InfoSeq: Quantification of Information Content in genomic datasets

Motivation

- We usually discuss the predictability of tracks using each other
- Uniform analysis of predictability of the data can reveal basic understanding of how genomic tracks relate to each other
- ***Quantity:*** How do we quantify the amount of information in genomic datasets?
  - Which datasets give the most amount of information?
- ***Predictability:*** How do we quantify (correct) predictability of one dataset from other datasets?
  - Which datasets can be predicted best from the others?

Entropic Measures from PrivaSeq

- Given N tracks (random variables) $X_1, X_2, \ldots, X_N$; we compute the predictability of Y as:

$$1 - \frac{H(Y|X_1, X_2, \ldots, X_N)}{H(X_1, X_2, \ldots, X_N, Y)}$$

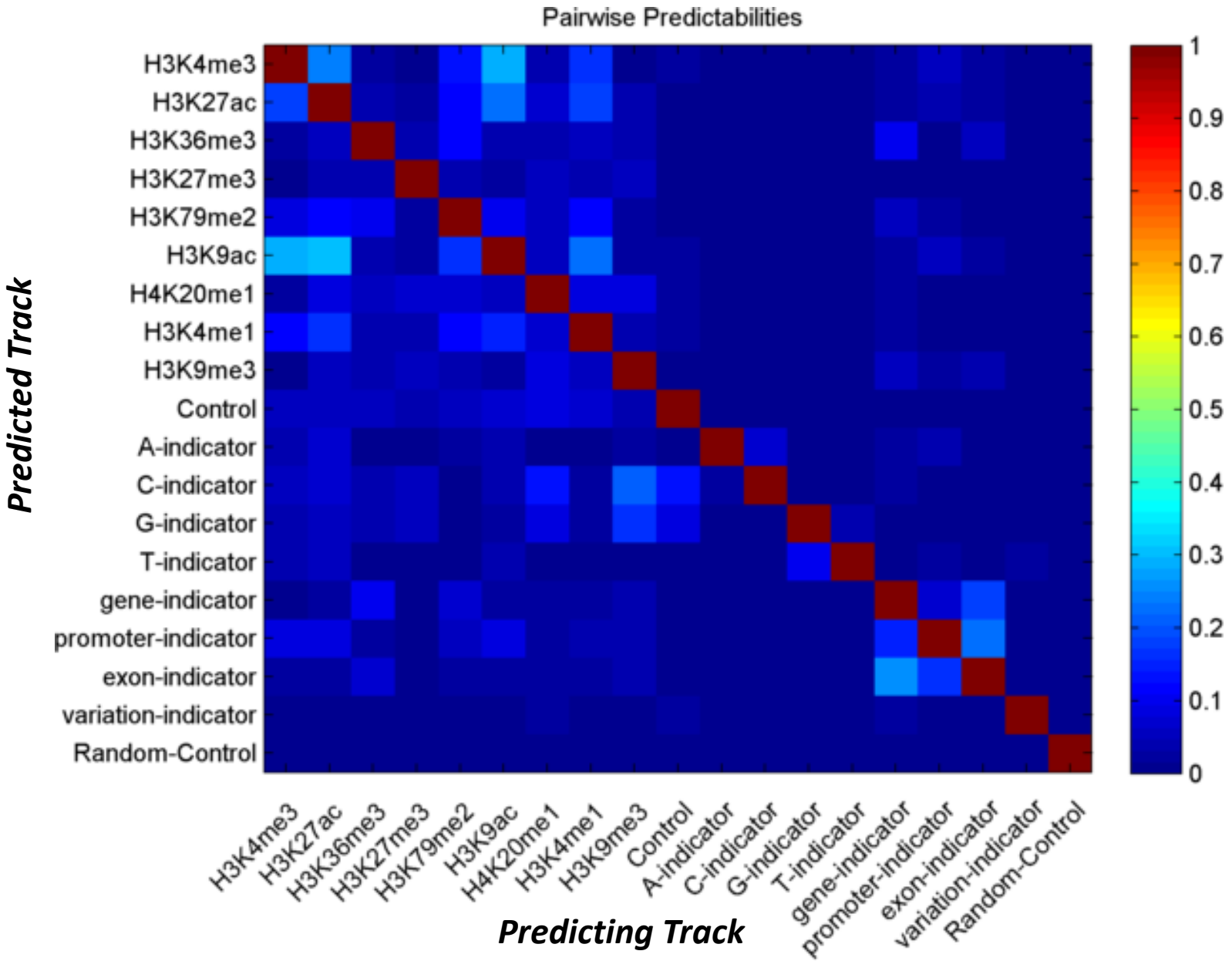
where $H(X_1, X_2, \ldots, X_N, Y)$ is the joint entropy and $H(Y|X_1, X_2, \ldots, X_N)$ is the conditional entropy of Y given other tracks

  - We estimate the entropies using the observed datasets as the sample entropies. Thus the quantities that we compute are data dependent

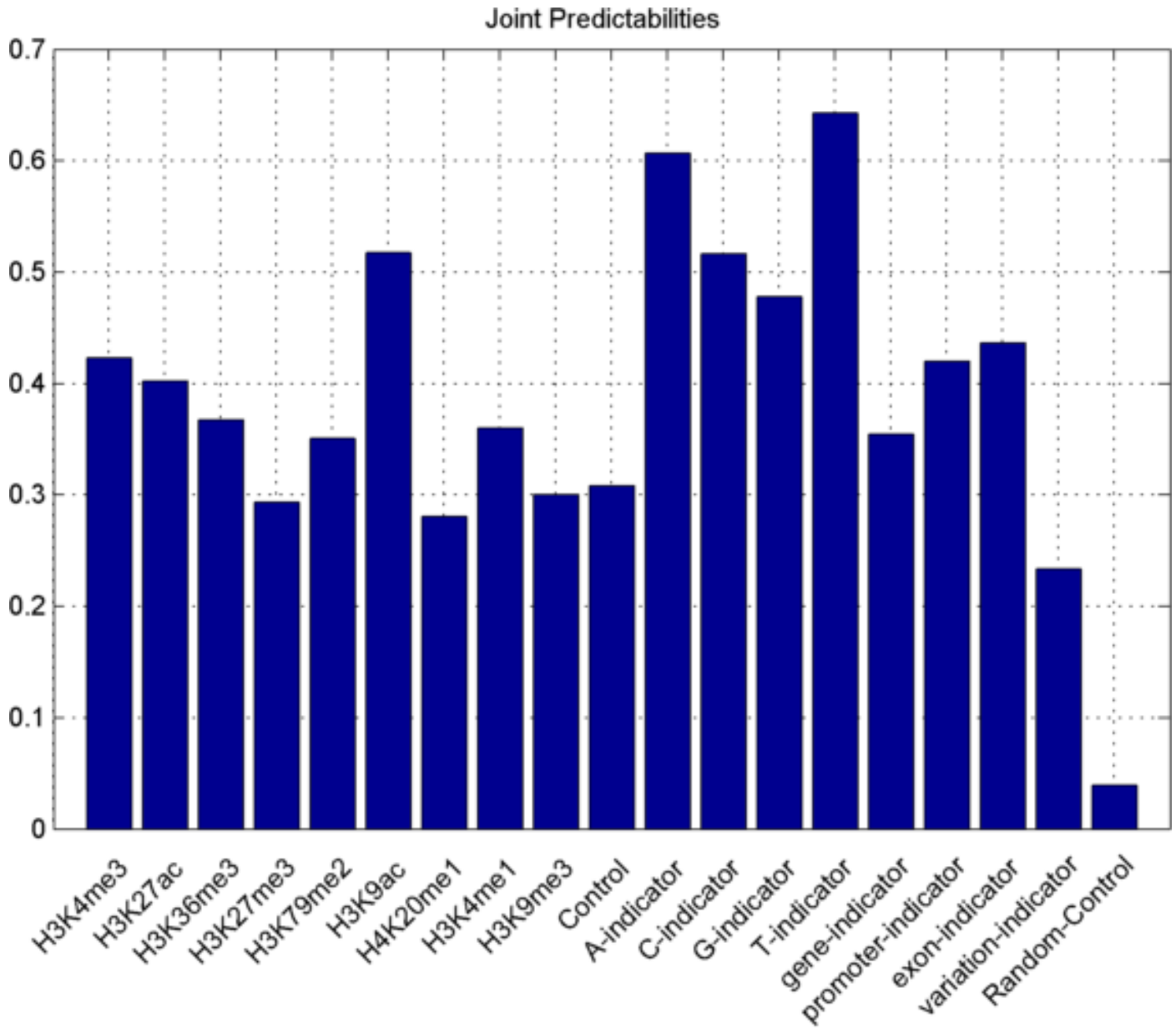
Entropic Measures from PrivaSeq

- Assign: $X_1 = H3K4me1, X_2 = H3K4me3, \ldots, X_N = H3K9me3$
  - H3K4me1, H3K4me3, H3K27ac, H3K36me3, H3K27me3, H3K9me3, H3K9ac, H3K79me2, H4K20me1, Control,
  - Sequence indicators (A,C,G,T)
  - 1000 Genomes variants (<0.1 allele frequency)
  - Gene/Promoter/Exon indicators
  - Randomized Control (random Bernoulli track): Must have zero predictability.
- Bin the signal tracks with 1,000 base pair long bins and generate the sample for each track
- Use $\lfloor \log_{10}(total\ signal) \rfloor$ to generate the tracks
- Estimate the sample entropies from histograms

Predictability of Tracks Using Each of the others



Joint Predictability (one from others)



Next..

- ***Effect of Data Representations:*** How does different representations of the data effect quantification of information?
  - Peaks versus signal tracks
- How to spin this to not overlap with other efforts in ENCODE?