Problem Set 2
Solutions

1. The easy ones first:

$$
\begin{aligned}
& \operatorname{Pr}(\mathrm{IBS}=0 \mid \mathrm{IBD}=2)=0 \\
& \operatorname{Pr}(\mathrm{IBS}=1 \mid \mathrm{IBD}=2)=0 \\
& \operatorname{Pr}(\mathrm{IBS}=2 \mid \mathrm{IBD}=2)=1
\end{aligned}
$$

The IBD $=1$ cases are pretty simple, too:

$$
\begin{aligned}
\operatorname{Pr}(\mathrm{IBS}=0 \mid \mathrm{IBD}=1) & =0 \\
\operatorname{Pr}(\mathrm{IBS}=1 \mid \mathrm{IBD}=1) & =\text { marker heterozygosity } \\
& =1-\sum_{i} p_{i}^{2} \\
\operatorname{Pr}(\mathrm{IBS}=2 \mid \mathrm{IBD}=1) & =\sum_{i} p_{i}^{2}
\end{aligned}
$$

The IBD $=0$ cases are harder. We're taking two random draws from the genotypes

$$
\begin{array}{cccc}
\left(a_{1}, a_{1}\right) & \left(a_{1}, a_{2}\right) & \ldots & \left(a_{1}, a_{k}\right) \\
& \left(a_{2}, a_{2}\right) & \ldots & \left(a_{2}, a_{k}\right) \\
& & \ddots & \vdots \\
& & & \left(a_{k}, a_{k}\right)
\end{array}
$$

with probabilities

$$
\begin{array}{cccc}
p_{1}^{2} & 2 p_{1} p_{2} & \ldots & 2 p_{1} p_{k} \\
& p_{2}^{2} & \ldots & 2 p_{2} p_{k} \\
& & \ddots & \vdots \\
& & & p_{k}^{2}
\end{array}
$$

and we want to find the probability they share 0,1 , or 2 alleles by state.
First:

$$
\begin{aligned}
\operatorname{Pr}(\text { IBS }=2 \mid \text { IBD }=0) & =\operatorname{Pr}[(11,11),(22,22), \ldots,(k k, k k),(12,12),(13,13), \ldots, \text { etc. }) \\
& =\sum_{i} p_{i}^{4}+\sum_{i} \sum_{j: j>i}\left(2 p_{i} p_{j}\right)^{2} \\
\text { [now we simplify] } & =\sum_{i} p_{i}^{4}+2 \sum_{i} p_{i}^{2} \sum_{j: j \neq i} p_{j}^{2} \\
& =\sum_{i} p_{i}^{4}+2 \sum_{i} p_{i}^{2}\left(\sum_{j} p_{j}^{2}-p_{i}^{2}\right) \\
& =\sum_{i} p_{i}^{4}+2\left\{\left(\sum_{i} p_{i}^{2}\right)^{2}-\sum_{i} p_{i}^{4}\right\} \\
& =2\left\{\sum_{i} p_{i}^{2}\right\}^{2}-\sum_{i} p_{i}^{4}
\end{aligned}
$$

The other two are similar; with (painful) simplification, we get:

$$
\begin{aligned}
& \operatorname{Pr}(\mathrm{IBS}=1 \mid \mathrm{IBD}=0)=4\left\{\sum p_{i}^{2}+\sum p_{i}^{4}-\sum p_{i}^{3}-\left(\sum p_{i}^{2}\right)^{2}\right\} \\
& \text { and } \operatorname{Pr}(\mathrm{IBS}=0 \mid \mathrm{IBD}=0)=1-4 \sum p_{i}^{2}-3 \sum p_{i}^{4}+4 \sum p_{i}^{3}+2\left(\sum p_{i}^{2}\right)^{2}
\end{aligned}
$$

Note: The biggest issues are the coefficients and the ranges of the summations (e.g., $\sum_{i} \sum_{j: j>i}$ or $\sum_{i} \sum_{j: j \neq i}$ or $\sum_{i} \sum_{j}$ ). Be precise!

Special case: $p_{1}=p_{2}=p_{3}=p_{4}=1 / 4$.

|  | IBS |  |  |
| :---: | :---: | :---: | :---: |
| IBD | 0 | 1 | 2 |
| 0 | $21 / 64$ | $36 / 64$ | $7 / 64$ |
| 1 | 0 | $3 / 4$ | $1 / 4$ |
| 2 | 0 | 0 | 1 |

2. Let $M=$ parental mating type, $G=$ kids' genotypes, and $\mathrm{DSP}=$ "discordant sibpair."

$$
\begin{aligned}
\operatorname{Pr}(\mathrm{IBD}=v \mid \mathrm{DSP}) & =\sum_{M, G} \operatorname{Pr}(\mathrm{IBD}=v \mid M, G, \mathrm{DSP}) \operatorname{Pr}(G \mid M, \mathrm{DSP}) \operatorname{Pr}(M \mid \mathrm{DSP}) \\
& =\sum_{M, G} \operatorname{Pr}(\mathrm{IBD}=v \mid M, G) \operatorname{Pr}(G \mid M, \mathrm{DSP}) \operatorname{Pr}(M \mid \mathrm{DSP})
\end{aligned}
$$

Calculating $\operatorname{Pr}(M \mid \mathrm{DSP})$ is similar to that for the affected sibpair, as calculated in class:

| M | $\operatorname{Pr}(M)$ | $\operatorname{Pr}(\mathrm{DSP} \mid M)$ | $\operatorname{Pr}(M \mid$ DSP $)$ | $\begin{gathered} \operatorname{Pr}(M \mid \mathrm{DSP}) \\ \text { when } p=0.05 \\ \hline \end{gathered}$ |
| :---: | :---: | :---: | :---: | :---: |
| $\mathrm{DD} \times \mathrm{Dd}$ | $4 p^{3}(1-p)$ | 1/2 | $\alpha \cdot 2 p^{3}(1-p)$ | $\sim 0.0656$ |
| $\mathrm{Dd} \times \mathrm{Dd}$ | $4 p^{2}(1-p)^{2}$ | 3/8 | $\alpha \cdot(3 / 2) p^{2}(1-p)^{2}$ | $\sim 0.9344$ |

where $\alpha=1 /\left[2 p^{3}(1-p)+(3 / 2) p^{2}(1-p)^{2}\right]$
Then we calculate $\operatorname{Pr}(G \mid M, \mathrm{DSP})$ and $\operatorname{Pr}(\operatorname{IBD}=v \mid M, G)$ for all possible $M, G$ :

|  |  |  | $\operatorname{Pr}(\mathrm{IBD}=v \mid M, G)$ |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: |
| $M$ | $G$ | $\operatorname{Pr}(G \mid M, \mathrm{DSP})$ | 0 | 1 | 2 |
| DD $\times$ Dd | DD,Dd | 1 | $1 / 2$ | $1 / 2$ | 0 |
| Dd $\times$ Dd | DD,Dd | $2 / 3$ | 0 | 1 | 0 |
| Dd $\times$ Dd | DD,dd | $1 / 3$ | 1 | 0 | 0 |

We then sum up to get $\operatorname{Pr}(\operatorname{IBD}=v \mid \mathrm{DSP})$ :

| 0 | 1 | 2 |
| :---: | :---: | :---: |
| 0.344 | 0.656 | 0 |

3. Let $K=\mathrm{IBD}$ status at disease gene and $X=\mathrm{IBD}$ status at marker.

$$
\begin{aligned}
\operatorname{Pr}(X=v \mid \mathrm{DSP}) & =\sum_{k} \operatorname{Pr}(X=v \mid \mathrm{DSP}, K=k) \operatorname{Pr}(K=k \mid \mathrm{DSP}) \\
& =\sum_{k} \operatorname{Pr}(X=v \mid K=k) \operatorname{Pr}(K=k \mid \mathrm{DSP})
\end{aligned}
$$

For $r=0.05$, the transition matrix $\operatorname{Pr}(X=x \mid K=k)$ is the following:

|  | $X$ |  |  |
| :---: | :---: | :---: | :---: |
| $K$ | 0 | 1 | 2 |
| 0 | 0.819 | 0.172 | 0.009 |
| 1 | 0.086 | 0.828 | 0.096 |
| 2 | 0.009 | 0.172 | 0.819 |

Note that the rows sum to 1 .
We multiply each row by the result for $\operatorname{Pr}(K=k \mid \mathrm{DSP})$ from problem 1, and obtain the following for $\operatorname{Pr}(X=x \mid \mathrm{DSP})$.

| 0 | 1 | 2 |
| :---: | :---: | :---: |
| 0.338 | 0.602 | 0.059 |

