1 Probability Theory

1.1 Classical Terminology [DeGroot 1.3-1.4]

- Experiment E.g. toss a coin 10 times or sequence a genome
- Outcome A possible result of an experiment,
  - E.g HHTHTTHHHT or ACGCTTATC
- Sample space The set of all possible outcomes of some experiment
  - E.g. $\{H, T\}^{10}$ or $\{A, C, G, T\}^*$.
- Event Any subset of the sample space
  - E.g. ≥ 4 heads; DNA seqs w/no run of > 50 As.

1.2 Goals

- Compute probabilities of events given probability of each possible outcome.
- Revise probabilities when new info is obtained

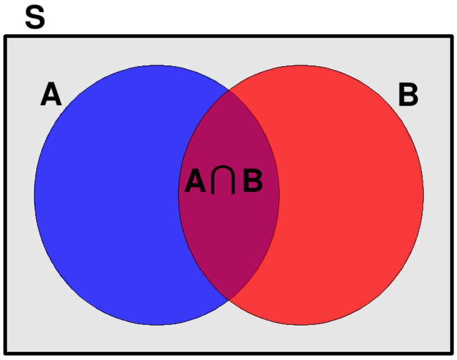
1.3 Definitions, axioms, simple theorems [DeGroot 1.5]

- If S is a sample space and $A \subseteq S$ is an event, then $Pr(A)$ is a number representing the probability that the event will occur – i.e., the probability that the outcome of the experiment will be in the set of outcomes constituting the event.
- Axiom 1 For any event A, $Pr(A) \geq 0$
- Axiom 2 If S is a sample space, $Pr(S) = 1$.
- Events A, B are disjoint iff $A \cap B = \emptyset$. The set $\{A_1, A_2, ...\}$ is disjoint iff every pair is disjoint. Disjoint events are mutually exclusive.
- Axiom 3 For any finite or infinite collection of disjoint events $A_1, A_2, ...$,

$$Pr(\cup_i A_i) = \sum_i Pr(A_i)$$

- Theorem $Pr(\emptyset) = 0$.
- Theorem For any event A where A^c is the complement of A, $Pr(A^c) = 1 - Pr(A)$.

- Theorem For any event A, $0 \leq Pr(A) \leq 1$.
- Theorem If $A \subseteq B$, then $Pr(A) \leq Pr(B)$.
- Theorem $Pr(A \cup B) = Pr(A) + Pr(B) - Pr(A \cap B)$.



2 Finite Sample Spaces [DeGroot 1.6]

- When $S = \{s_1, ..., s_n\}$, s_i is called an elementary event. $p_i \equiv Pr(s_i)$.
- The axioms imply
  - $p_i \geq 0, i = 1$ to n
  - $\sum_{i=1}^{n} p_i = 1$
- If $p_i = 1/n$ for $i = 1, ..., n$, the events $\{s_i\}$ are called equiprobable.
  - Then if A is an event and $|A| = M$, $Pr(A) = M/n$.

3 Permutations - Sampling without replacement [DeGroot 1.7]

- E.g. picking 3 cards from a deck of n.
  - Outcomes are 3-place vectors, each place filled by a different card
  - # of possible outcomes is $n(n-1)(n-2)$
  - Each outcome is called a permutation. (vector would be more intuitive.)
- When k cards are selected, # of permutations (vectors) is
  - $P_{n,k} = n(n-1)...(n-k+1)$
  - "The number of permutations of n elements taken k at a time."

  - Another way to write this is $P_{n,k} = \frac{n!}{(n-k)!}$
  - When k = n, $P_{n,k} = n(n-1)...1 = n!$. (0! = 1 by convention)

4 Combinations [DeGroot 1.8]

- How many distinct subsets of k elements can be chosen from n?
- Each subset is a combination of k elts. (subset would be more intuitive.)
- Order is irrelevant. No two combos (subsets) have the same elements.
- How many combos (subsets) of k elements can be selected from a set of n elements? (Written $C_{n,k}$)
  - E.g. the combos (subsets) of 2 elts from $\{a, b, c, d\}$ are

$$\{a, b\}\{a, c\}\{a, d\}\{b, c\}\{b, d\}\{c, d\} : C_{4,2} = 6$$

- In general, $C_{n,k} = \frac{n!}{(n-k)!k!}$. Also written $\binom{n}{k}$.
- Derivation: For each combo of k elements from n, there are $k!$ permutations. So # of permutations of n elements= $k!$ # of combos, or $P_{n,k} = k!C_{n,k}$.

$$C_{n,k} = \frac{P_{n,k}}{k!} = \frac{n!}{(n-k)!k!}$$

- Example: Probability of exactly 3 heads on 10 tosses of a fair coin. 2^{10} equiprobable outcomes, so

$$Pr(3H \text{ out of 10 tosses}) = \frac{\binom{10}{3}}{2^{10}}$$

- Think: A genome contains n genes of which s encode enzymes in the tricarboxcylic acid (TCA) cycle. After cells are treated with rapamycin, d change in expression level, of which x encode enzymes in the TCA cycle. How many gene sets of size d are there that contain exactly x TCA cycle genes? To answer this, break it down into two sub problems:

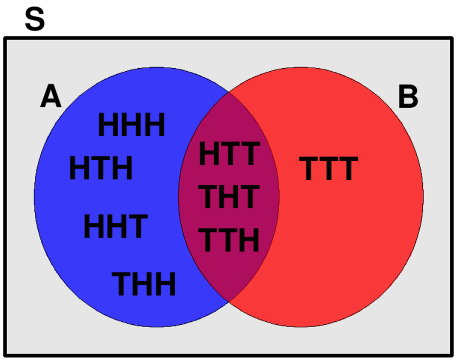
  1. How many sets of TCA cycle genes of size x are there?
  2. How many sets of non TCA-cycle genes of size $d - x$ are there?

  A union of any set of x TCA cycle genes and any set of $d-x$ non TCA-cyle meets the requirements – i.e. it is a set of d genes of which s are TCA cycle genes. The number of such unions has a practical application that will be discussed later.

5 Conditional Probability [DeGroot 2.1]

- Suppose A and B are events in S and we know that the outcome of a given experiment was in B (i.e. B occurred).
- What is the probability that the outcome was also in A?
- Conditional probability of A given B, written $Pr(A|B)$.
- Definition: $Pr(A|B) = \frac{Pr(A \cap B)}{Pr(B)}$ (Memorize this!)
- Example: Given that the number of heads on tossing three fair coins is less than two, what is the probability that it is greater than 0?

$$A : \#H > 0, B : \#H < 2$$



$$Pr(A \cap B) = 3/8, Pr(B) = 4/8, Pr(A|B) = \frac{3/8}{4/8} = 3/4$$

Result is same as direct count of remaining outcomes.

6 Independence [DeGroot 2.2]

- If $Pr(A|B) = Pr(A)$, we say A is independent of B.
  - Then $\frac{Pr(A \cap B)}{Pr(B)} = Pr(A)$ so $Pr(A \cap B) = Pr(A)Pr(B)$.
- If A is independent of B, then B is independent of A.
- A and B are independent.

7 Discrete Random Variables [DeGroot 3.1]

- Definition: A random variable (r.v.) is a function from a sample space S into the real numbers ($\mathbb{R}$)
  - E.g. flip a coin 10 times. $S = \{H, T\}^{10}$. For any $s \in S$, let $X(s)$ be the # times H occurs in s. X is a r.v. w/range $\{0..10\}$.
- Equations and inequalities involving random variables are interpreted as events. If X is a r.v., S is its sample space, and $a \in \mathbb{R}$, then $X = a$ is equivalent to the event $\{s \in S$ such that $X(s) = a\})$.
  - Therefore, if $a \in \mathbb{R}, Pr(X = a) \equiv Pr(\{s : X(s) = a\})$.
  - Any statement about the values of an r.v. can be interpreted as an event. E.g. $X < 2.7$ is equivalent to $\{s$ such that $X(s) < 2.7\})$.
  - Any fact that is true of all events is also true of all statements about the values of r.v.'s.
- A r.v. whose range is a finite or countably infinite set $\{x_1, x_2, ...\}$ is called discrete. Otherwise, it is continuous.
- The probability function of a discrete r.v. X is the function that maps $a \in \mathbb{R}$ to $Pr(X = a)$.
- We denote the probability function of a r.v. X as $f(x) \equiv \Pr(X = x)$, where the lower case letter x ranges over the real numbers.
- Also write $\Pr(x)$ as shorthand for $\Pr(X = x)$. Probability fn of X is also called the *distribution of* X.
  - Example: $\Pr(x) = 1/2^x$ for $x \in \{1, 2, ...\}$ is short for $\Pr(X = x) = 1/2^x$
- If $H \subseteq S$ is a possible outcome of an experiment or a set of possible outcomes it is convenient to write $Pr(X = H)$, even though H is not a number. This is equivalent to $Pr(Y = 1)$ where Y is a r.v. defined by $Y(s) = 1$ if and only if $s \in H$.

7.1 Example: Bernoulli and binomial distributions [DeGroot 5.2]

- Consider an experiment in which a single coin is flipped. Let X be a random variable that maps heads to 1 and tails to 0.

- The probability function for X has the form $\Pr(X = 1) = \Theta$ and $\Pr(X = 0) = (1 - \Theta)$, for some $\Theta \in [0, 1]$ (the interval between 0 and 1). *Bernoulli distribution* on X.

- If the coin is flipped N times, the probability of a specific sequence of outcomes $x_1, \ldots, x_n$ ($x_i \in 0, 1$) is

$$\Theta^{\sum x_i}(1 - \Theta)^{N - \sum x_i}$$

- Let Y be an r.v. that maps outcomes of N samples from a Bernoulli distribution, $x_1, \ldots x_n$, to their sum. The probability function of Y is

$$Pr(Y = y) = \binom{N}{Y} \Theta^Y (1 - \Theta)^{N-Y}$$

  for $y \in 0 \ldots N$ and 0 otherwise. I.e. the number of different binary sequences with Y 1's times the probability of any particular binary sequence with Y 1's.

7.2 Example: Hypergeometric distribution

- Genomics experiments frequently yield sets of genes. E.g., the set of genes whose expression levels are elevated in liver cancer cells.

- Most basic basic analysis is to ask whether certain types of genes are present in the result set more often than would be expected by chance. E.g. genes in a given signaling pathway.

- G: The set of all genes in a particular pathway (or other gene set) of interest.

- The genome contains n genes of which s are in G. The experiment yields a set of d genes of which x are in G.

- Given n, s, and d, what is the probability that exactly x of the d will be in G?

- The *experiment* is selecting a set of d genes at random from the n genes in the genome.

- The *outcome* is the set of genes selected.

- The function mapping the set of selected genes (outcome) to the number of selected genes that are in the predetermined set G is a *discrete random variable* that we will call X.

- What is the *probability function* of X?

    1. How many outcomes are there in total?
    2. How many of these outcomes are there in which exactly x selected genes are in the set G? To make such an outcome, one can take the union of any set x genes in G with any set of $d - x$ genes that are not in G.

- This probability function is called the *Hypergeometric distribution* with parameters n, s, and d. All must be integers of which $n > s, n > d$, and $d > x$.

- Let f be the cumulative probability function

  $$f(m) = \sum_{i=0}^{m} \Pr(x = i)$$

  Then $1 - f(x) + \Pr(x)$ is the probability that x *or more* of the d selected genes will be in the set G.

- This probibility is used in *statistical hypothesis testing* to test the null hypothesis that x of the d selected genes are in G by chance, as a result of the process described above. This null hypothesis is rejected if the probability is less than a user selected threshold. When it is rejected, the conclusion is that there is some reason for the large overlap – i.e. that the process of selecting the d genes (e.g. cells becoming cancerous) is related to the gene set G (e.g. because the expression levels of some of the genes in G must be altered to produce the cancerous phenotype). This is described by saying that the selected genes are *encriched for* genes in G.

- Suppose that the selected genes are not enriched for genes in G. That does **not** imply that the genes in G are unimportant for the selection process. E.g a treatment applied to cells could produce a visible phenotype of interest. Because you're interested in the phenotype, you do an experiment to determine which genes are differentially expressed after the treatment. Suppose the treatment results in both a set of 300 differentially expressed genes of which one is in the TCA cycle. Even though the differentially expressed genes are not enriched for TCA cycle genes, that one TCA cycle gene might be the one responsible for the phenotype of interest.

7.3 Continuous Random Variables [De Groot 3.2, 3.3]

- For a continuous r.v. Θ, probability of any particular value is zero.

- Use a probability density function (p.d.f.) $f(\Theta)$ where

$$\Pr(y \le \Theta \le z) = \int_y^z f(\Theta)\, d\Theta$$

(i.e. area under the pdf between y and z).

- Note: $Pr(-\infty \le \Theta \le +\infty) = 1$
- Example: Uniform p.d.f $f(\Theta) = 1$ for $0 \le \Theta \le 1$, $f(\Theta) = 0$ elsewhere.

$$\Pr(y \le \Theta \le z) = z - y$$

- Example: exponential p.d.f $f(\Theta) = ce^{-c\Theta}$ for $0 \le \Theta$, $f(\Theta) = 0$ elsewhere. c is a positive constant affecting the shape of the exponential.

$$\Pr(y \le \Theta \le z) = -e^{-cz} + e^{-cy}$$

- For continuous r.v.'s X and Y with joint p.d.f. $f(x, y)$ and *marginal* p.d.f.s $f_1(x)$ and $f_2(y)$, we define the *conditional p.d.f.* $g(x|y)$ as

$$g(x|y) = \frac{f(x, y)}{f_2(y)}$$

- The p.d.f.s of continuous r.v.s can often be treated like the p.f.s of discrete r.v.s by replacing summations with integrals.
- The cumulative distribution function (abbreviated c.d.f.) F of a random variable X is the function

$$F(x) = \Pr(X \le x), -\infty < x < \infty$$

- This definition of c.d.f. works for both discrete and continuous random variables.
- To calculate the c.d.f. of a continuous random variable with p.d.f f, you can use the integral:

$$F(x) = \int_{-\infty}^{x} f(z)\, dz$$

- To calculate the c.d.f. of a discrete random variable wtih probability function f, you can use the summation:

$$F(x) = \sum_{-\infty}^{x} f(z)$$

- This explains why random variables with countably infinite ranges are called discrete – the summation works for them.

7.4 Joint probability distributions [DeGroot 3.4]

- Multiple r.v.'s can be defined on outcomes of the same experiment. E.g. sampling from the space of all people in the United States, X might represent the person's height (in centimeters) and Y his weight (in kilos). Intuitively, X and Y are not independent – knowing a person's height is useful for guessing his weight, and vice-versa.

- Whenever we discuss two random variables, assume they are defined on outcomes of the same experiment.

- $Pr(x, y)$, the joint distribution of X and Y, is the probability that the outcome s of an experiment is such that $X(s) = x$ and $Y(s) = y$.

- For discrete r.v.'s X and Y,
  - $Pr(x|y) = \frac{Pr(x,y)}{Pr(y)}$ if $\Pr(y) > 0$; if $\Pr(y) = 0$ then $\Pr(x|y)$ is undefined.
  - X and Y are independent iff $Pr(x|y) = Pr(x)$ for all $x, y \in \mathbb{R}$

8 Four rules for manipulating probability expressions

8.1 Chain rule

Example:

$$\begin{aligned} Pr(x_1, x_2, x_3) &= \frac{Pr(x_1, x_2, x_3)}{Pr(x_2, x_3)} \frac{Pr(x_2, x_3)}{Pr(x_3)} Pr(x_3) \\ &= Pr(x_1|x_2, x_3) Pr(x_2|x_3) Pr(x_3) \end{aligned}$$

8.2 Bayes rule [DeGroot 2.3]

Example:

$$\begin{aligned} Pr(x_1|x_2)Pr(x_2) &= Pr(x_1, x_2) \\ &= Pr(x_2|x_1)Pr(x_1) \\ Pr(x_1|x_2) &= \frac{Pr(x_2|x_1)Pr(x_1)}{Pr(x_2)} \end{aligned}$$

Similarly,

$$Pr(x_1|x_2, x_3) = \frac{Pr(x_2|x_1, x_3)Pr(x_1, x_3)}{Pr(x_2, x_3)}$$

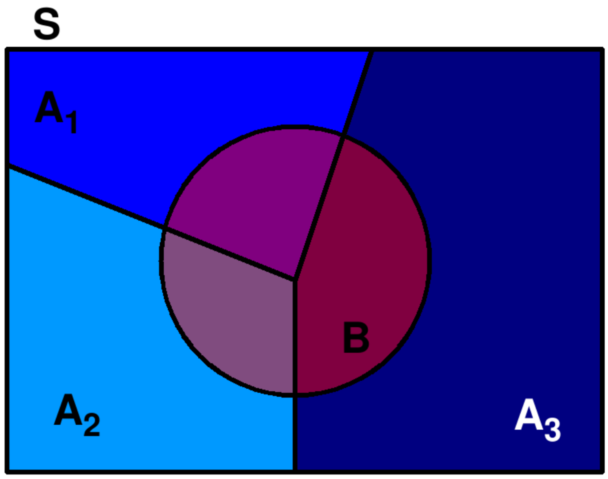
Hence,

$$Pr(x_1|x_2, x_3) = \frac{Pr(x_2|x_1, x_3)Pr(x_1|x_3)}{Pr(x_2|x_3)}$$

Extra variables behind the conditioning are carried along.

8.3 Summing out (Marginalizing) [DeGroot 3.5]

- Suppose $A_1, A_2, ...$ are disjoint events w/union S, the sample space.
- Then $(B \cap A_1), (B \cap A_2), ...$ are disjoint, w/ union B.



$$\begin{aligned}\sum_i Pr(B \cap A_i) &= Pr(\cup_i (B \cap A_i)) \\ &= Pr(B)\end{aligned}$$

- Let X, Y be discrete r.v.'s and let $y_1, y_2, ...$ be all possible values of Y.
- Let $A_i = \{s|Y(s) = y_i\}$ and $B = \{s|X(s) = x\}$
- The A_i are disjoint, so $\sum_i Pr(B \cap A_i) = Pr(B)$
- Translating back into r.v. notation: $\sum_i Pr(x, y_i) = Pr(x)$

8.4 Exhaustive Conditionalization

$$\begin{aligned}\sum_y Pr(x|y)Pr(y) &= \sum_y Pr(x, y) \\ &= Pr(x)\end{aligned}$$

9 Parameter estimation

- Suppose the probability function of a random variable belongs to a known family of distributions. Figure out which member of the family.
- Example: a biased coin turns up heads w/ uknown prob $\Theta, 0 \leq \Theta \leq 1$.
  - Determine Θ, the parameter.
  - (Sometimes Θ stands for a vector of parameters)

9.1 Maximum likelihood estimation

- Likelihood function: Given a set of observed outcomes O, can compute $Pr(O|\Theta)$ as a function of Θ.
  - Example: $Pr(x \text{ heads in } N \text{ flips } |\Theta) = \frac{N!}{x!(N-x)!}\Theta^x(1-\Theta)^{N-x}$
  - To emphasize that the likelihood is a function of the parameters once the observations are known, the notation $L(\Theta|N, x)$ is sometimes used.
- When there is little data, ML tends to underestimate probabilities of rare events, relative to our intuition.
- Example: Estimate probs for an unfair die from 10 rolls.
  - Suppose die has 6 nearly symmetrical faces.
  - Observations: 1,3,4,2,4,6,2,1,2,2
  - ML estimate for $Pr(5) = \frac{0}{10} = 0$. Implausible given die shape.
- Maximum likelihood estimate is the high point of the likelihood function.
  - Given observations O, $\hat{\Theta}_{ML} = \arg\max_{\Theta} Pr(O|\Theta)$
  - E.g.: coin flipping, x heads in N flips. $\hat{\Theta}_{ML} = \frac{x}{N}$.
  - To prove, find the maximum of the log of the likelihood by equating its derivative to zero and solving for Θ.

9.2 Maximum a postiori estimation [DeGroot 7.1, 7.2]

- The maximium a posterior (MAP) estimate is the most probable value of the parameter – i.e. the max of the posterior distribution.
- Posterior Distribution on Θ

- If Θ has finitely many possible values we can treat it as a discrete r.v.:

$$Pr(\Theta|O) = \frac{Pr(O|\Theta)Pr(\Theta)}{Pr(O)}$$

  For a fixed set of observations,

$$Pr(\Theta|O) \propto Pr(O|\Theta)Pr(\Theta)$$

- Posterior is proportional to likelihood times prior
- Prior can be uninformed – don't know so use uniform prior
- Or used to encode actual knowledge about a problem
- If Θ is a continuous r.v. with prior p.d.f. $g(\Theta)$ then its posterior p.d.f. $f(\Theta|O)$ is given by:

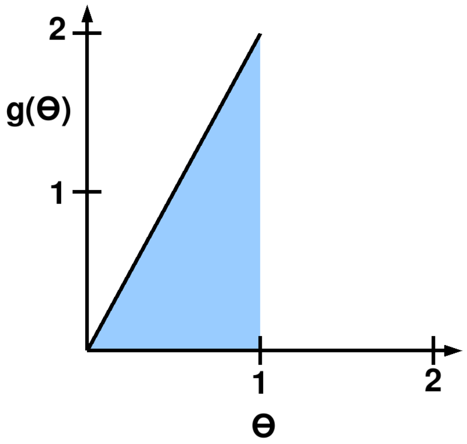
$$f(\Theta|O) = \frac{Pr(O|\Theta)g(\Theta)}{Pr(O)}$$

- Example: If Θ is the probability of flipping heads on a coin (i.e. the parameter of a Bernoulli distribution), possible priors $g(\Theta)$ include:
  - The uniform p.d.f: $g(\Theta) = 1$ for $0 \leq \Theta \leq 1$, $g(\Theta) = 0$ elsewhere. Then for any $y, z \in [0, 1]$:

$$Pr(y \leq \Theta \leq z) = z - y$$

  - A prior representing an expectation of coins biased toward more heads:

$$g(\Theta) = \begin{cases} 2\Theta & 0 \leq \Theta \leq 1 \\ 0 & \text{elsewhere} \end{cases}$$



  - Using the latter prior, the posterior p.d.f. f is given by:

$$f(\Theta|x \text{ heads in } N \text{ flips}) \propto \underbrace{\frac{N!}{x!(N-x)!}\Theta^x(1-\Theta)^{N-x}}_{\text{likelihood}}\underbrace{2\Theta}_{\text{prior}} \text{ for } 0 \leq \Theta \leq 1$$

$$\propto \Theta^{x+1}(1-\Theta)^{N-x} \text{ (or zero if } \Theta < 0 \text{ or } \Theta > 1)$$

9.3 Conjugate Priors [DeGroot 5.8]

- The two example priors given above, the uniform prior on $[0,1]$ and

  $$g(\Theta) = \begin{cases} 2\Theta & 0 \leq \Theta \leq 1 \\ 0 & \text{elsewhere} \end{cases}$$

  are both *conjugate priors* for the binomial likelihood function because the prior and the posterior have the same functional form. Distributions with this form are called *beta distributions.*

- In general, a beta distribution on Θ has the form

  $$\text{beta}(\Theta|a,b) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)}\Theta^{a-1}(1-\Theta)^{b-1}$$

  for $\Theta \in [0,1]$ and zero for $\Theta \notin [0,1]$. When n is a positive integer, $\Gamma(n) = (n-1)!$. Thus, when a and b are positive integers,

  $$\text{beta}(\Theta|a,b) = \frac{(a+b-1)!}{(a-1)!(b-1)!}\Theta^{a-1}(1-\Theta)^{b-1}$$

- The p.d.f. that is uniform on $[0,1]$ and 0 elsewhere is $\text{beta}(\Theta|a=1,b=1)$.

- The p.d.f. that is 2Θ on $[0,1]$ and 0 elsewhere is $\text{beta}(\Theta|a=2,b=1)$.

- When a beta prior p.d.f. with integer parameters a, b, is multiplied by a binomial likelihood of x heads in N trials, the posterior p.d.f. on Θ is

  $$f(\Theta|x,N,a,b) \propto \Theta^{x+a-1}(1-\Theta)^{N-x+b-1}$$

  for $\Theta \in [0,1]$ and 0 elsewhere. The proportionality constant ensures that the integral of the posterior over all values of Θ is 1. It can be shown (DeGroot, Section 5.10) that this implies the normalized posterior p.d.f. is:

  $$\frac{(N+a+b-2)!}{(x+a-1)!(N-x+b-1)!}\Theta^{x+a-1}(1-\Theta)^{N-x+b-1} \text{ (or zero if } \Theta < 0 \text{ or } \Theta > 1)$$

- Thus, when a prior p.d.f. is a beta distribution with parameters a, b and the likelihood is binomial, the posterior p.d.f. is a beta distribution with parameters $x + a$ and $N + a + b$. For this reason, the beta family of priors is said to be conjugate to binomial likelihood functions.

- The prior and posterior are always beta distributions – only the parameters change when data arrive.

- The beta distribution with parameters a and b takes on its maximum value when $\Theta = \frac{a-1}{a+b-2}$. (The derivation is just like the derivation of $\hat{\Theta}_{ML}$.)
  - Therefore, after observing x heads in N flips, the maximum a posteriori estimate is
$$\hat{\Theta}_{MAP} = \frac{x+a-1}{N+a+b-2}$$
  - Can continuously update the MAP estimate as new data come in.
- a and b can be thought of as pseudocounts or “imaginery data” for heads and tails, respectively.
- In the limit of large N, $\hat{\Theta}_{MAP}$ and $\hat{\Theta}_{ML}$ converge the same value.
- The larger a and b are, the more data it takes to overwhelm the prior. When they are large, the prior is said to be strong.

9.4 Posterior Predictive Distributions

- With a posterior pdf $g(\Theta|O)$ on parameters Θ given observations O, you can compute a distribution on future observations that does not depend on assuming any particular parameter values.
$$\Pr(X = x|O) = \int_{-\infty}^{\infty} \Pr(X = x|\Theta) g(\Theta|O) d\Theta$$
- This is exhaustive conditionalization on a continuous r.v. Θ.
- When the prior on Θ is beta(a, b), Y is a binary r.v. with $\Pr(Y = 1) = \Theta$, and N Bernoulli experiments have been observed in which $Y = 1$ occurred x times, the previous equation becomes:
$$\begin{aligned}\Pr(Y = 1|O) &= \int_0^1 \Theta \frac{(N+a+b-1)!}{(x+a-1)!(N-x+b-1)!} \Theta^{x+a-1}(1-\Theta)^{N-x+b-1} d\Theta \\ &= \frac{(N+a+b-1)!}{(x+a-1)!(N-x+b-1)!} \int_0^1 \Theta^{x+a}(1-\Theta)^{N-x+b-1} d\Theta \\ &= \frac{(N+a+b-1)!}{(x+a-1)!(N-x+b-1)!} \frac{(x+a)!(N-x+b-1)!}{(N+a+b)!} \\ &= \frac{x+a}{N+a+b}\end{aligned}$$
- The integral is derived in DeGroot section 5.10.
- Compare this posterior predictive to the MAP estimate of Θ.

  - MAP estimate of Θ is a point estimate while the posterior predictive considers all possible values of Θ.
  - As empirical data N and x grow large, the MAP estimate, posterior predictive, and ML estimate all converge on the same value.

9.5 Multinomial Distributions

- Formulas presented above for binary r.v.'s also apply to any variable with a finite number of possible values, with minor / obvious modifications.
- Binomial likelihood becomes multinomial.
- beta prior becomes *Dirichlet* prior.
- rv's with large numbers of possible values are common in bioinformatics.
- With many possible values, observations are often not sufficent to estimate parameters by ML.
- Dirichlet priors are common and important.

10 Expectation [DeGroot 4.1, 4.2]

- The expectation of a r.v. is its long-run expected average. For a discrete r.v.:
- $E[X] \equiv \sum_x Pr(x)x$
- If f is a real-valued function of X, $E[f(X)] = \sum_x Pr(x)f(X)$
- Example: If X is uniformly distributed over {1,2,3,4} and $f(X) = X^2$

$$E[f(X)] = \frac{1}{4} \cdot 1^2 + \frac{1}{4} \cdot 2^2 + \frac{1}{4} \cdot 3^2 + \frac{1}{4} \cdot 4^2 = \frac{30}{4}$$

- Expectation is <u>linear</u>. If $X_1, ...X_n$ are r.v.'s then $E(X_1 + ... + X_n) = E(X_1) + ...E(X_n)$.

11 Expectation Maximization

- Method for estimating parameters from experiments in which some key aspects of the outcomes are hidden.
- Example: A bag contains two types of six-sided dice. Each type has it's own probability of rolling the faces $1 \dots 6$.
  - A series of experiments is carried out. In each one, a die is chosen at random from the bag, rolled m times, and put back in the bag.
  - You are told the number that comes up on each roll, but not which type of die was used. (This is the hidden variable.)
  - You must estimate the probability of selecting a die of each type and the probability of rolling each number on a die of each type.
- Key idea 1 of EM approach
  - Let count(k,A) be the number of times face k was rolled on a die of type A.
  - If we knew the counts we could estimate Pr(face k|die type A) by M.L.:

$$\frac{\text{count}(k, A)}{\sum_{k=1}^{6} \text{count}(k, A)}$$

  - If we knew the counts we could also estimate Pr(die type A) by M.L.:

$$\frac{\sum_{k=1}^{6} \text{count}(k, A)}{\sum_{k=1}^{6} \text{count}(k, A) + \sum_{k=1}^{6} \text{count}(k, B)}$$

  - Can't get count(k, A) or count(k, B) from the data because die type is hidden.
  - Instead, use the expected counts with respect to the posterior distribution on the hidden variable (die type of each experiment).
- Formal derivation of expected counts for dice example.
  - Let $f_{i,j}$ be the face shown on the j^{th} roll of the i^{th} die selected.
  - Let D_i be the type of the i^{th} die chosen (A or B). Hidden variable.
  - Let

$$C_{i,j,k,A} = \begin{cases} 1 & \text{if } f_{i,j} = k \text{ and } D_i = A \\ 0 & \text{otherwise} \end{cases}$$

- Then

$$\text{count}(k, A) = \sum_{i,j} C_{i,j,k,A}$$

- So

$$\begin{aligned}
E[\text{count}(k, A)] &= E\left[\sum_{i,j} C_{i,j,k,A}\right] \\
&= \sum_{i,j} E\left[C_{i,j,k,A}\right] \\
&= \sum_{i,j} (\Pr(C_{i,j,k,A} = 0) \cdot 0 + \Pr(C_{i,j,k,A} = 1) \cdot 1) \\
&= \sum_{i,j} \Pr(C_{i,j,k,A} = 1) \\
&= \sum_{i,j \text{ s.t. } f_{i,j}=k} \Pr(D_i = A)
\end{aligned}$$

- We have some observations relevant to $\Pr(D_i = A)$, so we will use them by calculating the posterior probability $\Pr(D_i = A | f_{i,1}, f_{i,2}, \ldots)$.
- Key idea 2 of EM approach
  - Assume you know the probabilities. Start with random guesses.
  - Repeatedly improve probabilities by making max likelihood estimates from expected counts.
  - Use probabilities from the last round to compute expectations for the next.