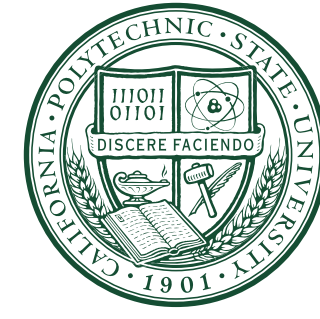


# Pyroprinting Sensitivity Analysis on the GPU



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## Overview

The biology department at Cal Poly, San Luis Obispo developed a fingerprinting method, pyroprinting, for differentiating between strains of bacteria. To investigate the sensitivity of pyroprinting, our research group has conducted an in-silico simulation on *E. coli* DNA sequences from the 16s-23s intergenic transcribed spacer (ITS) region. The simulation parameters consisted of the **dispensation sequence** (CCTCTACTAGAGCG20(TCGA)TT) and **primer** (TTGGATCAC). From these parameters, 24 unique alleles were determined from a mix of DNA sequences from NCBI reference *E. coli* genomes, manual sequencing (from Cal Poly), and from plasmids (from Cal Poly).

## Goal

We want to study and characterize pyroprinting sensitivity for the purpose of strain differentiation from a theoretical perspective. In particular, we investigate the quantity of simulated pyroprints that are deemed *similar*.

## Implementation

**Isolate Generation.** Generate every combination of seven alleles (unordered, with replacement). Each combination represents a unique theoretical isolate in our study.

**Pyroprint Generation.** For each isolate, construct its pyroprint:

- \* Pyrosequence each allele of the isolate
- \* Combine pyrosequenced alleles to create a single pyroprint

**Compute Correlations.** Compute the Pearson correlation coefficient for each pair of pyroprints.

**Histogram Generation.** Separate all computed correlation coefficients into a number of "buckets" based on their values.

## Simulation

**Pyroprint A**  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA

**Pyroprint B**  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA  
CTCCTTACCTTAAAGAAAGCGTCTTTGAAAGTGTCTGATGAAAAATAAATA

Figure 1.

A subset of 12 alleles from the 16s-23s ITS region of the reference *E. coli* DNA cassettes. These alleles are used for the sample pyroprints in Figure 2.

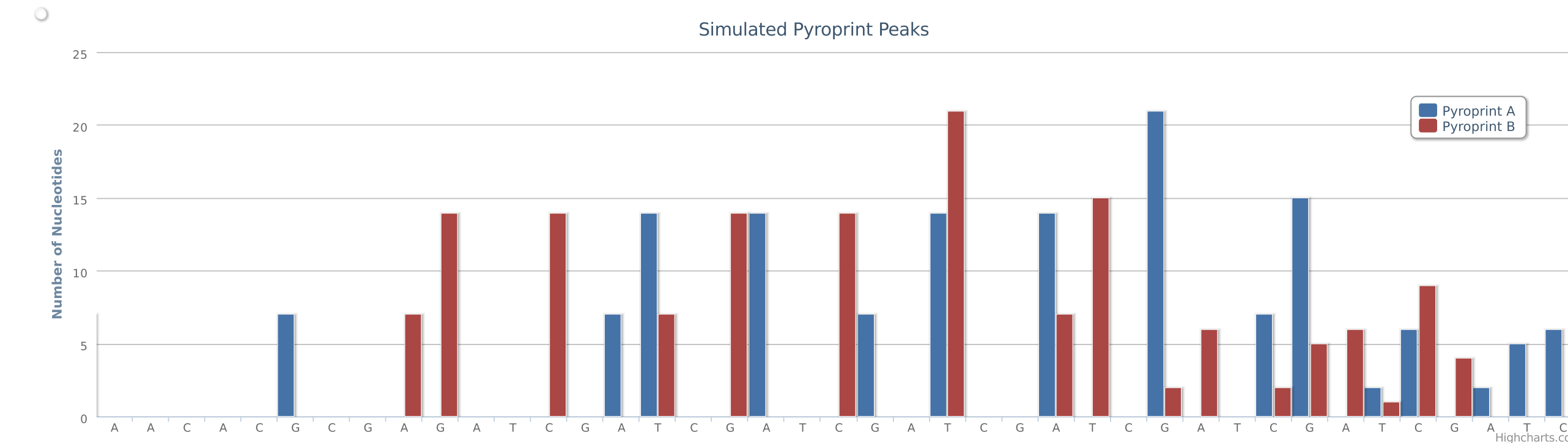
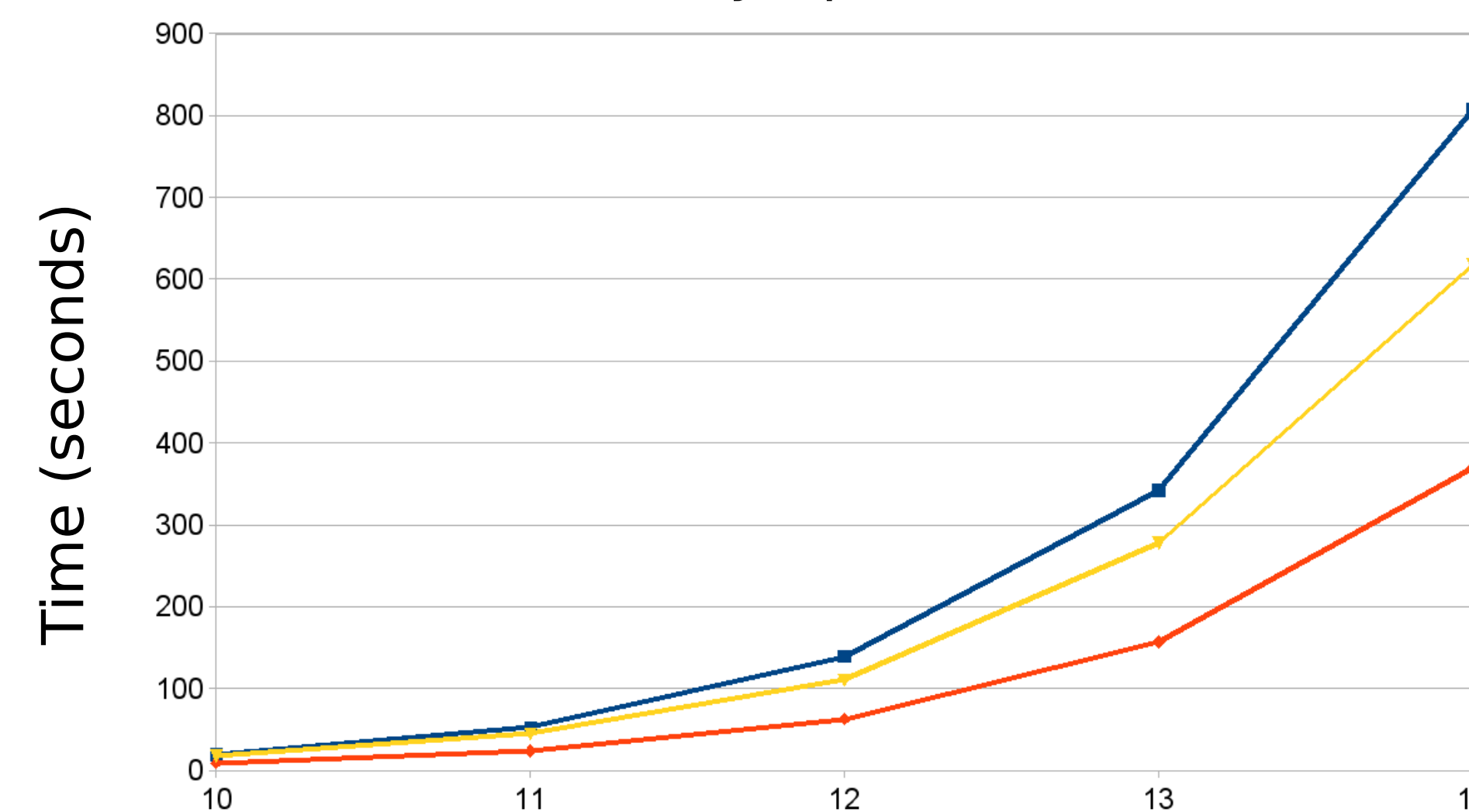


Figure 2.

Two sample pyroprints constructed using the 12 sample alleles in Figure 1. Each pyroprint is a combination of 7 alleles.

## Results

Runtime of Pyroprint Simulation

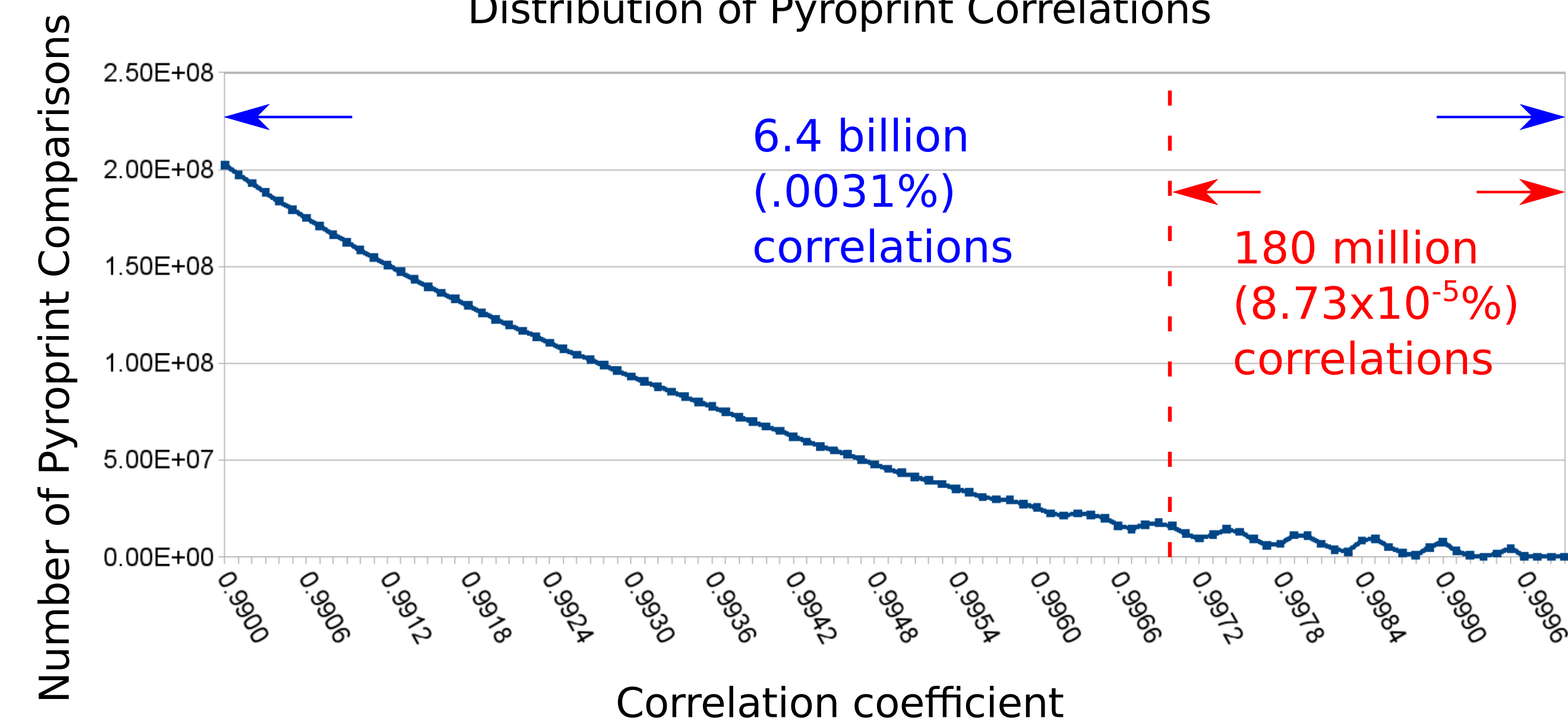


Number of Alleles

Dataset size based on Number of Alleles

# of Alleles	# of Isolates	# of comparisons
10	11,440	65,431,080
11	19,448	189,102,628
12	31,824	506,367,576
13	50,388	1,269,450,078
14	77,520	3,004,636,440
24	2,035,800	2,072,239,802,100

Distribution of Pyroprint Correlations



## Conclusion

For our simulation, over 99.96% ( $2.065 \times 10^{12}$ ) of all correlation coefficients fall below 99% similarity. In preliminary *in vitro* studies conducted on pyroprints, multiple pyroprints of the same isolate showed correlations above 99.7%. However we found that only  $8.73 \times 10^{-5}\%$  (180 million) of correlations fall into this category. This suggests that pyroprinting is sufficiently sensitive to distinguish bacterial strains.