? = mut1 or Y or +

↓

all winged progeny (F1) ⇒ recessive

Crossing F1 progeny:

winged (from F1) ♂ $\frac{mut1}{+}$ or $\frac{+}{Y}$ × winged (from F1) ♀ $\frac{mut1}{+}$

↓

no wingless females

♂ $\frac{mut1}{Y}$ (wingless) ; ♂ $\frac{+}{Y}$ (winged) ; ? ♀ $\frac{mut1}{+}$ (winged) offspring generated

∴ Mutant 1 is X-linked recessive with genotype $\frac{Mut1}{Y}$

Cross #2 to anlyze Mutant 2

mutant 2 wingless ♂ $\frac{mut2}{?}$ × wildtype winged ♀ $\frac{+}{+}$

? = mut2, Y, or +

↓

~50% winged (mix of sexes)
~50% wingless

∴ Mutant 2 is autosomal dominant and the genotype is heterozygous $\frac{mut2}{+}$

Cross #3 to analyze mutant 3

mutant 3 wingless ♂ $\frac{mut\,3}{?}$ × wildtype winged ♀ $\frac{+}{+}$

? = mut 3, +, or Y

↓

no wingless ♂'s or winged ♀'s.

only wingless ♀ $\frac{mut\,3}{+}$ and winged ♂ $\frac{+}{Y}$ offspring generated.

∴ mutant 3 is X-linked dominant with genotype $\frac{mut\,3}{Y}$

Cross 4 to analyze mutant 4

mutant 4 wingless ♂ $\frac{mut\,4}{?}$ × wildtype winged ♀ $\frac{+}{+}$

? = + or Y or mut 4

↓

all winged progeny ⟹ recessive

Crossing F1 progeny:

winged (from F1) ♂ $\frac{mut\,4}{+}$ or $\frac{+}{Y}$ × winged (from F1) ♀ $\frac{mut\,4}{+}$

↓

~75% winged

~25% wingless

∴ mutant 4 is autosomal recessive with genotype $\frac{mut\,4}{mut\,4}$

mutant 4 could have come from a true-breeding line (all flies homozygous for the mut4 allele. Additionally, mut1 and mut 3 could come from true-breeding lines where females are homozygous $\frac{X^{mut}}{X^{mut}}$ and males are $\frac{X^{mut}}{Y}$.

Mutant 2, however, must come from a cross.

4 a) Mechanism a

Wild type x wingless

AA aa

↓

Aa (F1 ♀ normal wings)

Aa x Aa

↓

1 AA : 2 Aa : 1 aa Phenotypically: 3 wt : 1 wingless

(25% F2 wingless)

Mechanism b

Wild type wingless

AABB x aabb

↓

AaBb (F1 ♀ normal wings)

AaBb x AaBb

↓

	AB	Ab	aB	ab
AB	ABAB	AABb	AaBB	AaBb
Ab	AABb	AAbb	AaBb	Aabb
aB	AaBB	AaBb	aaBB	aaBb
ab	AaBb	Aabb	aaBb	aabb

∴ phenotypically: 15 winged : 1 wingless (6.25% of F2 wingless).

Mechanism C

Wildtype × wingless

AABB × aabb, aaB-, A-bb

Since "-" means blank, it can be either allele (use table from mechanism b)

Phenotypically: 9 winged : 7 wingless (43.75% F2 wingless)

Mechanism d

Wildtype × wingless

AABB × $aaB^{D}-$

Again, look @ mechanism b table. However, since wingless mut is produced from recessive allele of 1 gene ("aa") but dominant allele of the other (BB or Bb), phenotypic ratio is 13 wt : 3 wingless (18.75% of F2 is wingless).

With Star Genetics

Cross mut ♂ to wt ♀, then cross any F1 ♂ to cross to any F1 ♀. Note F2 ratios to determine mechanism (make sure to generate enough F2 progeny for a significant result). Below is a REAL star genetics trial.

Mut 1 × wt → normal F1 ⟶ ~6% F2 wingless ⟹ Mechanism B

Mut 2 × wt → normal F1 ⟶ ~28% F2 wingless ⟹ Mech. A

Mut 3 × wt → normal F1 ⟶ ~17% F2 wingless ⟹ Mech. D

Mut 4 × wt → normal F1 ⟶ ~40% F2 wingless ⟹ Mech. C

Chi-Square Analysis

For a given model, let's take Mutant 2 as an example (mech A).

° Freedom = # phenotypic classes - 1 = 2 - 1 = 1

level of significance = 5% ⟹ p = 0.05

From Star Genetics, we get the following observed result out of a total of 168 offspring with mechanism A. From our calculations, we get the following expected results for F2

	expected	observed	$(E-O)^2$	$(E-O)^2/E$
wt	126	120	36	0.2857
wingless	42	48	36	0.8571

Total = χ^2 = 1.1428

Based on χ^2 table provided, P is between 10% and 50% probability (between p of 0.9 and 0.5). Since this is greater than the cutoff of 5%, a statistically significant result between the observed and expected results cannot be concluded (cannot reject null hypothesis).

Now, what if we assume mut 2 is mechanism D instead?

	E	O	$(E-O)^2$	$(E-O)^2/E$
wt	136.5	120	272.25	1.9945
wingless	31.5	48	272.25	8.643

Total = χ^2 = 10.6

∴ P is < 0.005. This is less than the cutoff of 0.05, so we reject the null hypothesis that mutant 2 exhibits mechanism D.

5. a) The trait is recessive. Neither the parents of individuals 3 or 2 exhibit the mutant phenotype.

b) Bayes Theorem: $P(X|Y) = \frac{p(Y|X) * p(X)}{[p(Y|X) * p(X)] + [p(Y|\bar{X}) * p(\bar{X})]}$

$$p(1 \text{ is a carrier, Aa} \mid 5 \text{ unaffected, A-}) = \frac{\frac{1}{2} \cdot \frac{2}{3}}{(\frac{1}{2} \cdot \frac{2}{3}) + (1 \cdot \frac{1}{3})} = \frac{\frac{1}{3}}{\frac{2}{3}} = \boxed{\frac{1}{2}}$$

c) $p(2^{nd} \text{ child with trait}) = p(1 \text{ is carrier}) * p(2 \text{ is carrier}) * p(\text{child will be affected})$

$$= (\tfrac{1}{2})(1)(\tfrac{1}{2}) = \boxed{\frac{1}{4}}$$

d) p(child has trait) = p(5 is a carrier) * p(6 is a carrier) * p(child will be affected)

$= (1)(1)\left(\frac{1}{4}\right) = \boxed{\frac{1}{4}}$

e) Since both 5 and 6 are Aa, an "unaffected child" does not change the probability of an affected child. It remains $\boxed{1/4}$ as in part d.

f) $p(X|Y) = p(1 \text{ is a carrier } X^+X^m \mid 5 \text{ is unaffected } X^+Y) = \frac{\frac{1}{2}\left(\frac{1}{2}\right)}{\left(\frac{1}{2}\cdot\frac{1}{2}\right)+\left(1\cdot\frac{1}{2}\right)} = \frac{\frac{1}{4}}{\frac{1}{4}+\frac{2}{4}} = \frac{\frac{1}{4}}{\frac{3}{4}} = \boxed{\frac{1}{3}}$

g) $p(X|Y) = p(4 \text{ is a carrier } X^+X^m \mid 6 \text{ is unaffected } X^+X^m) = \frac{\frac{1}{2}\left(\frac{1}{2}\right)}{\left(\frac{1}{2}\cdot\frac{1}{2}\right)+\left(1\cdot\frac{1}{2}\right)} = \boxed{\frac{1}{3}}$

h) p(6 is a carrier) = $\boxed{1}$ 3 is X^mY, so 6 must be a carrier

i) p(second daughter with trait) = p(3 is carrier) * p(4 is carrier) * p(daughter will be affected)

$= 1\left(\frac{1}{3}\right)\left(\frac{1}{2}\right) = \boxed{\frac{1}{6}}$

j) p(son with trait) = p(6 is carrier) * p(son will be affected)

$= 1\left(\frac{1}{2}\right) = \boxed{\frac{1}{2}}$

k) 6 IS a carrier, so the probability doesn't change due to one unaffected son. The chance of the 2nd son having the trait is still $\boxed{1/2}$