

# Extracting sparse mutational signatures via LASSO

***Daniele Ramazzotti<sup>1,2</sup>, Avantika Lal<sup>1</sup>, Keli Liu<sup>3</sup>, Luca De Sano<sup>4</sup>, Robert Tibshirani<sup>3</sup>, and Arend Sidow<sup>1,5</sup>***

<sup>1</sup>Department of Pathology, Stanford University, Stanford, CA , USA.

<sup>2</sup>Department of Computer Science, Stanford University, Stanford, CA , USA.

<sup>3</sup>Department of Statistics, Stanford University, Stanford, CA , USA.

<sup>4</sup>Dipartimento di Informatica Sistemistica e Comunicazione, Università degli Studi Milano Bicocca Milano, Italy.

<sup>5</sup>Department of Genetics, Stanford University, Stanford, CA , USA.

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**Overview.** Point mutations occurring in a genome can be divided into 96 categories based on the base being mutated, the base it is mutated into and its two flanking bases. Therefore, for any patient, it is possible to represent all the point mutations occurring in that patient's tumor as a vector of length 96, where each element represents the count of mutations for a given category in the patient.

A mutational signature represents the pattern of mutations produced by a mutagen or mutagenic process inside the cell. Each signature can also be represented by a vector of length 96, where each element represents the probability that this particular mutagenic process generates a mutation of the 96 above mentioned categories. In this R package, we provide a set of functions to extract and visualize the mutational signatures that best explain the mutation counts of a large number of patients.

*In this vignette, we give an overview of the package by presenting some of its main functions.*

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## 1 Changelog

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1.0.0 package released on Bioconductor in May 2018.

## 2 Algorithms and useful links

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Acronym	Extended name	Reference
SparseSignatures	De Novo Mutational Signature Discovery in Tumor Genomes using SparseSignatures	<a href="#">Publication</a>

## 3 Using the SparseSignatures R package

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We now present the main features of the package. To start, we show how to load data and transform them to a count matrix to perform the signatures discovery; first we load some example data provided in the package.

```
library("SparseSignatures")
## Loading required package: NMF
## Loading required package: pkgmaker
## Loading required package: registry
##
## Attaching package: 'pkgmaker'
## The following object is masked from 'package:base':
##
## isFALSE
## Loading required package: rngtools
## Loading required package: cluster
```

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```
## NMF - BioConductor layer [OK] | Shared memory capabilities [NO: synchronicity]
| Cores 23/24

## To enable shared memory capabilities, try: install.extras('
## NMF
## ')

data(ssm560_reduced)
head(ssm560_reduced)

##      sample chrom      pos ref alt
## 1: PD10014a     1 186484577   A   C
## 2: PD10014a     7 141761948   G   A
## 3: PD10014a     7  71266228   C   T
## 4: PD10014a     8  82304475   A   T
## 5: PD10014a     3 191275626   T   A
## 6: PD10014a     4 135265376   C   T
```

These data are a reduced version with only 3 patients of the 560 breast tumors provided by Nik-Zainal, Serena, et al. (2016). We can transform such input data to a count matrix to perform the signatures discovery with the function `import.counts.data`. To do so, we also need to specify the reference genome as a `BSgenome` object and the format of the 96 nucleotides to be considered. This can be done as follows, where in the example we use `hs37d5` as our reference genome.

```
library("BSgenome.Hsapiens.1000genomes.hs37d5")

## Loading required package: BSgenome
## Loading required package: S4Vectors
## Loading required package: stats4

##
## Attaching package: 'S4Vectors'

## The following object is masked from 'package:NMF':
##
##      nrun

## The following object is masked from 'package:pkgmaker':
##
##      new2

## The following object is masked from 'package:base':
##
##      expand.grid

## Loading required package: IRanges
## Loading required package: GenomeInfoDb
## Loading required package: GenomicRanges
## Loading required package: Biostrings
## Loading required package: XVector
```

## Extracting sparse mutational signatures via LASSO

```
##
## Attaching package: 'Biostrings'

## The following object is masked from 'package:base':
##
##   strsplit

## Loading required package: rtracklayer

bsg = BSgenome.Hsapiens.1000genomes.hs37d5
data(mutation_categories)
head(mutation_categories)

##   context alt   cat
## 1:   A:A C>A A[C>A]A
## 2:   C:A C>A C[C>A]A
## 3:   G:A C>A G[C>A]A
## 4:   T:A C>A T[C>A]A
## 5:   A:A C>G A[C>G]A
## 6:   C:A C>G C[C>G]A

imported_data = import.counts.data(input=ssm560_reduced,bsg=bsg,mutation_categories=mutation_categories)

## Warning in import.counts.data(input = ssm560_reduced, bsg = bsg, mutation_categories
= mutation_categories): Some samples have fewer than 100 mutations:
## PD10010a, PD10011a, PD10014a

head(imported_data)

##           A[C>A]A A[C>A]C A[C>A]G A[C>A]T A[C>G]A A[C>G]C A[C>G]G A[C>G]T A[C>T]A
## PD10010a      37      25       8       24      35       5       16      25      49
## PD10011a     103      59      16      73     113      54      31     102     116
## PD10014a     235     241      37     234     158      71      26     180     229
##           A[C>T]C A[C>T]G A[C>T]T A[T>A]A A[T>A]C A[T>A]G A[T>A]T A[T>C]A A[T>C]C
## PD10010a      31     100      42      21      15      17      30      48      20
## PD10011a      73     228     109      61      70      56     165     184     116
## PD10014a      89     178     186     105      90     126     174     261     122
##           A[T>C]G A[T>C]T A[T>G]A A[T>G]C A[T>G]G A[T>G]T C[C>A]A C[C>A]C C[C>A]G
## PD10010a      29      44       8       6      10      23      34      28       8
## PD10011a     113     169      77      41      73     105     105      75      30
## PD10014a     167     211      76      27      84      59     244     238      35
##           C[C>A]T C[C>G]A C[C>G]C C[C>G]G C[C>G]T C[C>T]A C[C>T]C C[C>T]G C[C>T]T
## PD10010a      23      15      19      20      26      48      37      55      43
## PD10011a     102      60      37      22      65      71      52     108     103
## PD10014a     243     107     105      40     144     136     124     144     197
##           C[T>A]A C[T>A]C C[T>A]G C[T>A]T C[T>C]A C[T>C]C C[T>C]G C[T>C]T C[T>G]A
## PD10010a      12       7      18      16      14      17      20      30       6
## PD10011a     116      80      89     103     103      78     102     158      40
## PD10014a     116     139     145     217     103     144     112     129      47
##           C[T>G]C C[T>G]G C[T>G]T G[C>A]A G[C>A]C G[C>A]G G[C>A]T G[C>G]A G[C>G]C
## PD10010a       8       5      13      31      22      11      22       6      12
## PD10011a      65      55     188      78      50      14      55      55      66
## PD10014a      54      70     107     146     126      24     160      63      70
##           G[C>G]G G[C>G]T G[C>T]A G[C>T]C G[C>T]G G[C>T]T G[T>A]A G[T>A]C G[T>A]G
## PD10010a       9      14      40      32      82      25       6       6       6
```

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```
## PD10011a      13      87      76      63      118      81      69      41      56
## PD10014a      25     120     141      99     180     163      62      66      83
##              G[T>A]T G[T>C]A G[T>C]C G[T>C]G G[T>C]T G[T>G]A G[T>G]C G[T>G]G G[T>G]T
## PD10010a      13      22       9      16      24       7       1       8      10
## PD10011a      86      96      62      82      93      56      46      35      99
## PD10014a     126     110      81     102     135      32      18      61      78
##              T[C>A]A T[C>A]C T[C>A]G T[C>A]T T[C>G]A T[C>G]C T[C>G]G T[C>G]T T[C>T]A
## PD10010a      40      40      12      48      54      37      12      85      67
## PD10011a      78      80      12      83     116     104      29     194     119
## PD10014a     202     191      17     253     198     159      33     325     188
##              T[C>T]C T[C>T]G T[C>T]T T[T>A]A T[T>A]C T[T>A]G T[T>A]T T[T>C]A T[T>C]C
## PD10010a      55      53      71      39      13       3      35      19      13
## PD10011a      94      78     126     121      43      64      91     125      79
## PD10014a     153      93     184     124      89      73     221     143     118
##              T[T>C]G T[T>C]T T[T>G]A T[T>G]C T[T>G]G T[T>G]T
## PD10010a      11      25      18      11      11      35
## PD10011a      83     113      68      90     140     251
## PD10014a      75     148      71      54      76     160
```

The function `import.counts.data` can also take a text file as input with the same format as the one shown above. Now, we show an example of a visualization feature provided by the package, and we show the counts for the first patient PD10010a in the following plot.

```
patient.plot(countMatrix=imported_data,patientName="PD10010a")
```

After the data are loaded, signatures can be discovered. To do so, we need to define a set of parameters on which to perform the estimation.

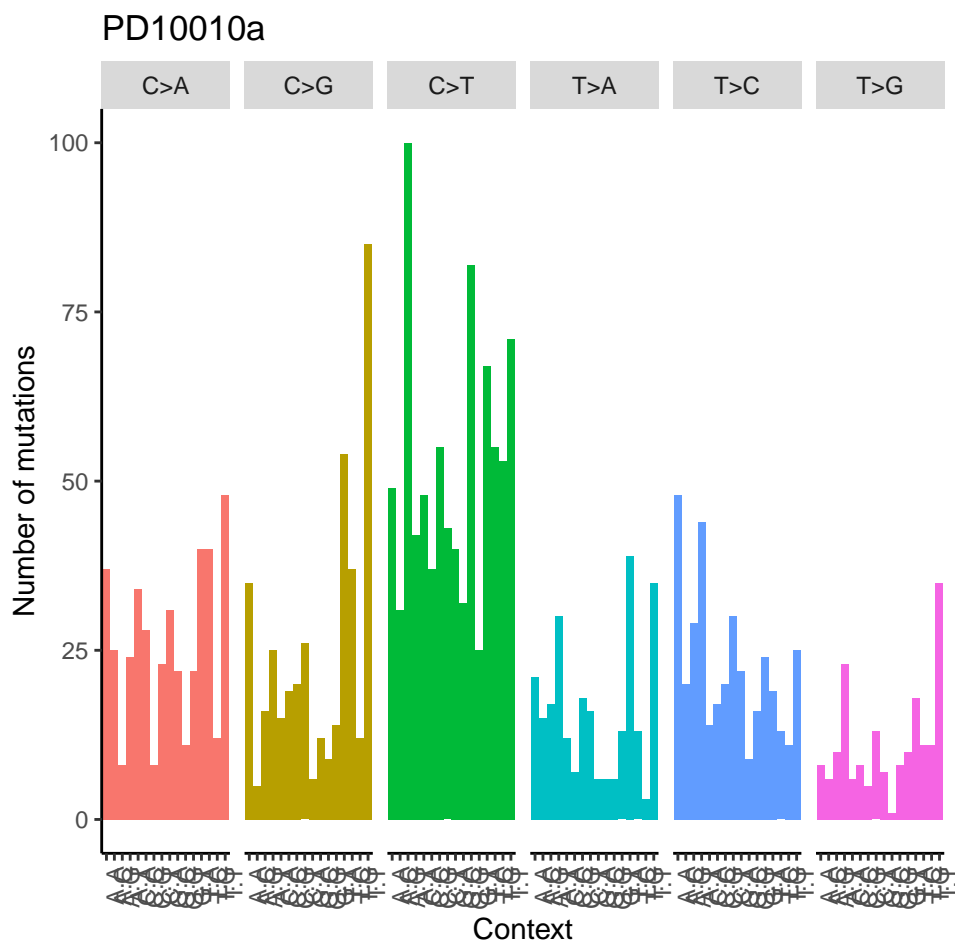
First of all, we need to specify the ranges for the number of signatures (variable *K*) and the LASSO penalty value (variable *lambda rate*) to be considered. The latter is more complicated to estimate, as it requires that the values in the range not to be too small in order to avoid dense signatures, but also should not be too high in order to still perform a good fit of the observed counts.

Besides these parameters, we also need to estimate the initial values of *beta* to be used during the estimation. We now show how to do this on the set of counts from 560 tumors provided in Nik-Zainal, Serena, et al. (2016).

```
data(patients)
head(patients)

##              A[C>A]A A[C>A]C A[C>A]G A[C>A]T A[C>G]A A[C>G]C A[C>G]G A[C>G]T A[C>T]A
## PD8623a      24      23       4      20      10      19       2      11      43
## PD8618a      29      19       2      15      11      12       2       8      31
## PD6418a      23      29       4      26      12       9       1      12      39
## PD7214a      19      20       5      18      11       5       4       7      30
## PD4968a      59      64       5      34      25      16       1      18      81
## PD4954a     102      87      19      82      80      48      13      88     117
##              A[C>T]C A[C>T]G A[C>T]T A[T>A]A A[T>A]C A[T>A]G A[T>A]T A[T>C]A A[T>C]C
## PD8623a      25      77      28      16      12      23      37      57       7
## PD8618a      17      91      24      10      10       8      18      50      23
## PD6418a      36     104      36      13      19      26      22      53      19
## PD7214a      22      65      21      12      18      17      18      41      12
```

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**Figure 1:** Visualization of the counts from patient PD10010a from the dataset published in Nik-Zainal, Serena, et al

##	PD4968a	57	246	70	26	46	53	66	93	39
##	PD4954a	53	125	79	64	48	37	52	97	41
##		A[T>C]G	A[T>C]T	A[T>G]A	A[T>G]C	A[T>G]G	A[T>G]T	C[C>A]A	C[C>A]C	C[C>A]G
##	PD8623a	30	42	12	6	8	16	32	21	6
##	PD8618a	31	59	1	3	6	7	18	15	3
##	PD6418a	32	57	7	4	6	8	24	19	2
##	PD7214a	23	43	4	5	3	9	15	13	1
##	PD4968a	47	85	17	6	7	16	45	27	10
##	PD4954a	64	97	26	11	38	41	100	90	18
##		C[C>A]T	C[C>G]A	C[C>G]C	C[C>G]G	C[C>G]T	C[C>T]A	C[C>T]C	C[C>T]G	C[C>T]T
##	PD8623a	26	13	13	4	19	32	40	73	31
##	PD8618a	14	4	9	4	3	21	33	61	30
##	PD6418a	23	15	15	4	8	42	36	71	51
##	PD7214a	10	7	5	2	12	31	32	48	40
##	PD4968a	53	13	15	14	27	82	88	145	79
##	PD4954a	83	77	48	22	65	90	64	84	99
##		C[T>A]A	C[T>A]C	C[T>A]G	C[T>A]T	C[T>C]A	C[T>C]C	C[T>C]G	C[T>C]T	C[T>G]A
##	PD8623a	10	10	10	11	14	15	15	23	3

## Extracting sparse mutational signatures via LASSO

##	PD8618a	6	4	7	5	11	17	10	13	4
##	PD6418a	6	13	9	14	19	8	13	14	6
##	PD7214a	9	4	3	6	8	9	9	8	0
##	PD4968a	13	25	20	36	22	24	29	37	7
##	PD4954a	41	48	55	57	46	53	40	74	17
##		C[T>G]C	C[T>G]G	C[T>G]T	G[C>A]A	G[C>A]C	G[C>A]G	G[C>A]T	G[C>G]A	G[C>G]C
##	PD8623a	7	14	15	13	20	3	13	9	2
##	PD8618a	4	6	5	17	13	9	14	2	10
##	PD6418a	8	8	14	20	20	9	16	5	6
##	PD7214a	7	8	12	24	7	2	8	6	6
##	PD4968a	10	7	24	35	25	12	30	9	13
##	PD4954a	19	37	42	53	67	13	42	40	28
##		G[C>G]G	G[C>G]T	G[C>T]A	G[C>T]C	G[C>T]G	G[C>T]T	G[T>A]A	G[T>A]C	G[T>A]G
##	PD8623a	1	6	33	24	61	29	3	11	6
##	PD8618a	0	5	23	33	67	29	3	12	4
##	PD6418a	3	5	35	39	94	34	7	12	9
##	PD7214a	3	4	31	47	50	24	1	8	6
##	PD4968a	1	11	68	62	190	65	8	21	14
##	PD4954a	1	63	72	69	85	67	19	29	22
##		G[T>A]T	G[T>C]A	G[T>C]C	G[T>C]G	G[T>C]T	G[T>G]A	G[T>G]C	G[T>G]G	G[T>G]T
##	PD8623a	6	15	10	6	23	1	3	5	4
##	PD8618a	5	17	10	8	23	0	1	1	0
##	PD6418a	8	36	11	22	22	1	3	3	6
##	PD7214a	8	26	12	8	18	1	3	2	2
##	PD4968a	18	43	19	29	35	6	3	3	11
##	PD4954a	49	61	37	34	54	12	7	32	36
##		T[C>A]A	T[C>A]C	T[C>A]G	T[C>A]T	T[C>G]A	T[C>G]C	T[C>G]G	T[C>G]T	T[C>T]A
##	PD8623a	34	24	8	31	22	20	1	32	119
##	PD8618a	22	17	10	25	15	14	1	30	47
##	PD6418a	34	23	5	35	9	12	2	24	43
##	PD7214a	14	22	6	24	9	7	2	24	52
##	PD4968a	79	57	9	87	64	27	8	120	464
##	PD4954a	92	109	11	106	158	89	17	279	166
##		T[C>T]C	T[C>T]G	T[C>T]T	T[T>A]A	T[T>A]C	T[T>A]G	T[T>A]T	T[T>C]A	T[T>C]C
##	PD8623a	59	52	98	29	15	6	18	25	17
##	PD8618a	26	37	37	20	4	3	13	21	12
##	PD6418a	56	52	65	31	9	9	15	25	17
##	PD7214a	38	41	62	14	8	7	16	19	14
##	PD4968a	177	157	337	127	20	19	42	41	42
##	PD4954a	114	48	150	62	44	27	71	58	38
##		T[T>C]G	T[T>C]T	T[T>G]A	T[T>G]C	T[T>G]G	T[T>G]T			
##	PD8623a	11	26	9	11	10	27			
##	PD8618a	12	16	4	3	6	11			
##	PD6418a	9	36	9	6	9	20			
##	PD7214a	13	22	4	10	8	19			
##	PD4968a	23	44	15	8	15	38			
##	PD4954a	30	57	40	29	37	62			

First, we can estimate the initial values of beta as follows.

## Extracting sparse mutational signatures via LASSO

```
starting_betas = starting.betas. estimation(x=patients,K=3:12,background_signature=background)
```

Then, we also need to explore the search space of values for the LASSO penalty in order to make a good choice. To do so, we can use the function `evaluate.lambda.range` to test different values as follows.

```
lambda_range = evaluate.lambda.range(x=patients,K=10,beta=starting_betas[[8,1]],  
                                     lambda_values=c(0.05,0.10))
```

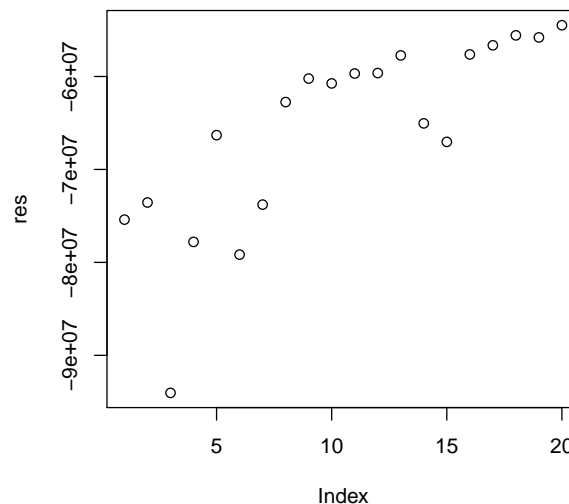
As the executions of these functions can be very time-consuming, we also provide as examples together with the package a set of pre-computed results by the two functions `starting.betas.estimation` and `evaluate.lambda.range` obtained with the commands above.

```
data(starting_betas_example)  
data(lambda_range_example)
```

To evaluate the best lambda range, we need to carefully consider the log-likelihood of the solutions at each iteration of our method. This can be done by exploiting the `as.` functions that we provide. Here are some examples.

```
# example of using too small a value of lambda  
# the log-likelihood is very unstable across the iterations  
res = as.loglik.progression.in.range(lambda.range.result=lambda_range_example,lambda_value=0.01)
```

```
plot(res)
```



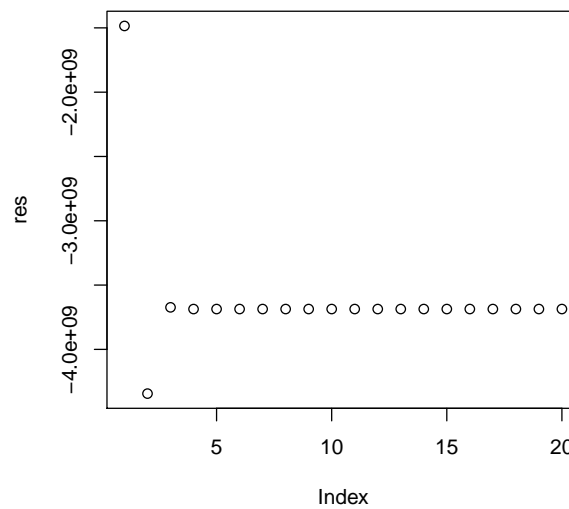
**Figure 2:** Example of using too small a value of lambda: the log-likelihood is very unstable across the iterations

```
# example of using too high a value of lambda  
# the log-likelihood drops after the first iteration  
res = as.loglik.progression.in.range(lambda.range.result=lambda_range_example,lambda_value=0.30)
```

```
plot(res)
```



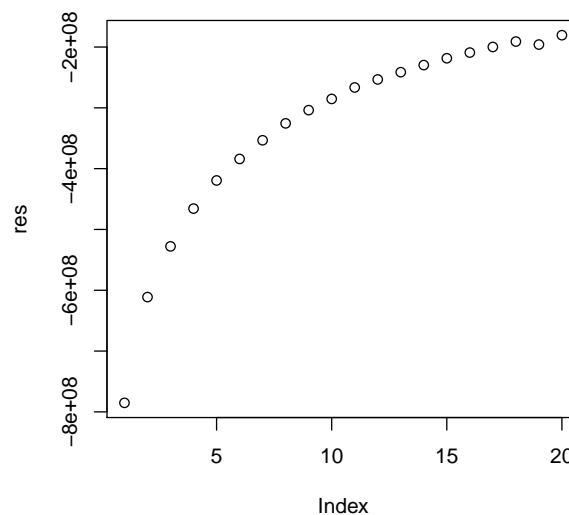
## Extracting sparse mutational signatures via LASSO



**Figure 3:** Example of using too high a value of lambda: the log-likelihood drops after the first iteration

```
# example of using a good value of lambda
# the log-likelihood is increasing across the iterations
res = as.loglik.progression.in.range(lambda.range.result=lambda_range_example, lambda_value=0.15)

plot(res)
```



**Figure 4:** Example of using a good value of lambda: the log-likelihood is increasing across the iterations

Now that we have evaluated all the required parameters, we need to decide which configuration of number of signatures and lambda value is the best. To do so, we rely on cross-validation.

## Extracting sparse mutational signatures via LASSO

```
cv = nmf.LassoCV(x=patients,K=3:10)
```

We notice that the computations for this task can be very time consuming, especially when many iterations of cross validations are specified (see manual) and a large set of configurations of the parameters are tested. To speed up the execution, we suggest using the parallel execution options. Also, to reduce the memory requirements, we advise splitting the cross validation in different runs, e.g., if one wants to perform 100 iterations, we would suggest making 10 independent runs of 10 iterations each. Also in this case, we provide as examples together with the package a set of pre-computed results obtained with the above command and the following settings:  $K = 3:10$ , cross validation entries = 0.10, lambda values =  $c(0.05, 0.10, 0.15)$ , number of iterations of cross-validation = 2.

```
data(cv_example)
```

We can now estimate the best configuration of the parameters in terms of median mean squared error by cross validation, where the best configuration is the one with lowest error.

```
res = as.mean.squared.error(cv_example)$median
res_best = which(res==res[which.min(res)],arr.ind=TRUE)
best_K = rownames(res)[res_best[1]]
best_lambda = colnames(res)[res_best[2]]
best_K

## [1] "5_signatures"

best_lambda

## [1] "0.1_lambda"
```

Finally, we can compute the signatures for the best configuration, i.e.,  $K = 5$  and  $\lambda = 0.10$ .

```
beta = starting_betas_example[["5_signatures","Value"]]
res = nmf.LassoK(x=patients,K=5,beta=beta,background=background,lambda_rate=0.10,
               iterations=5,num_processes=NA)

## Performing the discovery of the signatures by NMF with Lasso...
## Performing a total of 5 iterations...
## Progress 20%...
## Progress 40%...
## Progress 60%...
## Progress 80%...
## Progress 100%...
```

We conclude this vignette by plotting the discovered signatures.

```
signatures = as.beta(res)
signatures.plot(beta=signatures, xlabels=FALSE)
```

## Extracting sparse mutational signatures via LASSO

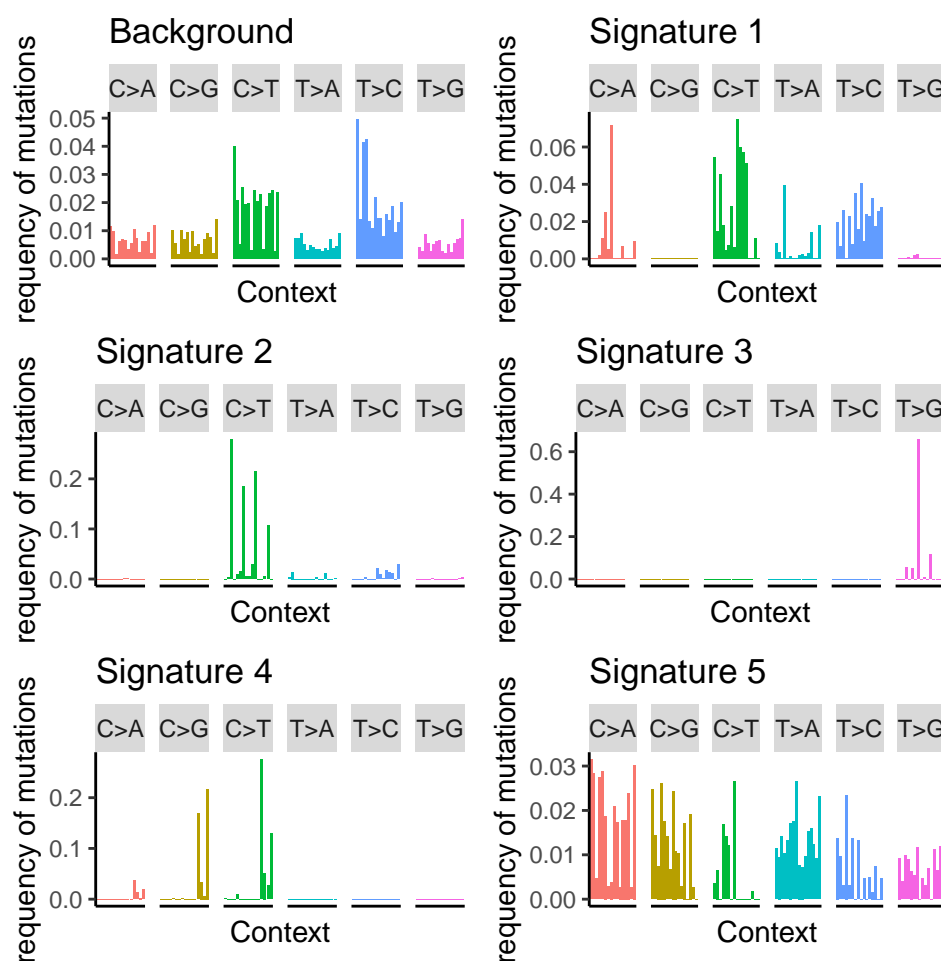


Figure 5: Visualization of the discovered signatures

## 4 sessionInfo()

- R version 3.5.1 Patched (2018-07-12 r74967), x86\_64-apple-darwin15.6.0
- Locale: C/en\_US.UTF-8/en\_US.UTF-8/C/en\_US.UTF-8/en\_US.UTF-8
- Running under: OS X El Capitan 10.11.6
- Matrix products: default
- BLAS:  
/Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRblas.0.dylib
- LAPACK:  
/Library/Frameworks/R.framework/Versions/3.5/Resources/lib/libRlapack.dylib
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, stats4, utils

## Extracting sparse mutational signatures via LASSO

- Other packages: BSgenome 1.50.0, BSgenome.Hsapiens.1000genomes.hs37d5 0.99.1, Biobase 2.42.0, BiocGenerics 0.28.0, Biostrings 2.50.0, GenomeInfoDb 1.18.0, GenomicRanges 1.34.0, IRanges 2.16.0, NMF 0.21.0, S4Vectors 0.20.0, SparseSignatures 1.2.0, XVector 0.22.0, bigmemory 4.5.33, cluster 2.0.7-1, knitr 1.20, pkgmaker 0.27, registry 0.5, rngtools 1.3.1, rtracklayer 1.42.0
- Loaded via a namespace (and not attached): BiocManager 1.30.3, BiocParallel 1.16.0, BiocStyle 2.10.0, DelayedArray 0.8.0, GenomeInfoDbData 1.2.0, GenomicAlignments 1.18.0, Matrix 1.2-14, R6 2.3.0, RColorBrewer 1.1-2, RCurl 1.95-4.11, Rcpp 0.12.19, Rsamtools 1.34.0, SummarizedExperiment 1.12.0, XML 3.98-1.16, assertthat 0.2.0, backports 1.1.2, bibtex 0.4.2, bigmemory.sri 0.1.3, bindr 0.1.1, bindrcpp 0.2.2, bitops 1.0-6, codetools 0.2-15, colorspace 1.3-2, compiler 3.5.1, crayon 1.3.4, data.table 1.11.8, digest 0.6.18, doParallel 1.0.14, dplyr 0.7.7, evaluate 0.12, foreach 1.4.4, ggplot2 3.1.0, glue 1.3.0, grid 3.5.1, gridBase 0.4-7, gridExtra 2.3, gtable 0.2.0, highr 0.7, htmltools 0.3.6, iterators 1.0.10, labeling 0.3, lattice 0.20-35, lazyeval 0.2.1, magrittr 1.5, matrixStats 0.54.0, munsell 0.5.0, nnlasso 0.3, nnls 1.4, pillar 1.3.0, pkgconfig 2.0.2, plyr 1.8.4, purrr 0.2.5, reshape2 1.4.3, rlang 0.3.0.1, rmarkdown 1.10, rprojroot 1.3-2, scales 1.0.0, stringi 1.2.4, stringr 1.3.1, tibble 1.4.2, tidyselect 0.2.5, tools 3.5.1, withr 2.1.2, xtable 1.8-3, yaml 2.2.0, zlibbioc 1.28.0