Ubiquitous Genomics: Hackathon 1

Maya Anand
mva2112@columbia.edu

Anne Bozack
akb2134@cumc.columbia.edu

Cheyenne Parsley
cep2141@columbia.edu

Robert Piccone
rap2186@columbia.edu

Daniel Speyer
dls2192@columbia.edu

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Problem 1

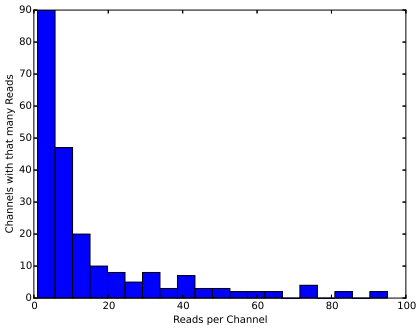
Number of 1D and 2D reads classified as failed: 3364
Number of 1D and 2D reads classified as passed: 3243
Number of 2D reads classified as failed: 540
Number of 2D reads classified as passed: 1081
Fraction of 2D reads in failed folder: 0.160523186683
Fraction of 2D reads in passed folder: 0.333333333333

Problem 2

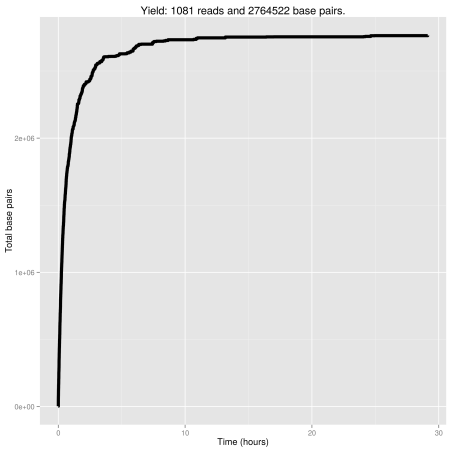
218 channels had at least one read, and 137 had at least five. This compares with 434 "active" channels during initialization, and 651 immediately after loading fuel

The average channel had 14.8 reads. Channel 212 had 95 reads, which was the most.

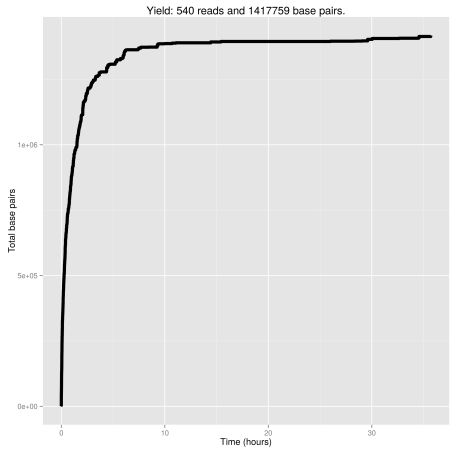
Just for fun, here's a histogram of reads per channel



Problem 3



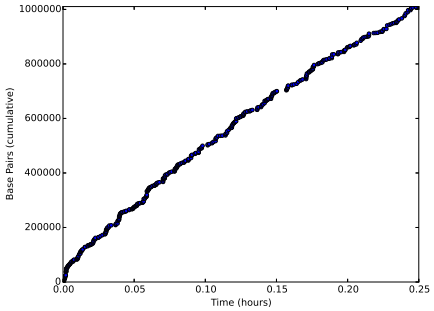
Passed Reads

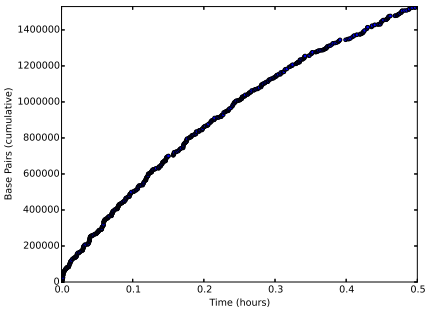


Failed Reads

Problem 4

Let us zoom in a little on the previous graphes:





The first quarter hour appears linear, but the first half hour does not.

To estimate the amout of time needed to sequence the human genome once, we used data from the first quarter hour due to its linearity. We hypothesize that the change in sequencing rate is due to a decrease in the molar concentration of DNA, and therefore the rate at which a DNA molecule encounters a given pore is rate-limiting, rather than a decrease in the effeciecy of the MinION. Therefore, in our calculation, we made the assumption that DNA concentration does not change over time and there is only one copy of the genome present to avoid sequencing $>$ 1x coverage.

Problem 5

Passed 2D Reads

Mean Quality Score=10.3775
Std. Dev.=1.83151
n=2764522

Failed 2D Reads

Mean Quality Score=9.48623
Std. Dev.=2.06174
n=1417759

T-test comparison

T-Statistic=451.124
P-Value=0

The P-value was confirmed to be returned as 0 from Python/numpy. We believe that the true value is above 0 but beneath the lowest threshold of Python's float value (2.2250738585072014e-308).

Passed 2D Reads - First Hour

Mean Quality Score=10.3668
Std. Dev.=1.82208
n=1970130
Median=10

Passed 2D Reads - Last Hour

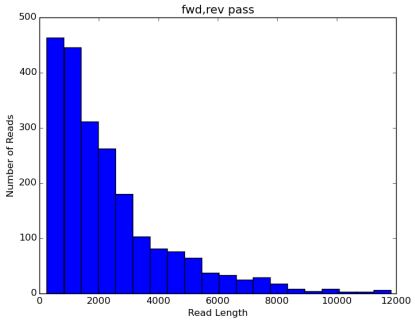
Mean Quality Score=11.5651
Std. Dev.=2.12032
n=968
Median=11

The quality of the reads does not appear to have degraded over the timespan of the sequencing (on the contrary, there is a slight increase).

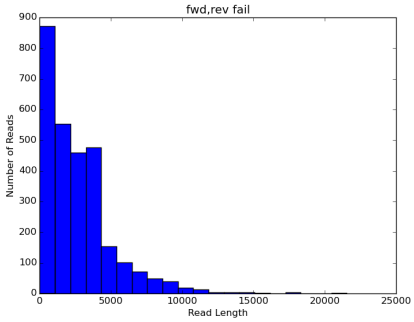
Problem 6

1D reads

The following histograms show the length distribution of 1D reads (both template and complement) for passes and fails.



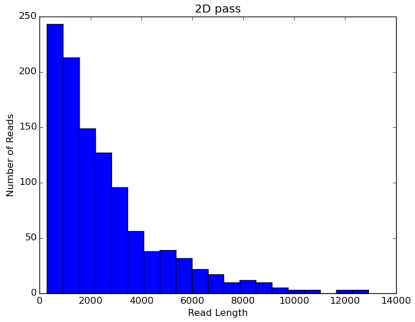
Passed Reads



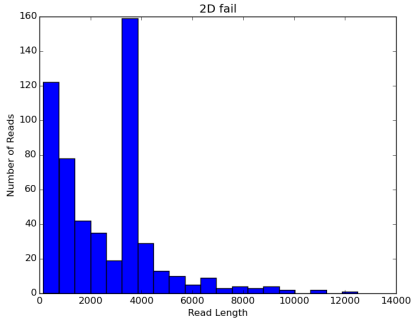
Failed Reads

2D reads

The following histograms show the length distribution of 2D reads for passes and fails.



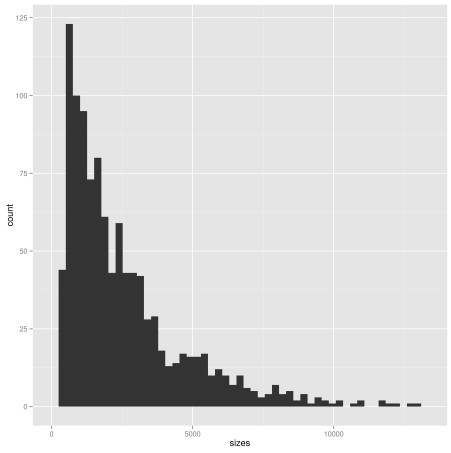
Passed Reads



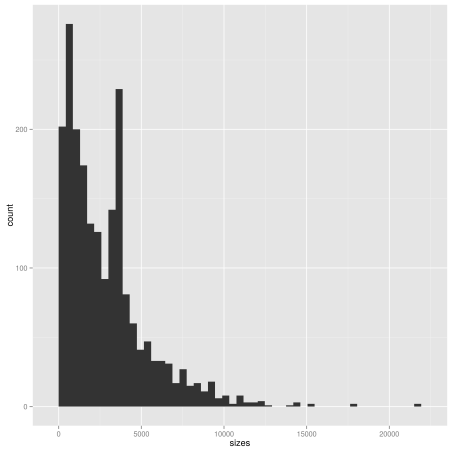
Failed Reads

1D and 2D reads

The following histogramss show the cumulative length distribution of both 1D and 2D reads for passes and fails.



Passed Reads



Failed Reads

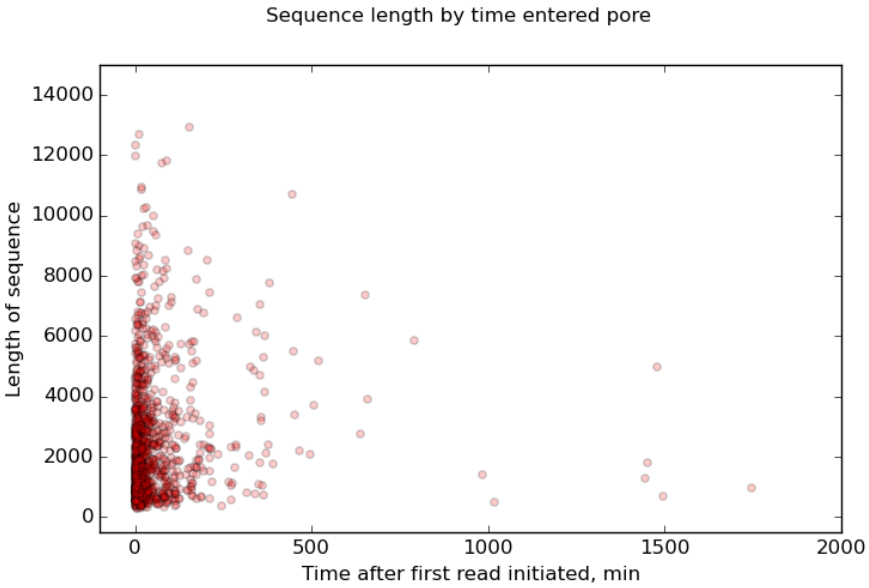
Problem 7

LONGEST TEMPLATE READ
From file: MINION02_4teamawesome_2446_1_ch312_file44_strand.fast5
Number of nucleotides: 11820

LONGEST COMPLEMENT READ
From file: MINION02_4teamawesome_2446_1_ch312_file44_strand.fast5
Number of nucleotides: 11498

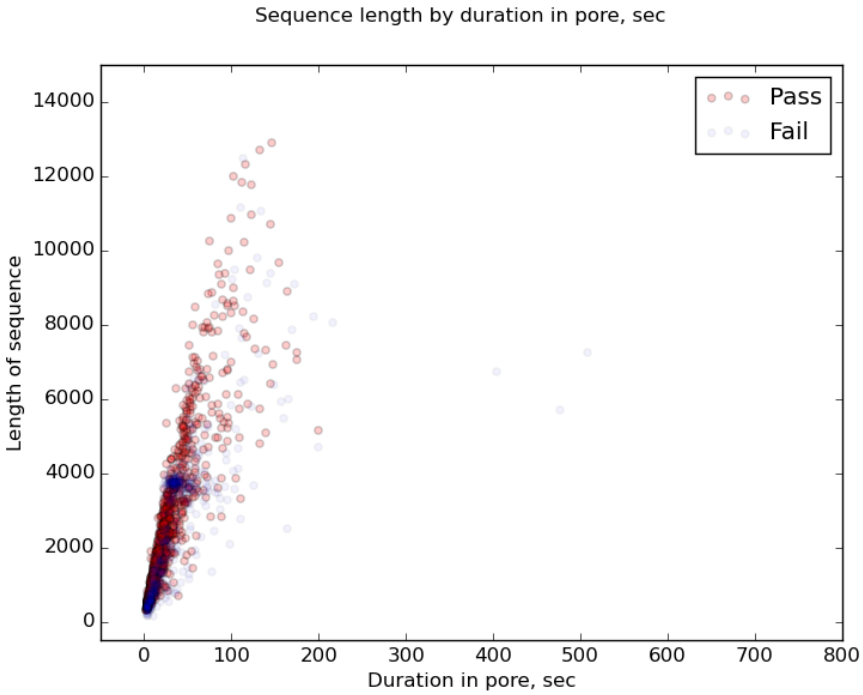
LONGEST 2D READ
From file: MINION02_4teamawesome_2446_1_ch312_file44_strand.fast5
Number of nucleotides: 12916

Problem 8



This graph was generated from the 2D pass reads, and time was calculated as time (in minutes) that each read was initiated from the time the first read was initiated. Those reads that initiated late did not achieve a long read length.

Problem 9



Problem 10

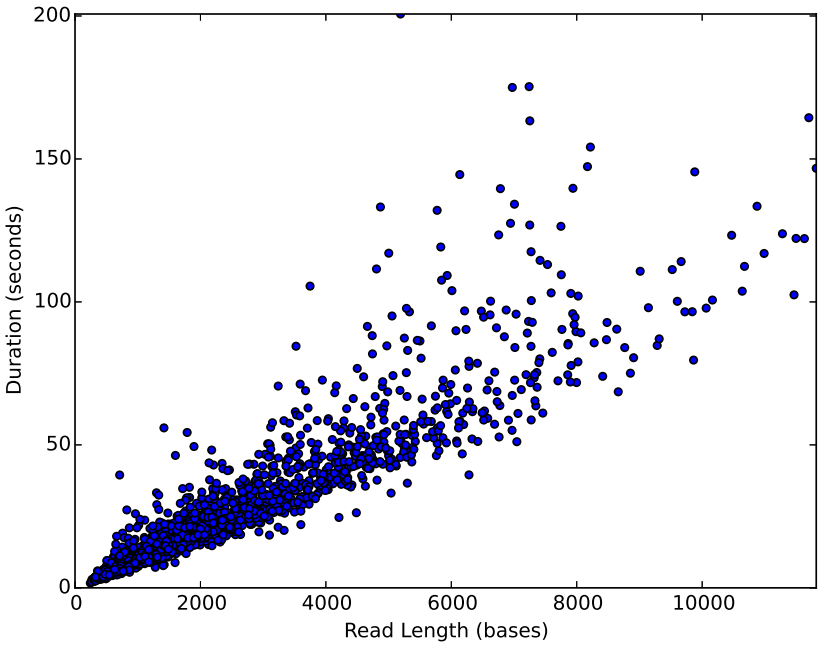
Computing nucleotide composition of passed reads...
Failed reads %Composition
% A: 26.8544936058
% C: 22.6248607838
% T: 26.8972371186
% G: 23.6234084919

Computing nucleotide composition of failed reads...
Passed reads %Composition
% A: 27.8932849874
% C: 21.7440845108
% T: 27.990263778
% G: 22.3723667238

Problem 11

Simple Model

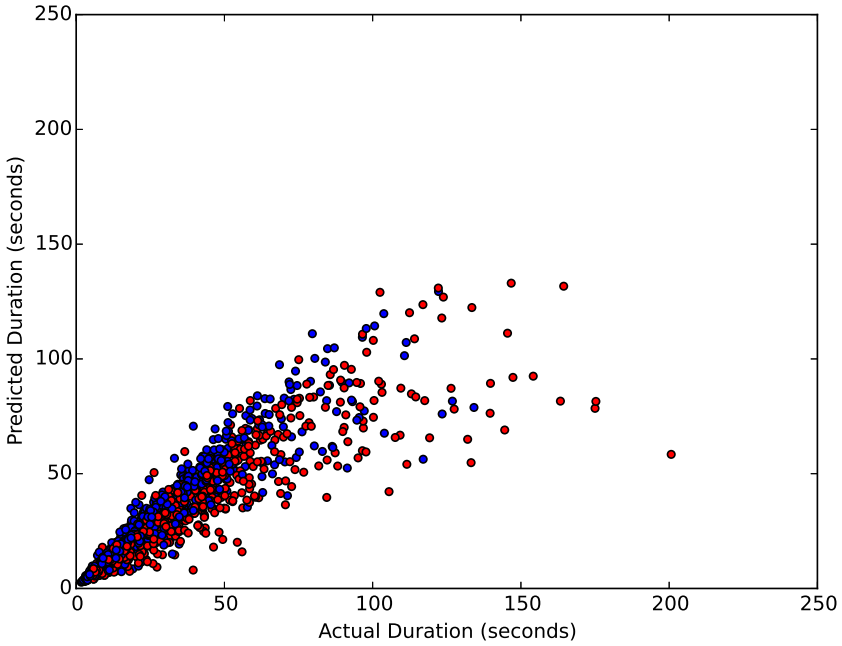
The simplest possible model is the one in which the number of nucleotides determines the read duration, possibly with some constant term for getting started. To consider this, we start with a scatterplot of bases against time with a linear fit.



We might be tempted to include a constant term in our fitting, but as should be apparent, it would be negative. How long it would take to sequence an extremely short read is unclear. Fortunately, there are none in our sample.

This allows us to construct a trivial (and still pretty effective) model based on a fixed cost per nucleotide.

Cost per nucleotide: 11.25ms

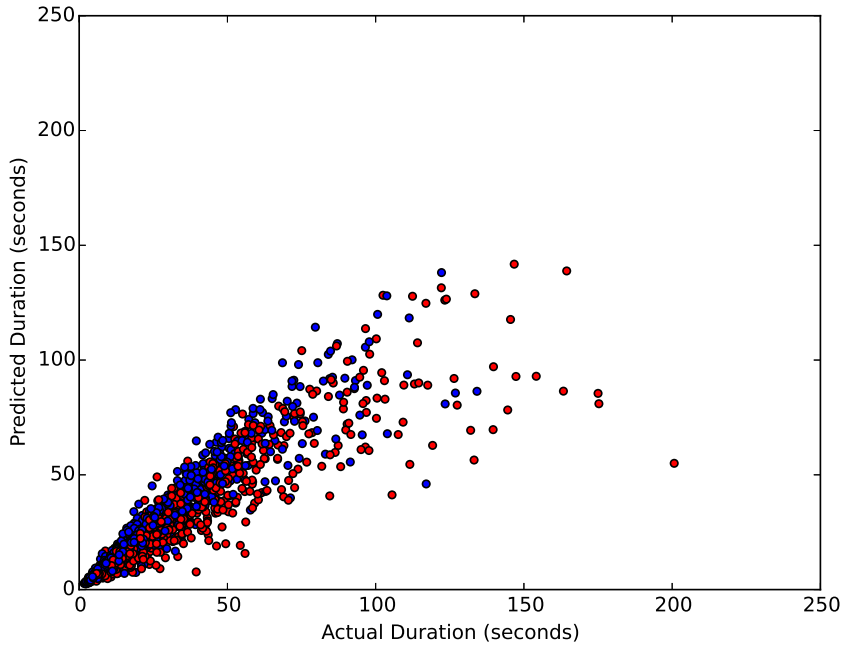


$r^2 = 0.84$

(Red circles are template strand; blue are complement. There appears to be no significant difference between them.)

Nucleotide Model

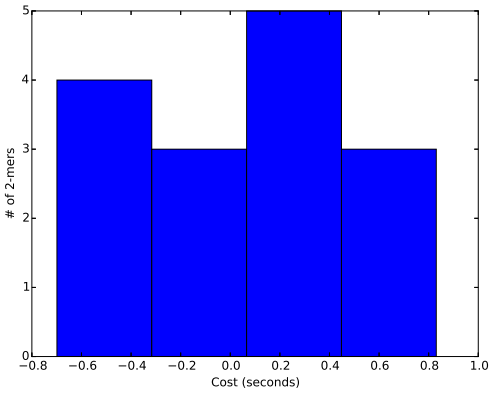
A slightly more complex model uses a differend cost for each type of nucleotide: A=32ms C=-07ms G=04ms T=12ms



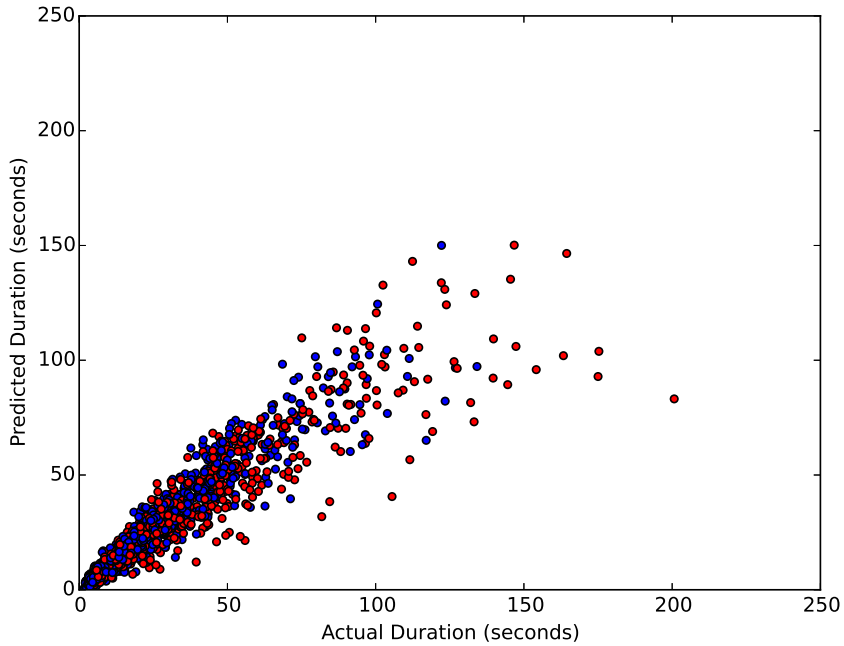
$r^2 = 0.84$

2mer Model

We can use a model in which each the time to extend by one nucleotide is determined by the 2-mer in the middle of the pore. We can not list all the costs, but here's a histogram:



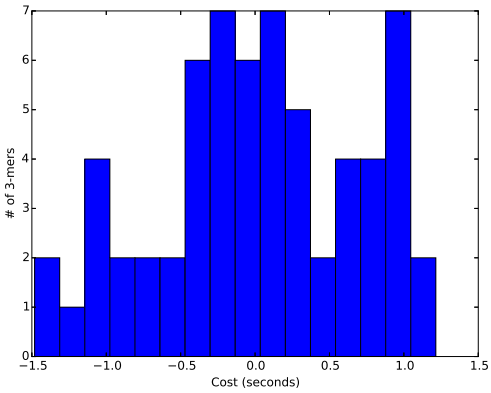
And here's the resulting predictions:



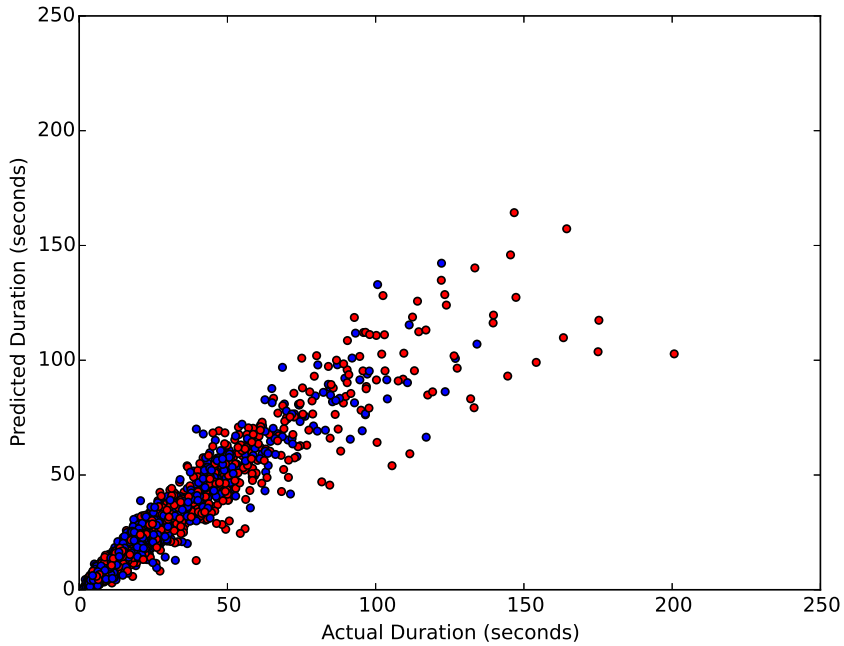
$r^2 = 0.88$

3mer Model

We can use a model in which each the time to extend by one nucleotide is determined by the 3-mer in the middle of the pore. We can not list all the costs, but here's a histogram:



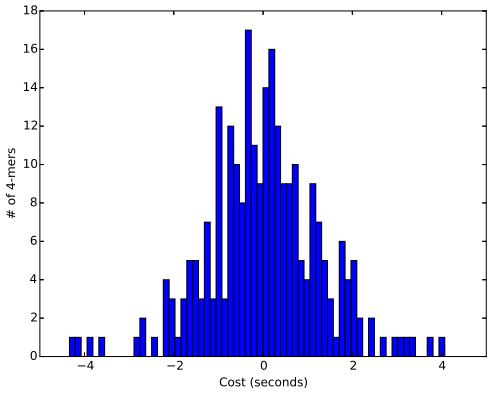
And here's the resulting predictions:



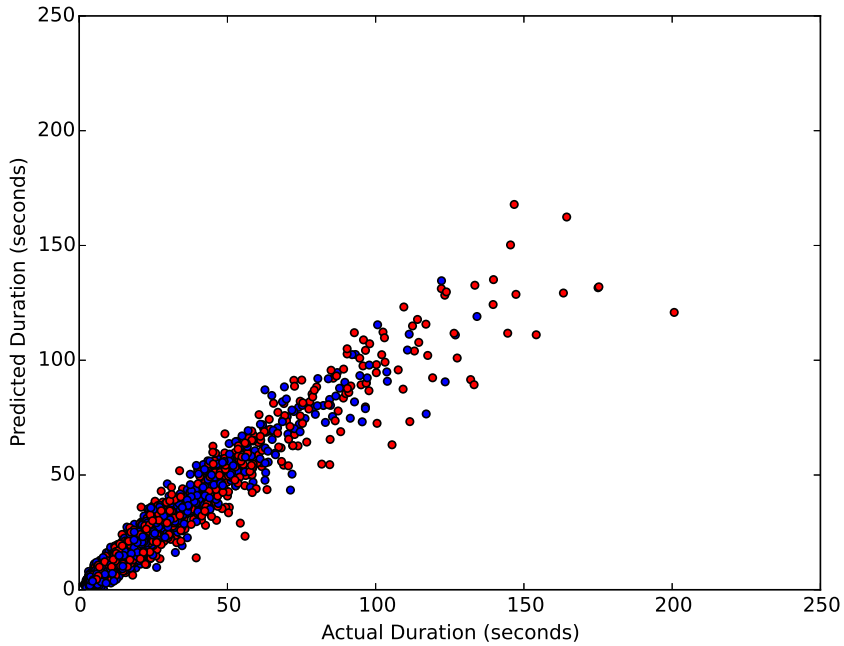
$r^2 = 0.91$

4mer Model

We can use a model in which each the time to extend by one nucleotide is determined by the 4-mer in the middle of the pore. We can not list all the costs, but here's a histogram:



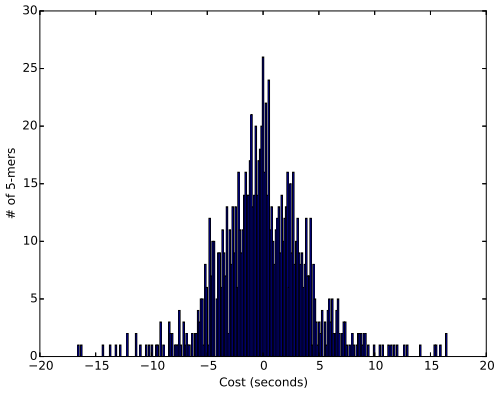
And here's the resulting predictions:



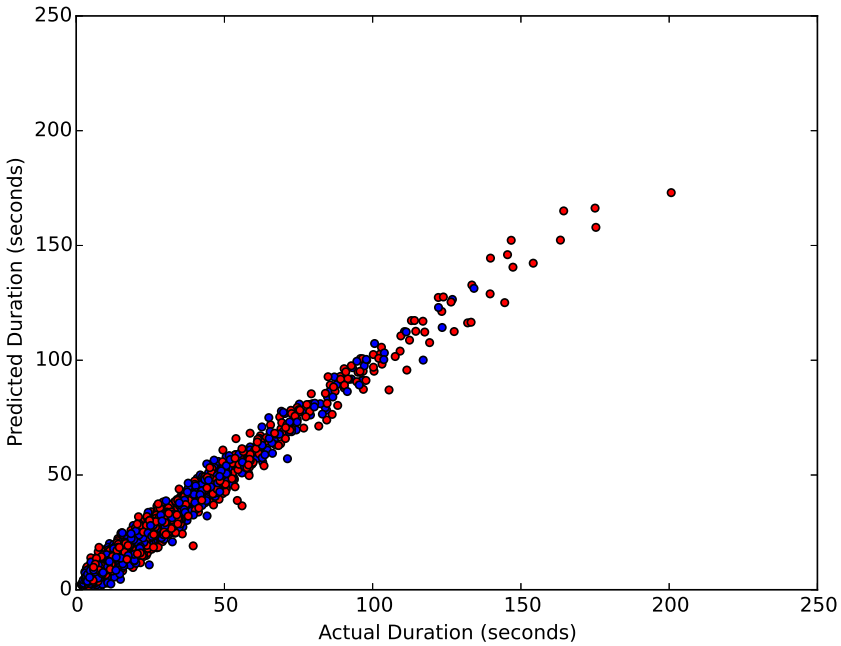
$r^2 = 0.94$

5mer Model

We can use a model in which each the time to extend by one nucleotide is determined by the 5-mer in the middle of the pore. We can not list all the costs, but here's a histogram:



And here's the resulting predictions:



$r^2 = 0.98$

At this point our model has 1024 degrees of freedom for 2162 datapoints, so a good fit may reveal more overfitting than model appropriateness.