Solutions to Genetics Problems

This chapter is much more than a solution set for the genetics problems. Here you will find details concerning the assumptions made, the approaches taken, the predictions that are reasonable, and strategies that you can use to solve any genetics problem. The value of this chapter depends on you. In every case, before you look here, you should struggle with the problem, design your own approach, and make your own mistakes. Only then should you look at the solutions given here.

(1) PROBLEMS INVOLVING ONLY ONE GENE

(1.1) One gene; two alleles; simple dominance

(1.1.1)
a) GG × GG. A plant homozygous for the G allele is crossed to another plant homozygous for the G allele. Each parent has only the G allele to give to its offspring, so the Punnett square used to predict the offspring would look like this:

	G	G
G	GG green	GG green
G	GG green	GG green

This predicts all offspring (100%) will have the genotype of GG and green flower color is the dominant trait, so all have green flowers.

Because both parents produce only one type of gamete, you can simplify the Punnett square to:

	G
G	GG green

b) gg × gg. A plant homozygous for the g allele is crossed to another plant homozygous for the g allele. Each parent has only the g allele to give to its offspring, so the Punnett square used to predict the offspring would look like this:

	g	g
g	gg blue	gg blue
g	gg blue	gg blue

or

	g
g	gg blue

This predicts all offspring (100%) will have the genotype of gg and blue flower color.

c) Gg × gg. A heterozygous plant is crossed to a plant homozygous for the g allele. The heterozygote will pass either the G or g allele to its offspring. The other parent has only the g allele to give. The Punnett square used to predict the offspring would look like this:

	G	g
g	Gg green	gg blue
g	Gg green	gg blue

or

	G	g
g	Gg green	gg blue

Because green flower color is dominant to blue flower color, the Gg offspring will have green flowers but the homozygous gg offspring will have blue flowers. Thus, you would expect 50% of the offspring to be Gg (green flowers) and 50% to be gg (blue flowers).

d) Gg × Gg. Two heterozygous plants are crossed. The Punnett square used to predict the offspring would look like this:

	G	g
G	GG green	Gg green
g	Gg green	gg blue

This predicts 25% GG offspring, 50% Gg offspring, and 25% gg offspring, a 1:2:1 genotypic ratio. However, because the Gg heterozygotes are indistinguishable from the GG homozygotes, what you see is 75% of offspring have green flowers and 25% of offspring have blue flowers, for a phenotypic ratio of 3:1.

e) Green × Green. There are two possible genotypes for a green individual: GG or Gg. This means that there are three possibilities for Green × Green:
1) GG × GG. This gives 100% GG with green flowers as in part (a) above.
2) Gg × Gg. This gives 75% green flowers (25% GG and 50% Gg) and 25% gg with blue flowers as in part (d) above.
3) GG × Gg. The Punnett square used to predict the offspring would look like this:

	G	g
G	GG green	Gg green
G	GG green	Gg green

This gives 50% GG and 50% Gg, but all offspring have green flowers.

Extra Challenge: Look at 1) and 3) above. If a green-flowered plant × a green-flowered plant gives all green-flowered offspring, how would you determine whether the parents were GG × GG or GG × Gg?

f) Blue × Blue
The only possible genotype for a blue individual is gg. Therefore, the cross must be gg × gg, which gives 100% gg (blue flowers) as in part (b) above.

(1.1.2)
a) In cross 1, a red-eyed mouse × a white-eyed mouse gives all red-eyed mice.
A possible model is that eye color is controlled by one gene with two alleles. Since the white-eyed phenotype is not seen in the offspring of this cross, it is likely that red eyes is the dominant phenotype. If so, cross 1 could be either:

A) red-eyed mouse (RR) × white-eyed mouse (rr) → all F_1 are Rr
B) red-eyed mouse (Rr) × white-eyed mouse (rr) → F_1 are either Rr or rr

Option (A) would give all red-eyed offspring, which is consistent with the observed results. Option (B) should give some white-eyed offspring with the genotype rr, so this does not fit the observed results.

In cross 2, a red-eyed offspring (F_1) × a red-eyed offspring (F_1) gives some red-eyed and some white-eyed offspring. We predict this cross to be: red-eyed mouse (Rr) × red-eyed mouse (Rr).

The expected results from this cross are:

	R	r
R	RR	Rr
r	Rr	rr

25% RR, 50% Rr, and 25% rr offspring, a 1:2:1 genotypic ratio. But in our model, the Rr heterozygotes are indistinguishable from the RR homozygotes, so what you see is that 75% of the offspring have red eyes and 25% of the offspring have white eyes, for a phenotypic ratio of 3:1.
The reported data of 36 red-eyed to 13 white-eyed fit this prediction well.

You could also have tried the alternative model, where white eyes are dominant. Some appropriate symbols are:

Allele	Contribution to phenotype
W	white eyes (dominant)
w	red eyes (recessive)

If so, cross 1 could be either:
A) red-eyed mouse (ww) × white-eyed mouse (Ww) where you would expect a 1:1 ratio of red eyes to white eyes. This is inconsistent with the data.

B) red-eyed mouse (ww) × white-eyed mouse (WW) where you would expect all Ww (white-eyed) offspring. This is also not observed, so this model is inconsistent with the data.

There is no need to check cross 2 since one piece of inconsistent data rules out this model. So, even if you did not conclude that red eyes were likely to be dominant, you can still propose a consistent model by ruling out models that do not fit the data.

Your complete model would be that eye color is controlled by one gene with two alleles where red eyes are dominant to white eyes.
Cross 1: RR × rr → all Rr
Cross 2: Rr × Rr → 36 (RR + Rr) and 13 (rr)

b) In cross 1, a long-eared mouse × a short-eared mouse gives some long-eared and some short-eared mice. A possible model is that ear length is controlled by one gene with two alleles. From these data, we cannot determine which allele is associated with the dominant phenotype, so we must look at the data from cross 2 before proposing a model.

In cross 2, a long-eared F_1 mouse × a long-eared F_1 mouse gives some long-eared and some short-eared mice. In this cross, long-eared parents produce mice with short ears, i.e., the short-eared phenotype was masked in the parents. Therefore, a likely model is that long ears is the dominant phenotype, and some appropriate symbols are:

Allele	Contribution to phenotype
L	long ears (dominant)
l	short ears (recessive)

Therefore, in cross 1, the long-eared parent could be LL or Ll, but the short-eared parent must be ll. So the cross could be either:

a) long-eared mouse (LL) × short-eared mouse (ll) where you would expect all (Ll) long-eared offspring. This is inconsistent with the data.

b) long-eared mouse (Ll) × short-eared mouse (ll) where you would expect a 1:1 ratio of (Ll) long ears to (ll) short ears. This is consistent with the data considering there are only 22 offspring to examine. 12:10 is approximately 1:1.

In cross 2, a long-eared F_1 mouse (Ll) × a long-eared F_1 mouse (Ll) should give offspring that have a ratio of three long-eared mice to one short-eared mouse. The data support this model.

You could also have tried an alternative model, where the short-eared phenotype is dominant. Some appropriate symbols are:

Allele	Contribution to phenotype
S	short ears (dominant)
s	long ears (recessive)

In this scenario, for cross 1 the short-eared parent could be SS or Ss, but the long-eared parent must be ss. So the cross could be either:

a) long-eared mouse (ss) × short-eared mouse (SS) where you would expect all short-eared offspring. This is inconsistent with the data.

b) long-eared mouse (ss) × short-eared mouse (Ss) where you would expect a 1:1 ratio of long ears to short ears. This is consistent with the data considering there are only 22 offspring to examine. 12:10 is approximately 1:1.

However, in cross 2, a long-eared F_1 mouse (ss) × a long-eared F_1 mouse (ss) should give only long-eared offspring, which is not seen. This model is inconsistent with the data.

So, even if you did not conclude that long ears were likely to be dominant, you can still propose a consistent model by ruling out models that do not fit the data.

(1.1.3)
a) The achondroplasia phenotype is dominant. If a novel phenotype that is not seen in the parents appears in their offspring, it suggests that the novel phenotype is recessive. By this reasoning, normal size is recessive to dwarf size, which is dominant. You can try the alternative model (dwarfism is recessive) and show that it is not consistent with these family data.

b) For the model that normal size is recessive to dwarf size, some appropriate symbols are:

Allele	Contribution to phenotype
D	dwarf (dominant)
d	normal height (recessive)

To have a dd (normal size) child, both parents must have at least one d allele. To be dwarves, they must both have at least one D allele. Thus, both parents must be Dd.

(1.1.4) Give all models that are consistent with the data.
a) red fly × red fly gives one blue fly progeny.
The model is: one color gene with two alleles where red color is dominant to blue color.
Appropriate symbols would be:

Allele	Contribution to phenotype
R	red (dominant)
r	blue (recessive)

The cross is red (Rr) × red (Rr) ⇒ blue (rr).

b) brown cow × white cow gives one brown cow progeny.
There are two possible models here:

1) There are two alleles of the color gene, and brown color is dominant to white color. Appropriate symbols would be:

Allele	Contribution to phenotype
B	brown (dominant)
b	white (recessive)

The cross would be brown (BB or Bb) × white (bb) ⇒ brown (Bb).

2) There are two alleles of the color gene, and white color is dominant to brown color. Appropriate symbols would be:

Allele	Contribution to phenotype
W	white (dominant)
w	brown (recessive)

The cross would be brown (ww) × white (Ww) ⇒ brown (ww).

The data are consistent with **both** of these models.

(V1)

a) There is no solution for this part.

b) i) YY × YY: the Punnett square predicts 100% YY; VGLII would give all yellow-wing and no red-wing.

ii) YY × Yy: the Punnett square predicts 50% YY and 50% Yy, both of which are yellow-winged; VGLII would give all yellow-wing and no red-wing.

iii) YY × yy: the Punnett square predicts 100% YY; VGLII would give all yellow-wing and no red-wing.

iv) Yy × Yy: the Punnett square would predict 75% Y_ (yellow-wing) and 25% yy (red-wing); in a VGLII problem, this would be observed as a mixture of yellow-wing and red-wing, with more yelloe-wing than red-wing.

v) Yy × yy: the Punnett square would predict 50% Yy (yellow-wing) and 50% yy (red-wing); in a VGLII problem, this would be observed as a mixture of yellow-wing and red-wing, with roughly equal numbers of each.

vi) yy × yy: the Punnett square would predict 100% yy (red-wing); VGLII would give all red-wing and no yellow-wing.

c) There is no solution for this part.

(1.1.5) These mice have one gene with two alleles for the coat color trait. Brown is dominant to white. Some appropriate symbols would be:

Allele	Contribution to phenotype
B	brown (dominant)
b	white (recessive)

Parental cross:

brown mouse (Bb) × white mouse (bb) ⇒ 10 brown mice (Bb) and 13 white mice (bb)

White F_1 mice are bb. Therefore, in a cross between two white F_1 mice, all of their progeny will be white (bb) as well.

Brown F_1 mice are heterozygotes (Bb). The Punnett square used to predict the offspring would look like this:

	B	b
B	BB	Bb
b	Bb	bb

This predicts 25% BB offspring, 50% Bb offspring, and 25% bb offspring, a 1:2:1 genotypic ratio. However, because the Bb heterozygotes are indistinguishable from the BB homozygotes, what you expect is that 75% of the offspring should be brown and 25% of the offspring should be white. The results of 28 brown to 10 white are consistent with this model.

(1.1.6) There are many possible models. Below are two:

a) One gene with two alleles where blue is dominant to red.

i) BB = blue, Bb = blue, bb = red

ii)Tarzan (Bb) × Jane (bb) ⇒ Fred (bb) and Alice (bb)

b) One gene with two alleles where red is dominant to blue.

i) BB = red, Bb = red, bb = blue

ii) Tarzan (bb) × Jane (Bb) ⇒ Fred (Bb) and Alice (Bb)

c) i) Cross Fred × Alice.

ii) If model 1 is correct, then Fred (bb) × Alice (bb) would give all bb offspring which would be red.

iii) If model 2 is correct, then Fred (Bb) × Alice (Bb) would give 75% red offspring and 25% blue offspring.

(1.1.7)

a) Rr × Rr gives 1/4 chance of an rr child, and rr children have a 1/2 chance of being left-handed. Therefore, the chance is 1/4 x 1/2 or 1/8.

b) Yes. A left-handed (rr) mother × a right-handed (Rr) father have a 50% chance of having an rr child and that rr child could be left-handed.

c) Yes. Two left-handed parents, rr × rr, could have an rr child. That rr child could be right-handed.

d) This model allows for many possible individual families. However, on average, left-handed parents should be more likely to have left-handed children than right-handed parents are. When looking at many families, if right-handed parents were just as likely as left-handed parents to have left-handed children, the model is unlikely to be correct.

(V2) There are no answers for this problem.

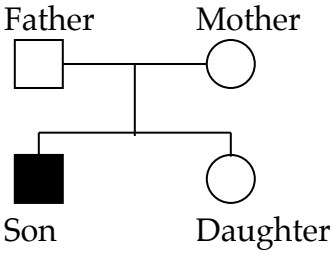
(1.2) Pedigrees involving one gene, I

(1.2.1)

a) i) You could use almost any letter for the cystic fibrosis gene; here is one example:

Allele	Contribution to phenotype
F	normal (dominant)
f	cystic fibrosis (recessive)

ii) Since pedigree symbols show only phenotype, the symbols for a carrier and a homozygous normal individual are identical. Therefore, the pedigree would look like this:



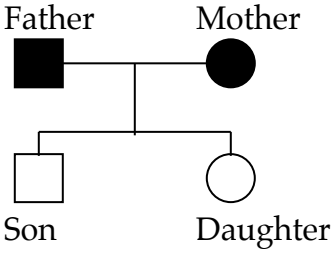
iii) From the information in the problem, the parents are carriers: Ff. The son with cystic fibrosis is ff. Using a Punnett square for these parents, the unaffected daughter could be either FF or Ff; this can also be written as F_. Without more information, it is not possible to know her genotype for certain.

iv) Using the Punnett square for these parents, 1/4 of the children, on average, would be expected to have cystic fibrosis. Therefore, the chance that the next child would have cystic fibrosis is 1/4 or 25%.

b) i) You could use almost any letter for the Marfan syndrome gene. Here is one example:

Allele	Contribution to phenotype
M	Marfan syndrome (dominant)
m	normal (recessive)

ii) The pedigree would look like this:



iii) In the case of an autosomal dominant trait, normal individuals can only be mm (if they had even one M allele, they would have Marfan syndrome). So the normal son must be mm.

iv) Without knowing anything about their children, the parents with Marfan syndrome could be either MM or Mm. You can figure out which genotype they have by considering their offspring. There are two ways to do this:

1) Try all three possibilities and see which can produce an mm (normal) child. If you try MM × MM, MM × Mm, or Mm × MM, none of these can produce an mm offspring. However, Mm × Mm can produce mm offspring. Therefore, both parents must be Mm. You might be surprised to see two out of two (100%) normal children when the Punnett square predicts only 1/4 of the children of these parents to be normal. This is not surprising since the number of offspring is small and statistical fluctuations are to be expected.

2) Work backward from the offspring. Consider the unaffected son; he must be mm. Since he got one of his alleles from his mother and one from his father, both mom and dad must have at least one m allele. Since mom and dad have Marfan syndrome, they each must have at least one M allele. Combining these, the parents must both be Mm.

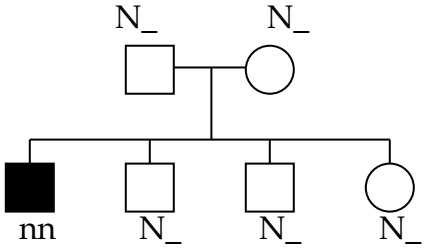
Either way, the parents must be Mm. Using a Punnett square, 3/4 of their offspring, on average, will have Marfan syndrome. So the risk that the next child in this family will have Marfan syndrome is 3/4 or 75%.

(1.2.2)
a) You can try both possibilities and see which works.

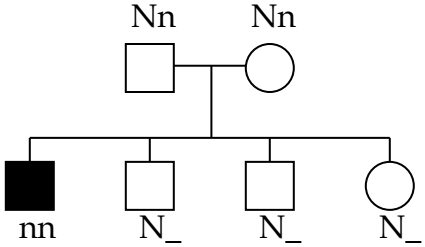
1) If having the disease is a recessive phenotype, then some appropriate symbols are:

Allele	Contribution to phenotype
N	normal (dominant)
n	diseased (recessive)

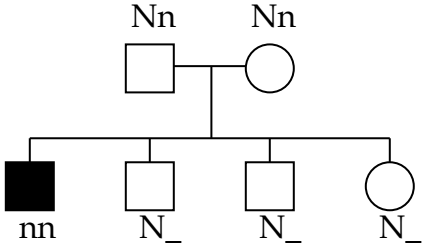
Start by writing the genotypes you are SURE of – the ones you can tell by phenotype alone. If the disease is inherited as an autosomal recessive trait, then you know that any diseased individuals must be nn. You also know that normal individuals must have at least one N in order to be normal. They could be either NN or Nn; you cannot be sure which without more information.



Then, work from what you know and see if the inheritance is possible. One place to start is the diseased son. He had to get an n from both parents, so they must be Nn:



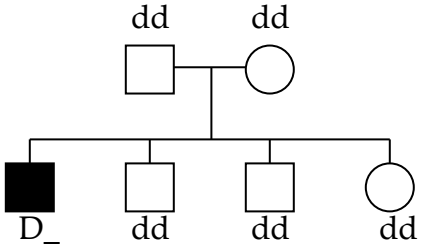
Finally, evaluate the other children. Is it possible for two Nn parents to have unaffected children with at least one N allele? The answer is yes, and without additional information, the genotype of the three unaffected children remains ambiguous. They could be either NN or Nn, so this model is consistent with the data. The genotypes are as follows:



2) On the other hand, if having the disease is a dominant phenotype, then some appropriate symbols are:

Allele	Contribution to phenotype
D	disease (dominant)
d	normal (recessive)

Start by writing the genotypes you are SURE of – the ones you can tell by phenotype alone. If the disease is inherited as an autosomal dominant trait, then you know that any normal individuals must be dd. You also know that diseased individuals must have at least one D in order to be diseased. They could be either DD or Dd; you cannot be sure which without more information.



Now, evaluate the pedigree and see whether the inheritance is possible. One place to start is the diseased son. He had to get a D from one of his parents, so at least one of them must have a D allele. However, if one of his parents had a D, he or she would be diseased. This is inconsistent with the pedigree so this disease cannot be inherited in an autosomal dominant manner.

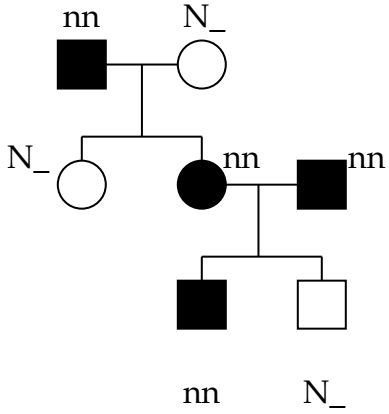
For part (a) above, we've shown that the pedigree is consistent with the disease being inherited as an autosomal recessive trait and inconsistent with the disease being inherited as an autosomal dominant trait. Therefore, the disease must be inherited in an autosomal recessive manner.

b) You can try both possibilities and see which works.

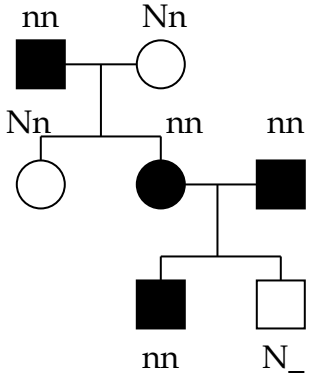
1) If having the disease is a recessive phenotype, then some appropriate symbols are:

Allele	Contribution to phenotype
N	normal (dominant)
n	diseased (recessive)

Start by writing the genotypes you are SURE of – the ones you can tell by phenotype alone. If the disease is inherited as an autosomal recessive trait, you know that any diseased individuals must be nn and normal individuals are N_.



Start from any of the diseased individuals. Try from the top down. To have a diseased daughter, the grandmother (top row; right) must have an n allele. It is possible for the grandparents (nn × Nn) to have both normal (Nn) and diseased (nn) offspring, so the first generation is consistent with the disease being a recessive trait.

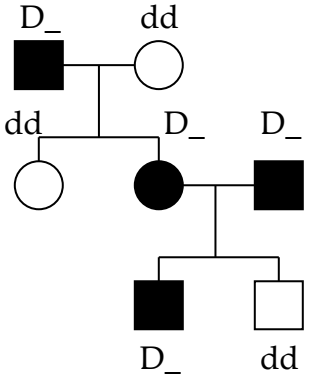


Now examine the second generation. The parents are nn × nn. The only offspring they can have are nn, so it is not possible for them to have normal children. The normal child at the lower right is inconsistent with this model. So this disease cannot be inherited in an autosomal recessive manner.

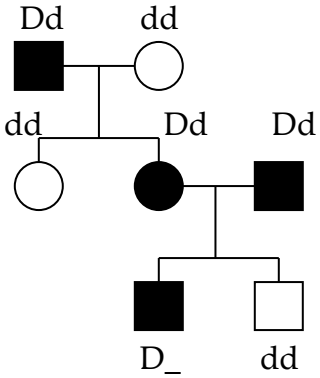
2) The alternative is that the disease is a dominant phenotype, and some appropriate symbols are:

Allele	Contribution to phenotype
D	diseased (dominant)
d	normal (recessive)

Start by writing the genotypes you are SURE of – the ones you can tell by phenotype alone. If the disease is inherited as an autosomal dominant trait, you know that any normal individuals must be dd and diseased individuals are D_.



You could start from any of the diseased individuals. To have a diseased daughter, one or both of the grandparents (top row) must have a D allele and show the disease. In addition, to have a normal daughter, both of the grandparents (top row) must have at least one d allele. Thus, the grandparents could be Dd × dd and be consistent with the disease as an autosomal dominant trait.



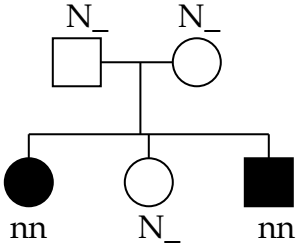
Now try the second generation. The parents are Dd × Dd. They could have DD, Dd, or dd offspring, so this pedigree is consistent with the disease being inherited as a dominant trait.

c) You can try both possibilities and see which works.

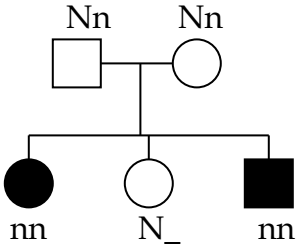
1) If having the disease is a recessive phenotype, then some appropriate symbols are:

Allele	Contribution to phenotype
N	normal (dominant)
n	diseased (recessive)

Start by writing the genotypes you are SURE of – the ones you can tell by phenotype alone. If the disease is inherited as an autosomal recessive trait, then you know that any diseased individuals must be nn. You also know that normal individuals must have at least one N in order to be normal. They could be either NN or Nn; you cannot be sure which without more information.



You know the parents must each have an n in order to produce nn children, so the parents must be Nn:



Then ask if Nn × Nn can produce normal offspring. They can have normal offspring that are Nn or NN. So this pedigree is consistent with the disease being inherited as a recessive trait.

2) If the disease is a dominant phenotype, then each generation must show the disease. In this pedigree, normal parents have diseased children, so the disease cannot be a dominant trait.

(1.2.3) a) Are the following statements true for autosomal recessive and/or autosomal dominant diseases:

i) *Diseased parents can have diseased offspring.* Yes, this is true for both autosomal dominant and autosomal recessive. Using the allele symbols defined in problem (1.2.2):

- Autosomal recessive: Two diseased parents (nn × nn) can have diseased offspring.
- Autosomal dominant: Two diseased parents (Dd × Dd) can have diseased offspring.

ii) *Normal parents can have normal offspring*. Yes, this is true for both autosomal dominant and autosomal recessive. Using the allele symbols defined in problem (1.2.2):

- Autosomal recessive: Two normal parents (Nn × Nn) can have normal offspring.
- Autosomal dominant: Two normal parents (dd × dd) can have normal offspring.

iii) *Even if both parents are normal, they can have diseased offspring*. This is only true for autosomal recessive.

- Autosomal recessive: Two normal parents (Nn × Nn) can have diseased offspring.
- Autosomal dominant: Two normal parents (dd × dd) cannot have normal offspring.

iv) *Even if both parents are diseased, they can have normal offspring*. This is true only for autosomal dominant.

- Autosomal recessive: Two diseased parents (nn × nn) cannot have normal (N_) offspring.
- Autosomal dominant: Two diseased parents (Dd × Dd) can have normal offspring.

b) The last two statements are diagnostic for particular modes of inheritance.

If you have two normal parents that have one or more diseased children, the disease cannot be inherited in an autosomal dominant manner. This can be used in problem (1.2.2), a and c, to rule out the autosomal dominant mode of inheritance. Note that you still have to check to be sure that autosomal recessive works.

If you have two diseased parents that have one or more normal children, the disease cannot be inherited in an autosomal recessive manner. This can be used in problem (1.2.2) b to rule out autosomal recessive. Note that you still have to check to be sure that autosomal dominant works.

(1.2.4) Fred would be at greater risk. Fred has an affected sister (dd) but his parents are normal so Fred's parents must be Dd × Dd. Therefore, the risk that Fred will be diseased is 1/4.

John's mother is dd, and his Dad is normal (DD or Dd). If Dad is DD, John cannot be affected; if Dad is Dd, John has a 1/2 chance of being affected. But because this is a rare disease, the chance that John's Dad is a carrier is very low. The actual risk can be calculated as 1/2 × (the chance that Dad is a carrier).

(1.2.5)
a) There is no right or wrong answer here, but it looks like Marfan syndrome runs in Anne's father's family. It appears that Charlie, John, and Peter have Marfan syndrome. This is consistent with autosomal dominant inheritance where affected children must have affected parents. It is also likely that Anne and probably David have Marfan syndrome.

b) Since Marfan syndrome is inherited in an autosomal dominant manner, children of an affected parent have a 50% chance of having Marfan syndrome.

(1.3) One gene; more complex models, I

(1.3.1) In *incomplete dominance*, the heterozygote has an *intermediate* phenotype, a phenotype different from either of the homozygotes. Some appropriate symbols would be:

Genotype	Phenotype
TT	tall
T′T′	short
TT′	medium, this is intermediate between tall and short

a) The parents would be TT × T′T′, giving all TT′ (medium height) offspring.

b) The parents can only be TT′ × TT′ giving:
25% TT – tall
25% T′T′ – short
50% TT′ – medium

(1.3.2) In *codominance*, the heterozygote has a *mixture of both* homozygote phenotypes. For example:

Genotype	Phenotype
LL	long hair
L′L′	short hair
LL′	a mixture of both long and short hair

a) The parents would be LL × L′L′, giving all LL′. The heterozygote offspring would have a mix of long and short hair.

b) The parents can only be LL′ × LL′, giving:
25% LL – long hair only
25% L′L′ – short hair only
50% LL′ – mixed long and short hair

(1.3.3)

Genotype	Phenotype
$C^B C^B$	blue
$C^R C^R$	red
c c	green
$C^B C^R$	blue
C^B c	blue
C^R c	red

(1.3.4) In cross 1, a blue-flowered plant × a white-flowered plant gives offspring that all have pale blue flowers. A plausible model is that color is controlled by one gene with two alleles and that color is incompletely dominant such that:

genotype	phenotype
BB	blue
BB′	pale-blue
B′B′	white

If so, cross 1 is: BB × B′B′ ⇒ all BB′, pale blue.

This would predict that cross 2 is: BB′ × BB′ ⇒ 1:2:1 blue flowers (BB) : pale blue flowers (BB′) : white flowers (B′B′).

For both cross 1 and cross 2, the predictions agree with the data.

(1.3.5) If you look at only cross 1, you see two phenotypes, green-eyed and white-eyed, so you could try a two-allele model. Cross 1 also tells us that we have heterozygote parents with green eyes that have some offspring with white eyes. This would indicate that green eyes are dominant to white eyes. You could use the symbols:

Genotype	Phenotype
GG	green eyes
Gg	green eyes
gg	white eyes

Cross 1 would have been Gg × Gg. You would then predict 25% GG, 50% Gg, and 25% gg or a ratio of 3 green-eyed : 1 white-eyed insects in the offspring. This is consistent with cross 1.

If you consider cross 2, however, you see three phenotypes. Both incomplete dominance and more than two alleles could explain three phenotypes, so where do you begin? If the three eye colors were due to incomplete dominance, you would expect to have seen red eyes in the first cross; the parents were not homozygotes because you had a mix of eye colors in the offspring. So you should consider the possibility that eye color is controlled by one gene with three alleles.

a) i) Thus, the three eye colors could be due to three alleles of the eye color gene where green eyes are dominant to white eyes. Some appropriate symbols would be:

E^R – allele associated with red eyes
E^G – allele associated with green eyes
E^W – allele associated with white eyes

ii) The parents in cross 1 would be: $E^GE^W \times E^GE^W$

iii)

	E^G	E^W
E^G	E^GE^G	E^GE^W
E^W	E^GE^W	E^WE^W

You would then predict 25% E^GE^G, 50% E^GE^W and 25% E^WE^W, or a ratio of 3 green-eyed : 1 white-eyed insects in the offspring. This is consistent with cross 1.

b) i) In cross 2, red-eyed × white-eyed → red-eyed and green-eyed offspring.

- The white-eyed phenotype is masked in the offspring so assume white eyes are recessive to both red and green eyes and thus the white-eyed parent would be: E^WE^W.
- Both red and green eyes are seen in the offspring; thus the red-eyed parent must have both the E^R and the E^G alleles, which means that red eyes are dominant to green eyes.

ii) Therefore, the parents in cross 2 are: red-eyed (E^RE^G) × white-eyed (E^WE^W).

(1.3.6) To begin, assign alleles to each of the parents. If both parents' genotypes are unambiguous, then predict the blood types possible in their offspring. If the parental genotypes are ambiguous, then predict blood types possible in the offspring for each combination.

i) type AB = I^AI^B , type O = ii: these parents could have I^Ai (type A) or I^Bi (type B) children.

ii) type A = I^AI^A or I^Ai, type O = ii.

If the type A parent is I^AI^A, then the couple could have only I^Ai (type A) children.

If the type A parent is I^Ai, then the couple could have I^Ai (type A) or ii (type O) children.

iii) type A = I^AI^A or I^Ai, type AB = I^AI^B.

If the type A parent is I^AI^A, then the couple could have I^AI^A (type A) or I^AI^B (type AB) children.

If the type A parent is I^Ai, then the couple could have I^AI^A (type A), I^AI^B (type AB), I^Ai (type A), or I^Bi (type B) children.

iv) type O = ii: these parents could have only ii (type O) children.

- Couple (iv) could have had only the baby with blood type O.
- The baby with type AB blood could have come only from couple (iii).
- Since couple (iii) had the AB baby, then the child with type B blood belongs to couple (i).
- This leaves the child with type A blood belonging to couple (ii).

(1.3.7) Remember a child receives one and only one allele from each parent.

- If George and Sallie are indeed Fred's parents, then Fred (type B blood) must have received the I^B allele from his father. Sallie with type A blood does not have the I^B allele.

- If George and Sallie are Fred's parents, then Sallie must have the genotype I^Ai, and Fred would have gotten the i allele from Sallie.

a) With only the blood type information, George and Sallie could be Fred's parents.

b) The information that George's father has type A blood and his mother has type B blood restricts George's genotype to I^Bi. This is still consistent with George and Sallie being Fred's parents.

c) The information that George has a sister with type O blood defines George's father as I^Ai and his mother as I^Bi, but this does not change the possibility that George and Sallie are Fred's parents.

d) The information that Sallie's father and mother are both I^AI^B means that Sallie (type A) has the genotype I^AI^A. This would prevent her from giving Fred the i allele. So if all the family information is true, then George and Sallie cannot be Fred's parents.

(1.3.8) The mother and the child are both type O and must have the genotype ii.

a) Bob with type A blood could be I^AI^A or I^Ai. If he is I^Ai, he could contribute the i allele, so he cannot be ruled out as the child's father.

b) Bob's mother (type A) could be I^AI^A or I^Ai and his father (type AB) must be I^AI^B. Bob could have type A blood (and the I^Ai genotype) if his mother contributed her i allele and his father contributed his I^A allele. Therefore, this information cannot exclude the man as the child's father.

c) If Bob's mother's parents are both type AB (I^AI^B), then Bob's mother must be I^AI^A, and she could not contribute an i allele to her son. Therefore, Bob must also be I^AI^A. This information would exclude him as the child's father.

(1.3.9) Begin by assigning the parental genotypes and the potential blood types of the children.

a) Couple #1 cannot be Rodger's parents.

> Tom must be I^AI^B and Ann is I^AI^A or I^Ai.
> If Ann is I^AI^A, then their children could be type A (I^AI^A) or type AB (I^AI^B).
> If Ann is I^Ai, then their children could be type A (I^AI^A or I^Ai), type AB (I^AI^B), or type B (I^Bi). But they cannot have a type O child. Therefore, they are not Rodger's parents.

Couple #2 cannot be Cathy's parents.

> Peter and Sally are both either I^BI^B or I^Bi. They can have type B children and, if they are both I^Bi, a type O child. They cannot have a type A child. Therefore, they are not Cathy's parents.

b) Since Ann's parents are both I^AI^B, she must be I^AI^A. Therefore, Ann and Tom (I^AI^B) can have only type A or AB children; they cannot have a type B child. In (a) you determined that they cannot have a type O child; therefore, they must be Cathy's parents.

c) Since Peter's parents are I^B_ and ii, he must be I^Bi. Since Sally's parents are both I^AI^B, she must be I^BI^B. Peter and Sally thus can have a type B child, but they cannot have a type O child. Therefore, Peter and Sally are Steve's parents.

(V3) There are no solutions for this part.

(1.3.10)

a) In cross 2, a purple plant is crossed to a blue plant and all the offspring are purple.

> i) Assume that color is controlled by one gene with two alleles, and that purple color is dominant to blue color. Some appropriate symbols would be:
>
> | Genotype | Phenotype |
> |---|---|
> | PP | purple |
> | Pp | purple |
> | pp | blue |
>
> ii) Cross 1 = purple (Pp) × blue (pp). Our model predicts 50% purple (Pp) and 50% blue (pp) offspring, which is what the data show.
> Cross 2 = purple (PP) × blue (pp). Our model predicts all purple (Pp) offspring, which is what the data show.

b) In these plants, you see three phenotypes. Both incomplete dominance and more than two alleles could explain three phenotypes, so where do you begin? If the three colors were due to incomplete dominance, then you could predict that the purple phenotype (which is intermediate between the blue and the red phenotypes) is associated with the genotype Pp. If this were true, then you would expect cross 3 and cross 4 to give identical results. Therefore, you should consider the possibility that color is controlled by one gene with three alleles.

Because crosses 3 and 4 give different offspring, you know that at least one parent in each cross is a heterozygote. However, all the parents in crosses 3 and 4 are purple, so purple is dominant to both red and blue.

Cross 5 indicates that blue is dominant to red.

Our model is that color is controlled by one gene with three alleles. Purple is dominant to both red and blue, and blue is dominant to red. Some appropriate symbols would be:

C^R – allele associated with red
C^B – allele associated with blue
C^P – allele associated with purple

c)
Cross 1 purple parent = C^PC^B or C^PC^R
Cross 2 purple parent = C^PC^P
Cross 3 purple parent = C^PC^B
Cross 4 purple parent = C^PC^R
Cross 5 purple parent = C^BC^B

Therefore:
Cross 3 = purple (C^PC^B) × purple (C^PC^B) ⇒ 3 purple (C^PC^P or C^PC^B) : 1 blue (C^BC^B)
Cross 4 = purple (C^PC^R) × purple (C^PC^R) ⇒ 3 purple (C^PC^P or C^PC^R) : 1 red (C^RC^R)
Cross 5 = blue (C^BC^B) × red (C^RC^R) ⇒ all blue (C^BC^R)

(1.3.11)
You see four coat colors in tribbles. Both incomplete dominance and more than two alleles could explain these phenotypes. Crosses 1 and 2 do not indicate that the colors are due to incomplete dominance. In fact, given crosses 1 and 2, you would predict that color is controlled by one gene with three alleles and that green is dominant to both red and white. In the progeny from cross 3 (where your F_1 tribbles are likely heterozygotes), you see what could be an intermediate phenotype.

Therefore, you should consider the possibility that color is controlled by one gene with three alleles, but some colors show incomplete dominance.

a) Our model is that color is controlled by one gene with three alleles. Green is dominant to both red and white, but the red and white phenotypes show incomplete dominance with each other. Some appropriate symbols would be:

Genotype	Coat color
$C^G\_$	green
C^RC^R	red
C^WC^W	white
C^RC^W	pink

The green F_1 tribbles from cross 1 are heterozygous C^GC^R. The green F_1 tribbles from cross 2 are heterozygous C^GC^W.
So cross 3 = green (C^GC^R) × green (C^GC^W) ⇒25% C^GC^G (green) : 25% C^GC^R (green) : 25% C^GC^W (green) : 25% C^RC^W (pink), giving the ratio of 3 (green) : 1 (pink) seen.

b) The cross is pink (C^RC^W) × green (C^GC^G) ⇒ 50% C^RC^G and 50% C^WC^G. Because green is dominant to both white and red, all progeny will be green.

(1.4) One gene; sex linkage

(1.4.1)

a) We are following an X-linked gene where red eyes is dominant to white eyes.

i) The white-eyed female can only be X^rX^r; the red-eyed male can only be X^RY.

The Punnett square is:

	X^r	X^r
X^R	X^RX^r red-eyed	X^RX^r red-eyed
Y	X^rY white-eyed	X^rY white-eyed

This would give:

50% X^RX^r red-eyed female
50% X^rY white-eyed male

ii) The red-eyed female can be X^RX^r or X^RX^R; the white-eyed male can only be X^rY.

The first Punnett square is:

	X^R	X^r
X^r	X^RX^r red-eyed	X^rX^r white-eyed
Y	X^RY red-eyed	X^rY white-eyed

This would give:

25% X^RX^r red-eyed female
25% X^rX^r white-eyed female
25% X^RY red-eyed male
25% X^rY white-eyed male

The second Punnett square is:

	X^R	X^R
X^r	X^RX^r red-eyed	X^RX^r red-eyed
Y	X^RY red-eyed	X^RY red-eyed

This would give:

50% X^RX^r red-eyed female
50% X^RY red-eyed male

b) We are following a Z-linked gene where red eyes are dominant to white eyes.

i) The white-eyed female can only be Z^rW; the red-eyed male can be either Z^RZ^r or Z^RZ^R.

The first Punnett square is:

	Z^r	W
Z^R	Z^RZ^r red-eyed	Z^RW red-eyed
Z^r	Z^rZ^r white-eyed	Z^rW white-eyed

This would give:

25% Z^RW red-eyed female
25% Z^rW white-eyed female
25% Z^RZ^r red-eyed male
25% Z^rZ^r white-eyed male

The second Punnett square is:

	Z^r	W
Z^R	Z^RZ^r red-eyed	Z^RW red-eyed
Z^R	Z^RZ^r red-eyed	Z^RW red-eyed

This would give:

50% Z^RW red-eyed female
50% Z^RZ^r red-eyed male

ii) The red-eyed female can only be Z^RW; the white-eyed male can only be Z^rZ^r.

The Punnett square is:

	Z^R	W
Z^r	Z^RZ^r red-eyed	Z^rW white-eyed
Z^r	Z^RZ^r red-eyed	Z^rW white-eyed

This would give:

50% Z^rW white-eyed female
50% Z^RZ^r red-eyed male

(1.4.2)
a) A combination that is inconsistent with autosomal recessive.
Two diseased parents having a normal child. The parents must both be nn, so the child can only be nn (diseased).

b) Combinations that are inconsistent with sex-linked recessive.

- Two diseased parents having a normal child. The father must be X^nY and the mother must be X^nX^n, so the sons will all be X^nY (diseased) and the daughters will all be X^nX^n (diseased).
- A normal father having a diseased daughter. The daughter must be X^nX^n. Therefore, she must have gotten an X^n from each parent. Therefore, the father has to be X^nY (diseased).
- A diseased mother having a normal son. The mother must be X^nX^n. Since the son gets his X from his mother, he must be X^nY (diseased).

c) A combination that is inconsistent with autosomal dominant.
A diseased child from two normal parents. The child has to have at least one D allele. That allele had to come from one of the parents. That parent would therefore have to have at least one D, which would make him/her diseased.

(V4) There are no solutions for this part.

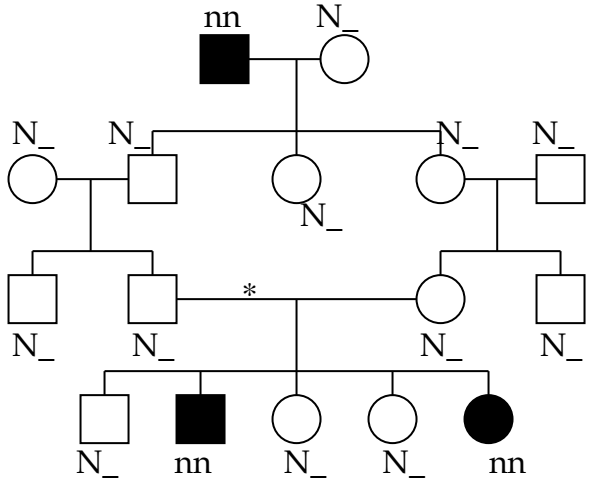
(1.5) Pedigrees involving one gene, II

(1.5.1)
a) There are two ways to solve parts (i) and (ii) of this problem. The first is the "brute force" method: try all three possible genetic models. This is time-consuming but guaranteed to get you the right answer.

1) First, try <u>autosomal recessive</u>:

<u>Genotype</u>	<u>Phenotype</u>
NN or Nn	normal
nn	affected

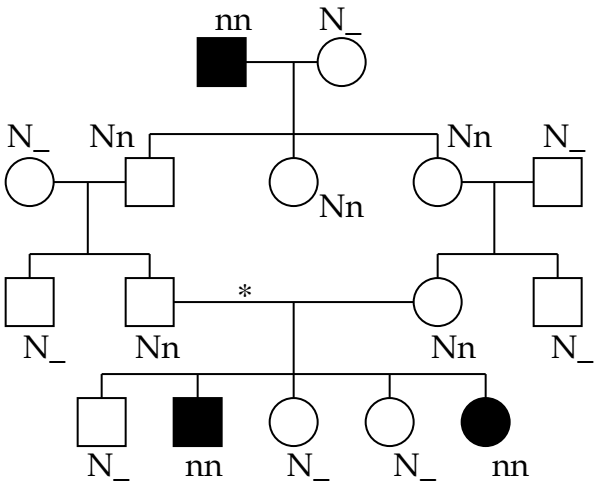
As before, assign the genotypes you know for sure. Individuals whose genotypes are ambiguous can be labeled as N_.



Begin with an affected individual (nn) on the bottom row; that individual has to get one (n) allele from each parent, so all ambiguous parents of affected individuals become (Nn). Thus, the parents of the affected son in the bottom row can be assigned as Nn. What about his siblings? It is possible for two Nn parents to have both affected and normal offspring, so without further information all his normal siblings remain (N_).

Now look at the affected male in the top row. All of his children have to get an n allele from him (since that is all he has to give). We don't know what the genotype of the top row female is, so she has to be marked as N_. (*Note that since the trait is rare, she is more likely to be NN.)

The pedigree incorporating this information is below.

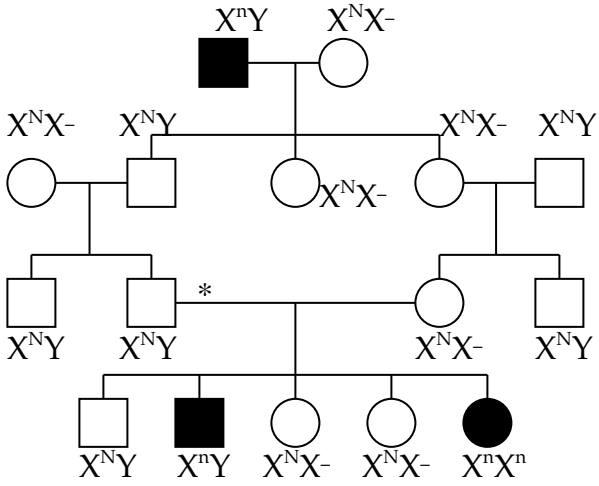


We cannot assign genotypes to the other individuals in the pedigree, so they must be marked N_. You can check to see that all the combinations of parents and offspring are possible. Therefore, this trait could be inherited in an autosomal recessive mode.

2) Now try sex-linked recessive:

Genotype	Phenotype
X^NX^N	normal female
X^NX^n	normal female
X^nX^n	affected female
X^NY	normal male
X^nY	affected male

This gives:

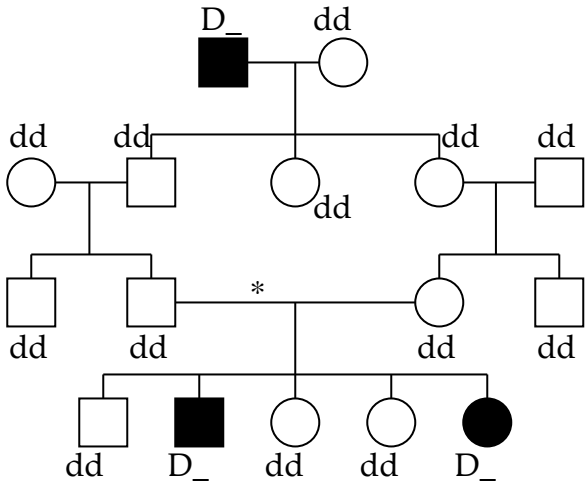


Begin with the affected son in the bottom row: he got his Y from his dad and his X^n from his mom. Therefore, his mom has to be X^NX^n. What about his affected sister? She had to get an X^n from her mom and an X^n from her dad. But if her dad had an X^n, he would have to be affected and he isn't. Therefore this pedigree is not consistent with a trait that is inherited in a sex-linked recessive manner.

3) Now try autosomal dominant:

Genotype	Phenotype
DD or Dd	affected
dd	normal

This gives:



Look at the affected son in the bottom row. One or more of his parents must have at least one D allele. But that would make them affected and they are normal, so this trait cannot be inherited in an autosomal dominant manner.

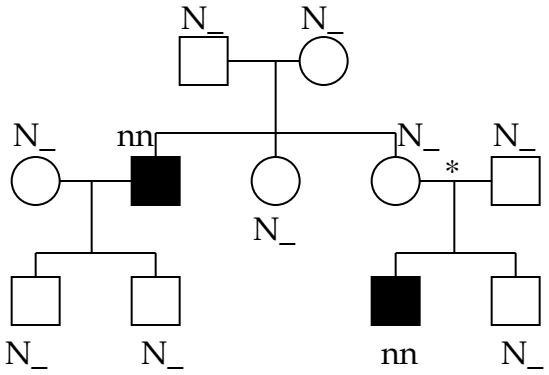
Here we tried all possible modes of inheritance. By process of elimination, this disease is consistent only with autosomal recessive inheritance.

iii) The couple marked with a * are Nn × Nn, so the risk that the next son will be diseased is 1/4 or 25%.

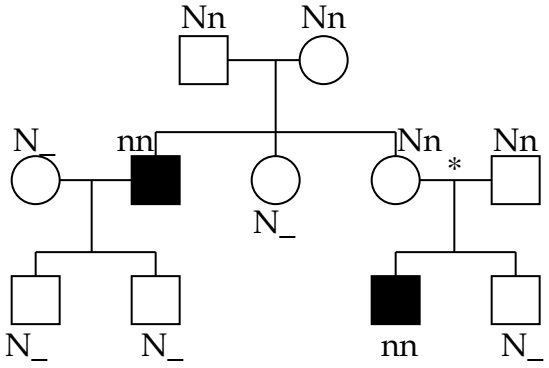
Another way to approach this pedigree is to use the rules that you created in an earlier problem (1.4.2) to rule out some of the models. Using those rules, the affected daughter in the bottom row eliminates two models. First, since her father is normal, the trait cannot be sex-linked recessive. Second, since both of her parents are normal, the trait cannot be autosomal dominant. You could then check to see if autosomal recessive works and it does.

b) Using the rules outlined in problem (1.4.2), we can immediately rule out autosomal dominant because both affected children have two normal parents. That leaves autosomal recessive and sex-linked recessive. No parts of the pedigree rule either of those two models out, so we must try each one to see how it works.

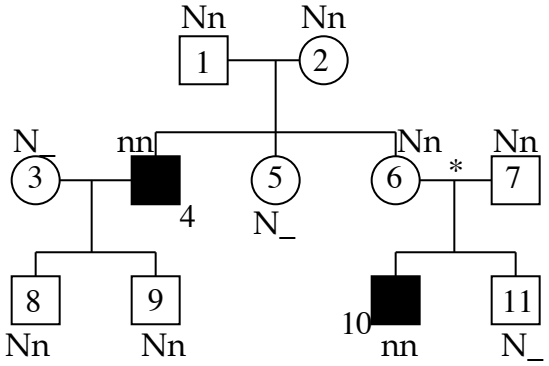
1) Try an autosomal recessive mode of inheritance. First fill in the genotypes we know for sure. All affected individuals would be nn and all unaffected individuals would have at least one N.



Begin with the affected male in the bottom row. He had to get an n from both parents. So they have to be Nn. Two Nn parents can have both normal and diseased children, so this part of the pedigree is consistent with an autosomal recessive mode of inheritance. Now look at the affected male in the middle row. As before, both of his parents have to be Nn. This information has been incorporated in the following pedigree.



Now look again at the affected male in the middle row. He must give an (n) to each of his children. Since none of his children are affected, they must be Nn. We do not have any other information that allows us to assign genotypes to the remaining individuals, so if the trait were inherited as an autosomal recessive trait, then the pedigree would be as follows.



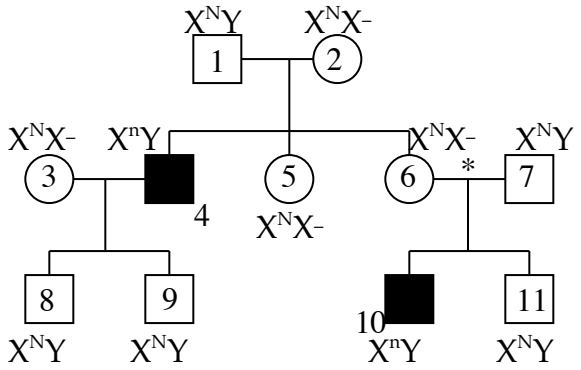
For the purposes of assessing how likely this mode of inheritance is we need to count the unrelated carriers; that is, unrelated people who have at least one allele associated with the trait. In this pedigree, there are three unrelated people with the trait allele: 1, 2, and 7. All the other people who have one or more n alleles got their n alleles from individuals 1, 2, or 7 or their descendants.

Going through each of the individuals:

1) Brought his n into the family. Unrelated carrier #1
2) Brought her n into the family. Unrelated carrier #2
3) Does not need to have an n to make the pedigree work.
4) Got his n's from 1 and 2.
5) If she has an n, she got it from 1 or 2.
6) Got her n from 1 or 2.
7) Brought his n into the family. Unrelated carrier #3
8) Got his n from 4.
9) Got his n from 4.
10) Got his n's from 6 and 7.
11) If he has an n, he got it from 6 or 7.

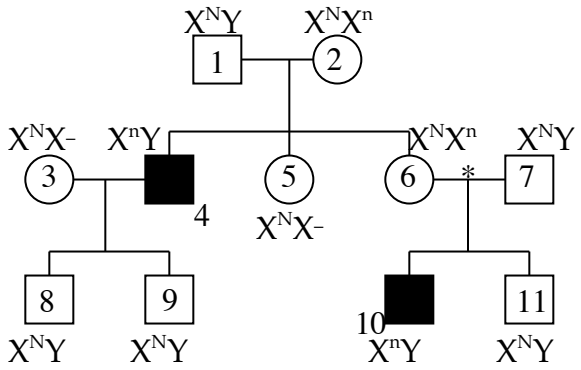
So for this trait to be inherited as an autosomal recessive trait, three unrelated carriers are required.

2) Now try a sex-linked recessive mode of inheritance; first fill in the genotypes you know for sure:



Begin with the affected male in the bottom row, individual 10. He got his Y from dad and his X^n from mom, so mom has to be X^NX^n. It is possible for $X^NX^n \times X^NY$ to have affected and normal sons, so this part of the pedigree is consistent with a sex-linked recessive mode of inheritance.

If you look at individual 4, his mom also has to be X^NX^n. Given this, the siblings of individual 4 are also possible so the pedigree remains consistent with a sex-linked recessive mode of inheritance. These genotypes are shown below.



Individuals 3 and 5 remain ambiguous.

Hence, this pedigree is also consistent with sex-linked recessive inheritance. To evaluate which mode is more likely, we once again count the number of unrelated carriers needed to make this mode of inheritance possible.
Individual:

1) Does not have an allele associated with the trait.
2) Brought her X^n in to the family. Unrelated carrier #1.
3) Does not necessarily have an allele associated with the trait.
4) Got his X^n from 2.
5) If she has an X^n, she got it from 2.
6) Got her X^n from 2.
7) Does not have an allele associated with the trait.
8) Does not have an allele associated with the trait.
9) Does not have an allele associated with the trait.
10) Got his X^n from 6.
11) Does not have an allele associated with the trait.

Therefore, a sex-linked recessive mode of inheritance requires only one unrelated carrier, whereas autosomal recessive inheritance required three unrelated carriers. If the trait is rare, then unrelated carriers are rare, so sex-linked recessive is a more likely mode of inheritance.

iii) Individuals 6 and 7 are X^NX^n and X^NY. The Punnett square is:

	X^N	X^n
X^N	X^NX^N	X^NX^n
Y	X^NY	X^nY

← sons

The sons will be 1/2 normal and 1/2 affected. Therefore, the chance that the next son will be affected is 1/2 or 50%.

(1.5.2)
a) First eliminate modes of inheritance that are not possible. Autosomal dominant inheritance is impossible because affected individuals 7, 8, and 13 have parents that are all normal.

Both autosomal recessive and sex-linked recessive modes are possible. However, a sex-linked recessive mode of inheritance is more likely because 1) there are five affected males and only one affected female, and 2) a sex-linked recessive mode requires only two unrelated carriers, individuals 1 and 2. (See solutions to problem [1.5.1] for more information on unrelated carriers.) Although this pedigree is consistent with inheritance of an autosomal recessive trait, this would require five unrelated carriers (1, 2, 3, 6, and 11).

b)

Genotype	Phenotype
X^NX^N	normal female
X^NX^n	normal female
X^nX^n	affected female
X^NY	normal male
X^nY	affected male

1: X^nY 2: X^NX^n 3: X^NY 4: X^NX^n 5: X^nX^n 6: X^NY 7: X^nY
8: X^nY 9: X^nY 10: X^NX^n 11:X^NY 12: X^NY 13: X^nY

(1.5.3)
a) First eliminate modes of inheritance that are not possible.

- not autosomal recessive: 4 and 5 are affected but they have a normal child (7).
- not sex-linked recessive: for two reasons:
  - 4 and 5 are affected but they have a normal child (7)
  - 1 is affected but she has a normal son (3)

Therefore, an autosomal dominant mode of inheritance is likely. It is important to work through the pedigree to make sure it is consistent.

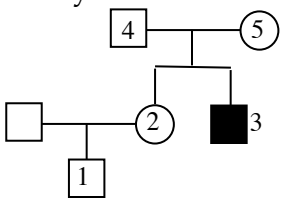
b)

Genotype	Phenotype
DD or Dd	affected (dominant)
dd	normal (recessive)

c) 1: Dd 2: dd 3: dd 4: Dd 5: Dd 6: Dd 7: dd

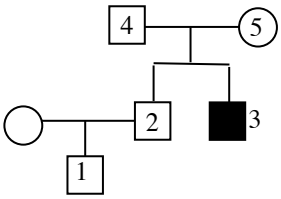
d) Dd × Dd gives 3:1 affected: normal. Therefore, there is a 75% chance that she will be affected.

(1.5.4) The pedigree for "a male those whose mother's brother is a hemophiliac" is represented below. Why should individual 1 be exempt from circumcision?



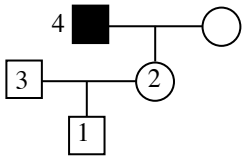
a) Individual 3 has hemophilia, although his parents do not have the disease. Thus, individual 5 must be a carrier (X^hX^H). Individual 3 would have received an X^h allele from his mother (individual 5) and a Y from his father (individual 4). Therefore, individual 2 has a 50% chance of being a carrier and if she is a carrier, the son (individual 1) will have a 50% chance of being a hemophiliac. This means that a male whose mother's brother is a hemophiliac has a 25% chance of being a hemophiliac. Exemption from circumcision makes sense.

b) This is not an oversight. See the pedigree below.



Again, individual 3 has hemophilia, although his parents do not have the disease. Thus, individual 5 must be a carrier (X^hX^H). However, individual 2 does not have the disease so he must have received the X^H allele from his mother. Individual 2 has the genotype X^HY, he does not carry the disease allele and cannot then pass it to the child. Therefore, individual 1 has no more risk for hemophilia than anyone in the general population.

c) Should an exemption be made for the son of a mother whose father is a bleeder? Explain.



Individual 4 has hemophilia. Thus, individual 2 would have received an X^h allele from her father and must be a carrier (X^hX^H). Since individual 2 is a carrier, individual 1 has a 50% chance of being a hemophiliac. An exemption from circumcision makes sense.

(1.5.5) We will use symbols outlined in earlier problems.

For autosomal recessive:

Genotype	Phenotype
NN or Nn	normal
nn	diseased

For sex-linked recessive:

Genotype	Phenotype
X^NX^N	normal female
X^NX^n	normal female
X^nX^n	diseased female
X^NY	normal male
X^nY	diseased male

For autosomal dominant:

Genotype	Phenotype
DD or Dd	diseased (dominant)
dd	normal (recessive)

a) First eliminate modes of inheritance that are not possible.

- A diseased mother has a normal son, so sex-linked recessive is not possible.
- Autosomal recessive is possible, but it requires four unrelated carriers.

  i) So an autosomal dominant mode of inheritance is more likely with only one unrelated carrier.

  ii) * = Dd

b) First eliminate modes of inheritance that are not possible.

- Two normal parents have a diseased child, so autosomal dominant is not possible.
- A diseased mother has a normal son, so sex-linked recessive is not possible.

  i) An autosomal recessive mode of inheritance is consistent with this pedigree.

  ii) * = Nn (not NN because the father is nn)

c) First eliminate modes of inheritance that are not possible.

- Two normal parents have a diseased child, so autosomal dominant is not possible.
- Autosomal recessive is possible, but it requires four unrelated carriers.
- Sex-linked recessive requires only two unrelated carriers.

  i) A sex-linked recessive mode of inheritance is more likely.
  ii) * = X^NX^n

d) First eliminate modes of inheritance that are not possible.

- Two normal parents have a diseased child, so autosomal dominant is not possible.
- A normal father has a diseased daughter, so sex-linked recessive is not possible.

i) Autosomal recessive is the only possible mode.
ii) * = Nn

e) First eliminate modes of inheritance that are not possible.

- Two normal parents have a diseased child, so autosomal dominant is not possible.
- Autosomal recessive is possible but requires four unrelated carriers.
- Sex-linked recessive requires only one unrelated carrier.

i) Sex-linked recessive
ii) * = X^nY

f) First eliminate modes of inheritance that are not possible.

- Two normal parents have a diseased child, so autosomal dominant is not possible.
- Autosomal recessive is possible but requires four unrelated carriers.
- Sex-linked recessive requires only one unrelated carrier.

i) Sex-linked recessive
ii) * = X^NX^n

g) All three modes are possible.

- Autosomal recessive is possible but requires three unrelated carriers
- Sex-linked recessive is possible but requires three unrelated carriers
- Autosomal dominant requires only one unrelated carrier.

i) Autosomal dominant
ii) * = dd

(1.6) One gene; more complex models, II

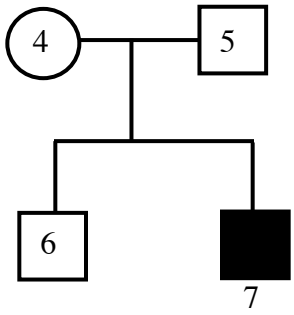
(V5) Virtual Genetics Lab V
There are no solutions for this part.

(V6) Virtual Genetics Lab VI
There are no solutions for this part.

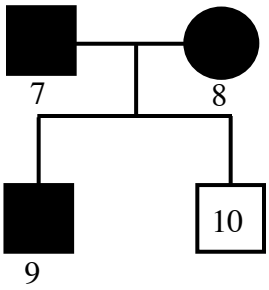
(3) CHALLENGE PROBLEMS

(3.1)

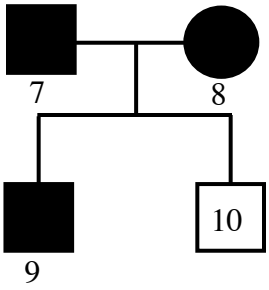
a) For autosomal dominant inheritance, affected children must have at least one affected parent. This part of the pedigree is inconsistent with an autosomal dominant mode of inheritance.



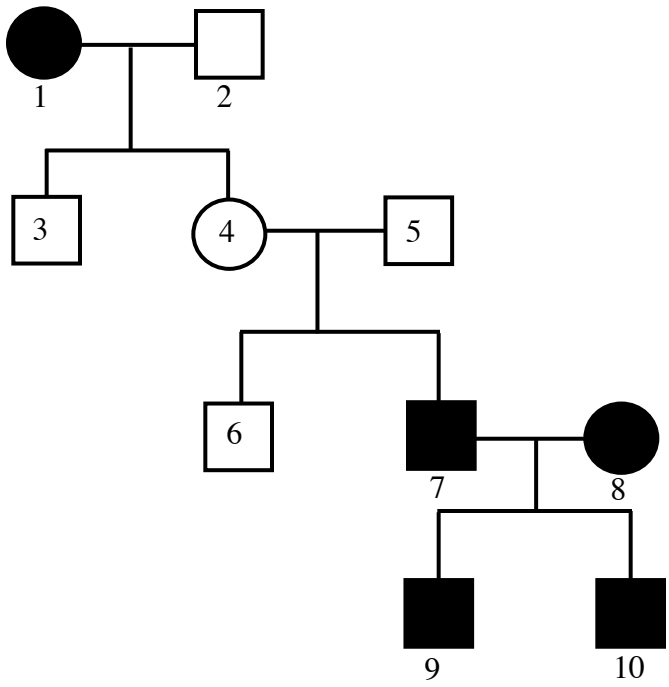
b) For autosomal recessive inheritance, two affected parents will have only affected children. This part of the pedigree is inconsistent with an autosomal recessive mode of inheritance.



c) For sex-linked recessive inheritance, all the sons from an affected mother will be affected. This part of the pedigree is inconsistent with a sex-linked recessive mode of inheritance.



d) If you change 10 from unaffected to affected, the pedigree is now consistent with an autosomal recessive mode of inheritance.



(3.2) In general, start with the simplest model you can think of and test it against the data.

a) There are three possible models to explain the phenotypes of these aliens.

1) One possibility is that blood type is controlled by one gene with the three alleles I^{α}, I^{β}, and I^{γ}. This theory fits only with crosses 4 and 5. The other crosses do not fit this theory.

2) Another way to explain the three phenotypes is to assume that blood type is due to one gene with two alleles, but the heterozygote is a different blood type than either homozygote. In cross 1, the three different phenotypes are present in the offspring, so one of the parents must be the heterozygote. For example:

TT type β
T′T type α
T′T′ type γ

If you apply these genotypes to cross 1, however, it is clear that this theory alone cannot explain the data.

3) If you examine cross 2 (male β × female γ) and cross 3 (male γ × female β), you see different results even though both crosses are β × γ. You also see that blood type is not evenly distributed between the sexes. This suggests that blood type is a sex-linked trait.

- First consider if XX = female and XY = male fit the data. Assume that blood type is due to one gene with two alleles where the heterozygote is a different blood type than either homozygote (see above). If XX = female and XY = male, then a heterozygote female will give male offspring of two different phenotypes, both of which are different from the phenotype seen in the heterozygote XX female.

- Next consider if ZZ = male and ZW = female fit the data. Assume that blood type is due to one gene with two alleles where the heterozygote is a different blood type than either homozygote (see above). If ZW = female and ZZ = male, then a heterozygote male will give female offspring of two different phenotypes, both of which are different from the phenotype seen in the heterozygote ZZ male.

Cross 1 fits the model that ZZ = male and ZW = female and that blood type is due to one gene with two alleles where the heterozygote is a different blood type from either homozygote. This model predicts that blood type is inherited in the following manner:

Z^AZ^A = male γ	Z^AW = female γ
Z^AZ^a = male α	
Z^aZ^a = male β	Z^aW = female β

The data from each cross are consistent with what is predicted by this model.

b) In the above model, blood type α is the phenotype of a heterozygote. Also in this model females carry only one sex chromosome (ZW = female). Therefore, it is not possible to have a female with type α blood.