

Assignment 1

posted Tuesday 16 January 2018

due Friday 26 January 2018 at 11.59pm

Submission policy: Report all plots (Question II parts 2, 3, 4, 5.1, 6 and Question III part 3) and your code in [this iPython notebook](#). Print your notebook as a PDF and attach it to the rest of your assignment. Turn in your assignment through gradescope. All enrolled students have been added to the gradescope. Let us know if you do not have access to gradescope for the class by dropping an email to ee372-win1718-staff@Stanford.edu.

Question I: Sanger sequencing

1. In a Sanger sequencing experiment, a bio-chemist observes that the masses of molecules that are terminated by ddATP are 400, 1200, and 1351. The masses of molecules terminated by ddCTP are 531, and 1482. The masses of the molecules terminated by ddGTP are 671, 813, and 961. The masses of the molecules terminated by ddTTP are 1093, and 1657. The primer used here is AGC. What is the molecule being sequenced?
2. Assume that A, G, C, T have the same molecular weight, and the masses measured have a tolerance of $\pm 0.05\%$. Give a bound on the maximum length that can be sequenced without error (assuming all measurements are within $\pm 0.05\%$ of the true value). How does this change when the molecular weights are different?

Question II: Base calling for Illumina sequencing

Consider the following base calling model studied in the class. We will focus on the A channel. Let $\mathbf{s} = [s(1), \dots, s(L)]^T$ be the binary sequence, obtained by setting $s(j) = 1$ if the j -th base is an A and 0 otherwise, and $\mathbf{y} = [y(1), y(2), \dots, y(L)]^T$ be the sequence of intensities observed in the A channel. Now, in the case of a large number N of strands in a cluster, the intensities and the DNA sequence can be related approximately as follows

$$\mathbf{y} = \mathbf{Q}\mathbf{s} + \mathbf{n}, \quad j = 1, 2, \dots, L,$$

where $\mathbf{Q} = [Q_{ij}]_{1 \leq i, j \leq L}$ is an $(L \times L)$ matrix with the (i, j) -th entry Q_{ij} being the probability that the j th base emits color in the i th cycle. $\mathbf{n} = [n(1), n(2), \dots, n(L)]^T$ is the noise vector.

Further assume that there is no possibility of a template leading, only lagging, *i.e.*, in the notation of the class $q = 0$. Assume $n(j)$ is Gaussian noise with zero mean and variance σ^2 (we are neglecting the effect that $y(j)$ is forced to be a positive real number, and we are also ignoring the amplitude a as that factor can be absorbed into σ^2 with a rescaling).

1. Express Q_{ij} in terms of i , j , and p . Given j and p , At which value of i is Q_{ij} maximized? **Bonus:** Can you connect the rows of \mathbf{Q} to the pmf of some well known distribution?
2. Simulate and plot $y(1), \dots, y(L)$ according to the probability model (for $s(t)$ being i.i.d. equally probable to be 0 or 1). Do this for various values of $p = 0, 0.01, 0.05, 0.1$, and 0.2 with $\sigma^2 = 0.1$.

- Write down the zero-forcing equalizer (i.e. matrix inversion) and the decoding rule. Simulate this rule and for different values of p plot its quality score as a function of position along the DNA sequence. Here the *Phred score* of a base is defined to be:

$$\text{Phred} = -10 \log_{10} p_e$$

where p_e is the probability of error of detecting the base. Do the Phred scores increase or decrease with the position of the base? Give an intuitive explanation.

- Write down the formula for the MMSE equalizer and the corresponding decoding rule. Simulate this rule and for different values of p plot the resulting quality score as a function of position along the DNA sequence. Compare it to the rule above.
- (Matched filter bound): In this section, we will try to calculate a lower bound on the probability of error for any rule. To do so, we invoke a bound called the matched filter bound in signal processing. Consider the following system. Suppose you want to decode $s(m)$ for a particular m . If there was no interference from any other symbol but you observe the intensities at all possible times, then we have

$$\tilde{y}(t) = Q_{im}s(m) + n(i), \quad i = 1, 2, \dots, L.$$

Given these observations, the optimal combining rule is called the matched filter rule in which a weighted average of the intensities

$$y_m = \sum_i Q_{im} \tilde{y}(i)$$

is calculated and followed by an appropriate detection rule to perform base calling. The probability of error of this rule is a lower bound to the probability of error of the optimal rule in the original problem because ignoring interference from other symbols will only improve performance.

- Find the appropriate detection rule and give an expression for the probability of error and the quality score of the optimal combining rule. Plot the quality score for a fixed $p = 0.05$ as a function of the position m . Compare this to the performance of the base calling rules in parts 3. and 4. *Hint:* Look at the likelihood ratio 0 and 1.
- What happens to this probability of error as a function of position in this case? What does this say about why the read length in Illumina sequencing is limited?
- Consider now the general case when $q \neq 0$. $p, q \in (0, 1)$. Write Q_{ij} in terms of $\{Q_{\ell,k}\}_{\ell \leq i-1, k \leq j}$. Give entries for the 10×10 matrix Q for $p = 0.1, q = 0.2$ *Hint:* Dynamic programming.

Question III: Playing around with reads

- We are given N reads of length L and a reference genome of length ℓ . Assuming reads were sampled uniformly from the entire genome, what is the expected number of times a base at a particular position will be sequenced? In other words, what is the *sequencing depth* of each base in the genome? What is the probability that we see the exact same read twice? You can assume that if a length- L sequence appears in the genome, it appears exactly once.
- Download the reference genome for *E. coli* [here](#), and download a set of reads obtained from an *E. coli* experiment [here](#) (you can right click each link and select "Save Link As", and you will need to [unzip](#) the fastq file containing the reads).
 - What is the length of the reference?
 - What is the length of each read?
 - How many reads are there?
 - What is the maximum number of times a read is repeated?

- What is the sequencing depth of each base in the reference for this experiment? *Hint*: Use the formula you got from above.
3. How many distinct 20-length substrings do you see across all reads? These substrings are commonly referred to as k -mers ($k = 20$ in this case). Count how often each distinct 20-mer appears and generate a histogram of the counts. *Hint*: Note that initializing a length- 4^{20} array may not be a viable approach. Consider using dictionaries!
 4. [Bowtie2](#) is a popular read aligner optimized for aligning large amounts of short reads to long references. Bowtie2 is preinstalled on Stanford's Rice cluster, but you can also install Bowtie2 on your local machine by downloading the [binary](#).
 - Build a Bowtie2 index from the *E. coli* reference genome (`bowtie2-build` command). You can copy the downloaded files from your computer to Rice using the `scp` command. Briefly describe the algorithms involved with building the index.
 - Using the default settings, use Bowtie2 to align the *E. coli* reads to the newly built Bowtie2 index. Use Bowtie2's `-t` option to obtain the runtime. How many reads have at least 1 reported alignment? What was the runtime?
 5. **BONUS:** Visually prove or disprove whether the reads are uniformly distributed across the reference. *Hint*: Use a sam/bam visualizer like [IGV](#) or [Bamview](#).