

Quick Permutation Test: feature filtering of n-gram data

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Introduction

N-grams (k-tuples) are vectors of n characters derived from input sequence(s). They may form continuous sub-sequences or be discontinuous. Important n-gram parameter is its position. Instead of just counting n-grams, one may want to count how many n-grams occur at a given position in multiple (e.g. related) sequences. Originally developed for natural language processing, n-grams are also used in genomics (Fang et al., 2011), transcriptomics (Wang et al., 2014) and proteomics (Guo et al., 2014).

	P1	P2	P3	P4	P5	P6
S1	1	2	4	4	3	1
S2	4	3	2	4	2	4
S3	2	4	1	3	1	4

Sample sequences. S - sequence, P - postion.

	1	2	3	4
S1	2	1	1	2
S2	0	2	1	3
S3	2	1	1	2

Unigram counts.

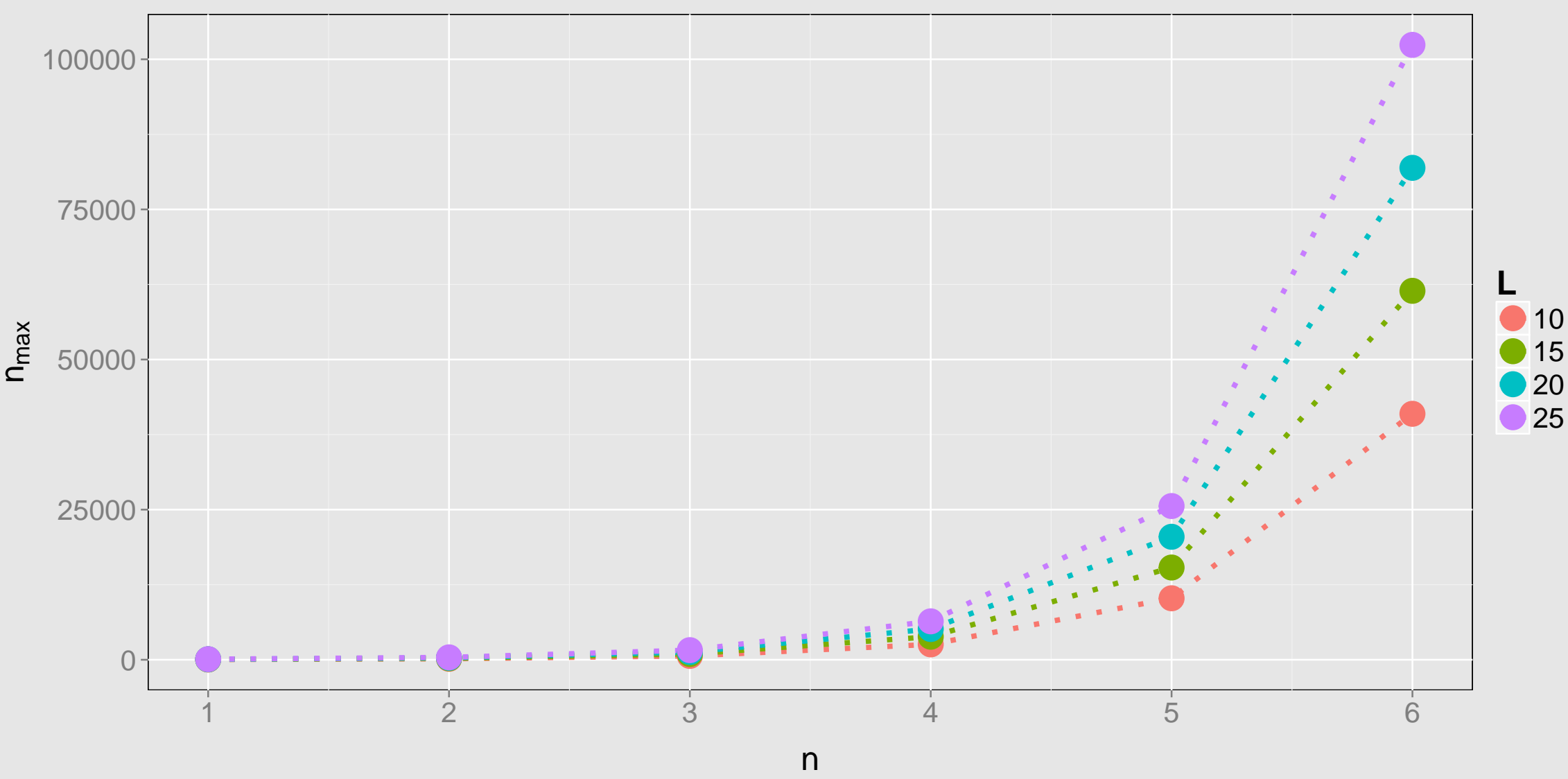
	P1.1	P2.1	P3.1	P4.1	P5.1	P6.1	P1.2	P2.2	P3.2	P4.2	P5.2	P6.2	P1.3
S1	1	0	0	0	0	1	0	1	0	0	0	0	0
S2	0	0	0	0	0	0	0	0	1	0	1	0	0
S3	0	0	1	0	1	0	1	0	0	0	0	0	0

A fraction of possible unigrams with position information.

Curse of dimensionality

Even when we limit ourselves to only continuous positioned n-grams, build on m possible characters, feature space grows rapidly with the number of elements in n-gram (n) and the length of the sequence (L). The number of possible positioned n-grams:

$$n_{\max} = L \times m^n$$



Feature selecting permutation tests

Model and statistic independent permutation tests can be used to filter features obtained through counting n-grams. During a permutation test class labels are randomly exchanged during computation of a significance statistic. p-values are defined as:

$$\text{p-value} = \frac{N_{T_P > T_R}}{N}$$

where $N_{T_P > T_R}$ is number of times when T_P (permuted test statistic) was more extreme than T_R (test statistic for non-permuted data). Permutation tests are computationally expensive (especially considering precise estimation of low p-values, because the number of permutations is inversely proportional to the interval between p-values).

QuiPT concept

In each permutation, for every observation, there are four possible results.

$$P(\text{Target}, \text{Feature}) = (1, 1) = p \cdot q$$

$$P(\text{Target}, \text{Feature}) = (1, 0) = p \cdot (1 - q)$$

$$P(\text{Target}, \text{Feature}) = (0, 1) = (1 - p) \cdot q$$

$$P(\text{Target}, \text{Feature}) = (0, 0) = (1 - p) \cdot (1 - q)$$

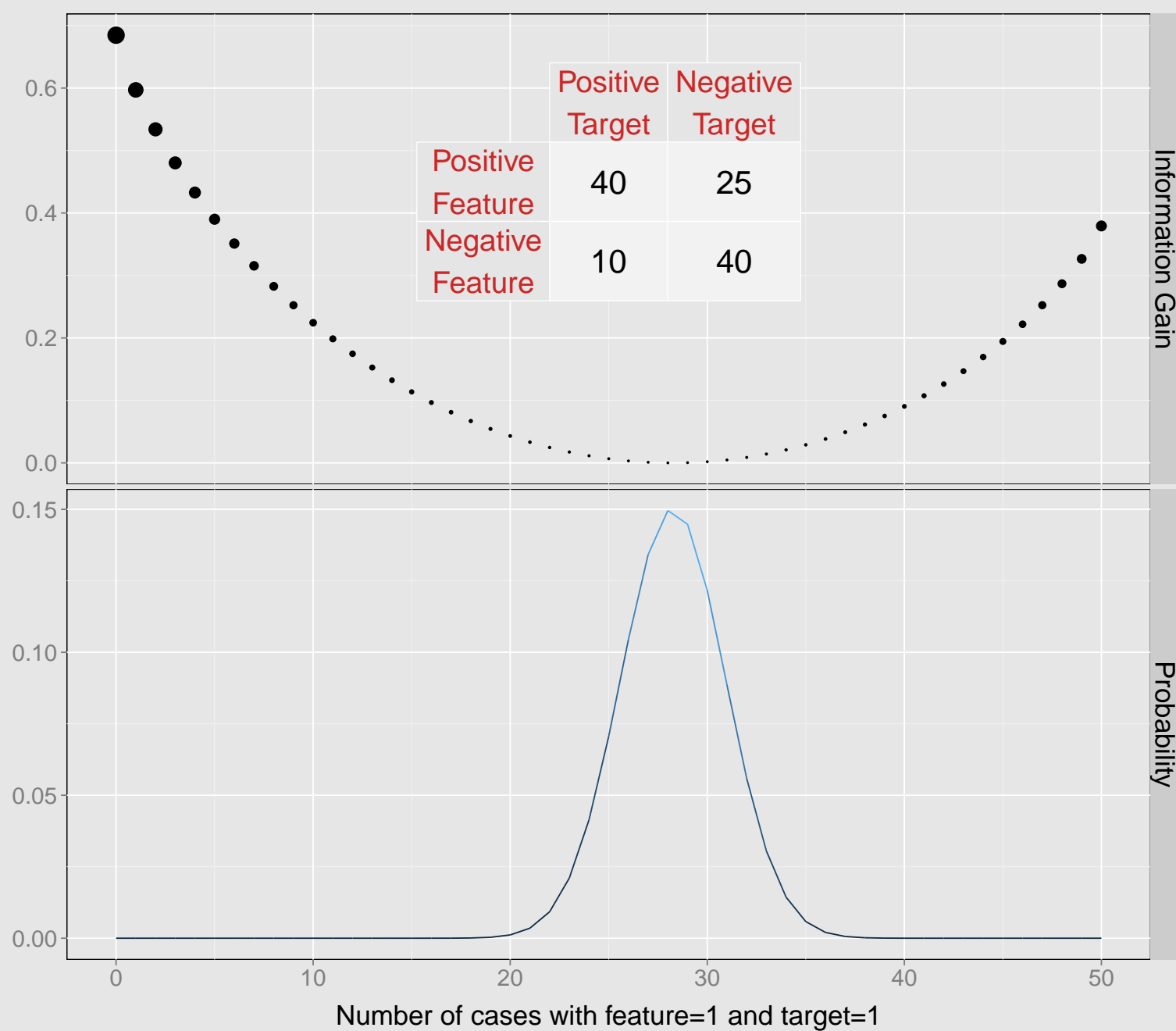
Where p and q are fractions of positive observations in target and feature respectively. An another view at permutation test is therefore that we get a contingency table, which is to be tested for independence. Computing probability of a such table with two constraints, $n_{1,\cdot} = n_{1,1} + n_{1,0}$ and $n_{\cdot,1} = n_{1,1} + n_{0,1}$, and conditioning on $n_{1,1}$, leads to hypergeometric distribution. $n_{i,j}$ denotes number of observations for which $(\text{Target}, \text{Feature}) = (i, j)$. This is in fact exact two-sided Fisher's test (Lehmann, 1986).

Computational cost

The cost of performing QuiPT is equal to computing a test statistic and probability of occurence for $n_{1,1} + n_{0,1}$ contingency tables. Suppose we consider 6-grams build on sequences of length 25 build of four characters. Then there are around 100,000 n-grams (features) to test. This means that for Benjamini-Hochberg procedure, we need to calculate p-values with accuracy of 0.05×10^{-5} . This requires at least 2 million permutations. Each permutation, apart from reshuffling labels, requires computation of a test statistic. Since n-gram features are very sparse vectors, QuiPT needs to evaluate only few contingency tables. The relative difference in speed between QuiPT and normal permutation tests depends on several factors, as a number of permutations and input data. For example, for simulation scheme presented below, QuiPT was on average 93 times faster than normal permutation test with 10^5 permutations.

Distribution of Information Gain for given contingency table

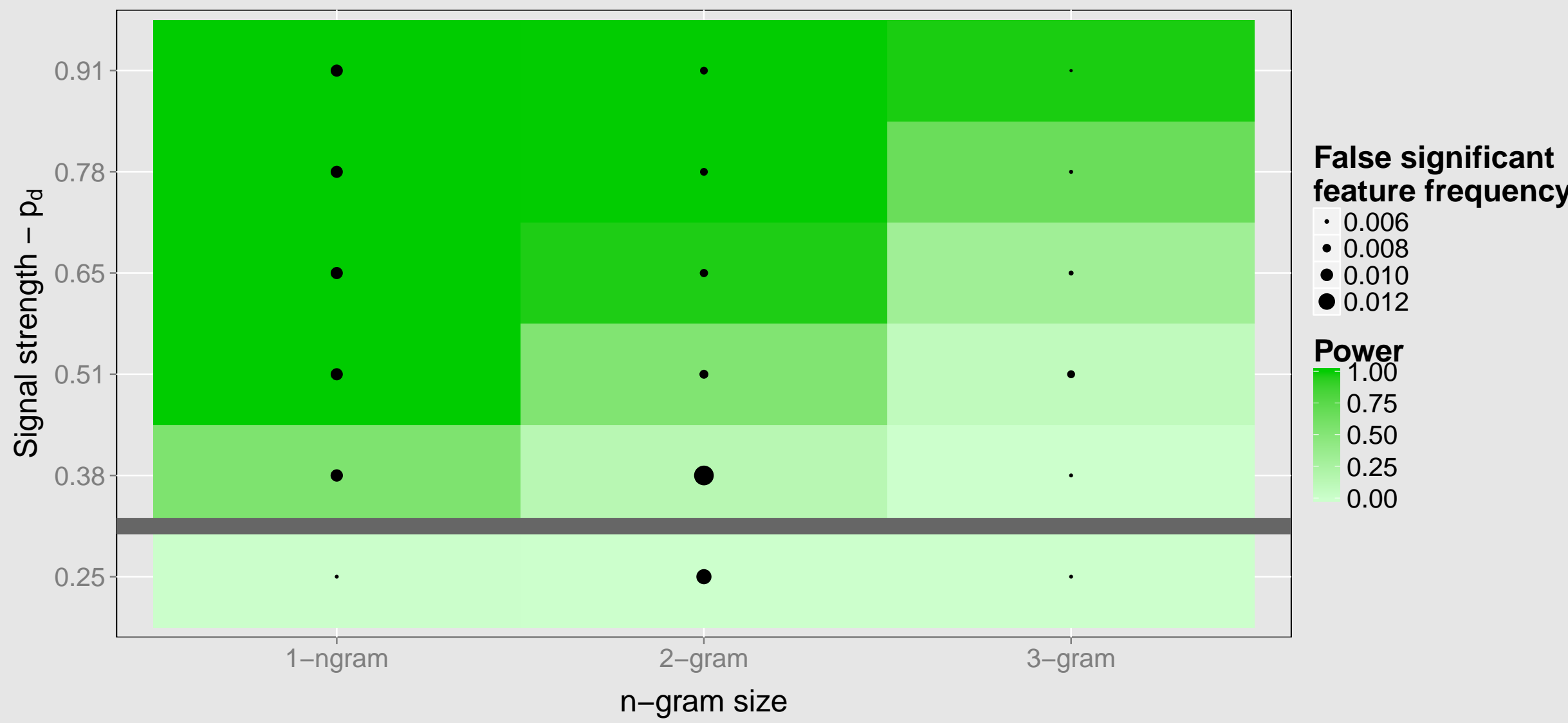
Given constraint on $n_{1,1} + n_{0,1}$, probability distribution on contingency tables, which permutations might produce, can be computed exactly.



Simulation scheme - genomics

1. Random 4000 sequences (20 nucleotides each). The half of the sequences has label 0.
2. Choose a single position between 3 and 18 (to avoid border cases).
3. Resample nucleotides at chosen position. The dominant nucleotide has probability of occurrence $p_d = 0.25$. Other nucleotides have probability of occurrence $p_o = (1 - p_d)/3$.
4. Perform QuiPT (Information Gain as test statistic) and choose significant features (with p-value < 0.001).
5. Iterate steps 1-4 over other values of p_d - 0.38, 0.51, 0.65, 0.78, 0.91.
6. Repeat steps 1-5 200 times.

Power and False discoveries



Summary

Quick permutation test is a powerful and quick equivalent of permutation test in binary feature-binary target testing scenario. It is especially useful when very precise p-values are required and features are sparse vectors.

Availability

QuiPT is a part of **biogram** R package devoted to the analysis of n-grams extracted from biological sequences: <http://cran.r-project.org/web/packages/biogram/>

Bibliography

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