# Quick Permutation Test: feature filtering of n-gram data

Piotr Sobczyk<sup>1\*</sup>, Michał Burdukiewicz<sup>2</sup>, Chris Lauber<sup>3</sup>, Paweł Mackiewicz<sup>2</sup>
\*Piotr.Sobczyk@pwr.edu.pl

<sup>1</sup>Wrocław University of Technology, Department of Mathematics, Poland <sup>2</sup>University of Wrocław, Department of Genomics, Poland

<sup>3</sup>Dresden University of Technology, Institute of Medical Informatics and Biometry, Poland

#### Introduction

N-grams (k-tuples) are vectors of n characters derived from input sequence(s). They may form continuous sub-sequences or be discontinuous. Another 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.

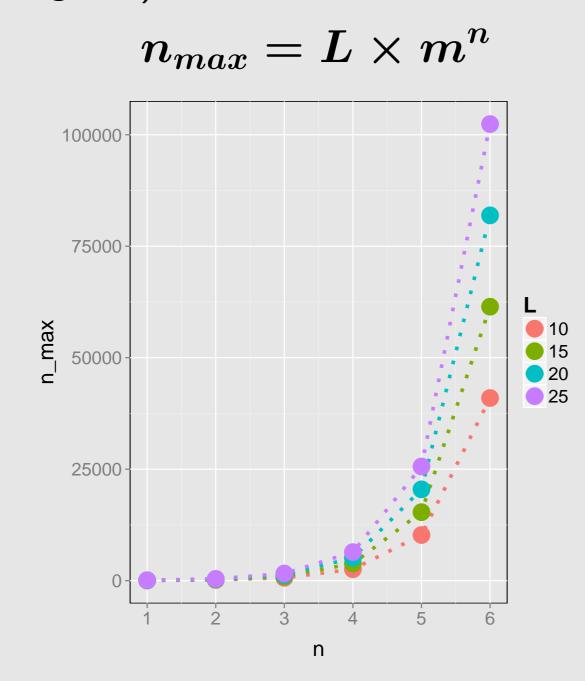
	P1	P2	P3	P4	P5	P6
S1	3	2	2	3	1	4
S2	4	4	2	4	2	3
<b>S</b> 3	3	4	1	4	3	1
	San	nnle	sea	lllen	ces	

_	P1_1	P2_1	P3_1	P4_1	P5_1	P6_1	P1_2	P2_2	P3_2	P4_2	P5_2
_	0	0	0	0	1	0	0	1	1	0	0
	0	0	0	0	0	0	0	0	1	0	1
	0	0	1	0	0	1	0	0	0	0	0
_	Λ.	f., at: a	sp of r	a a sai bl			i+b	acitic	n info	, kpo o ti d	<b>.</b>

A traction of possible unigrams with position information.

# Curse of dimensionality

Number of possible positioned n-grams (not taking into account distances between elemnts of n-gram):



# Permutation test

During permutation tests class labels are randomly exchanged during computation of significance statistic. p-values are defined as:

p-value 
$$=rac{N_{T_P>T_R}}{N}$$

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 model and statistic independent, but computationally expensive (especially precise estimation of low p-values, because the number of permutations is inversely proportional to the interval between p-values).

# QuiPT algorithm

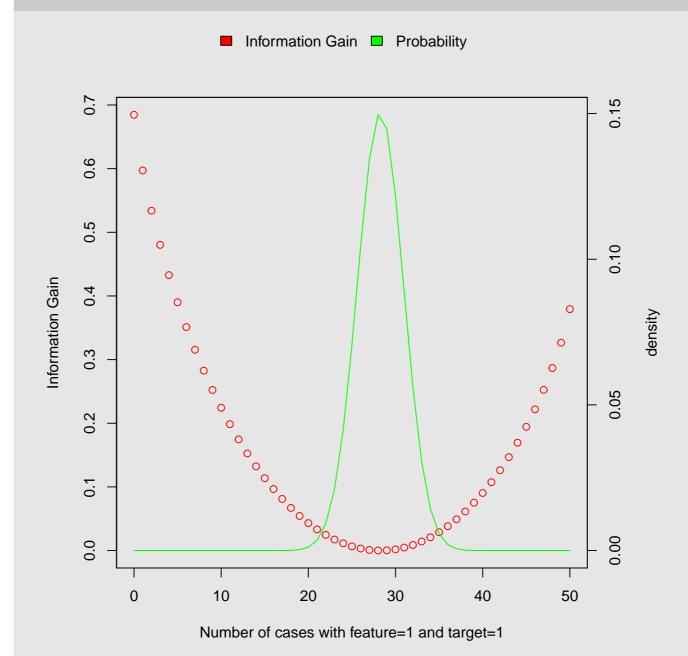
If probability that target equals 1 is  $oldsymbol{p}$  and probability that feature equals 1is q and feature and target are independent then each of them has the following probabilities

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

$$F(n_{1,1},n_{1,0},n_{0,1},n_{0,0}) = inom{n}{n_{1,1}} (p \cdot q)^{n_{1,1}} n - n_{1,1} \ inom{p \cdot (1-q)^{n_{1,0}}}{(n_{1,0})} (p \cdot (1-q))^{n_{1,0}} \ inom{n - n_{1,1} - n_{1,0}}{(n_{0,1})} ((1-p) \cdot q)^{n_{0,1}} \ inom{n - n_{1,1} - n_{1,0} - n_{0,1}}{n_{0,0}} \ inom{(1-p) \cdot (1-q)^{n_{0,0}}}{(1-p) \cdot (1-q)^{n_{0,0}}}$$

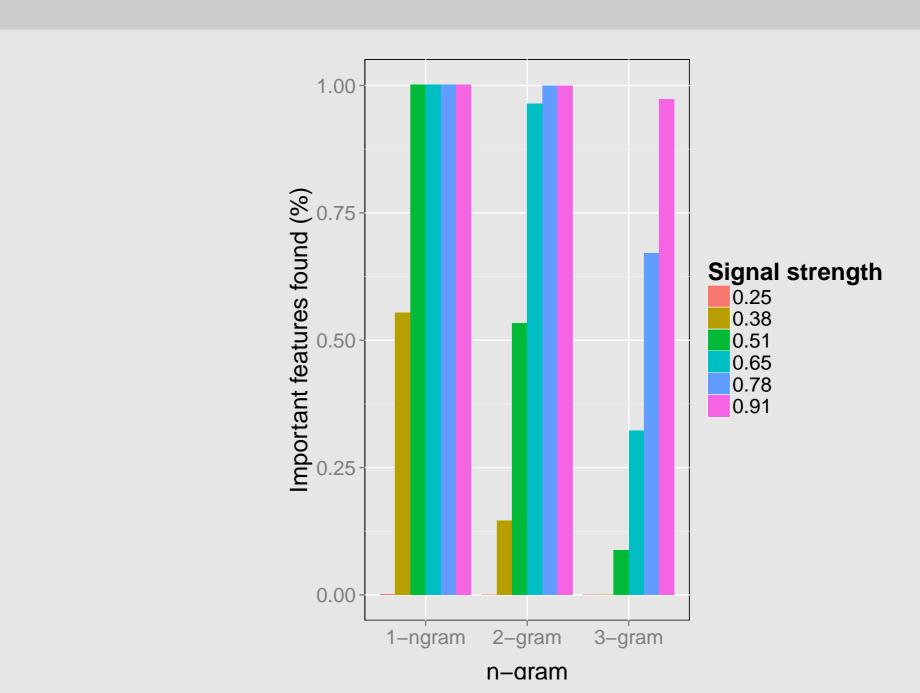
In addition to this:  $n_{1,\cdot}=n_{1,1}+n_{1,0}$  and  $n_{\cdot,1}=n_{1,1}+n_{0,1}$  are known and fixed.



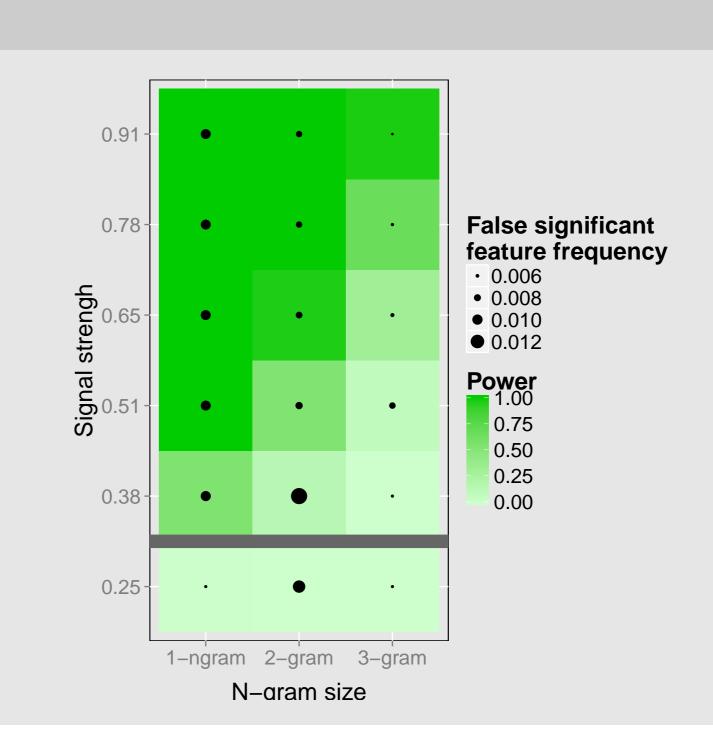


	Target	Feature	Freq
1 (	)	0	40
2 1	L	0	10
3 (	)	1	25
4 ]	L	1	40

### Test power



# False discoveries



# Summary

Quick permutation test is a powerful and quick equivalent of permutation test in binary feature-binary target testing scenario.

# **Avaibility**

biogram R package:

http://cran.r-project.org/web/packages/biogram/

# Bibliography