decompTumor2Sig

Identification of active mutational processes in individual tumors with the R package decompTumor2Sig

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The mutational processes responsible for the somatic mutations observed in tumor samples can be modeled by "**mutational signatures**" [1-3] which reflect the occurrences of base changes within their sequence contexts (i.e., in dependence on their flanking bases). The age-related mutations initiated by spontaneous deamination of 5-methylcytosine, for example, regard C>T transitions in the context of CpGs (because those are methylated; see Figures).

The first signature model described by **Alexandrov et al** [1,2] separately counts all possible nucleotide triplets whose central base is mutated (total of 6*4*4 = 96 possible triplet mutations, i.e., parameters).

The second model by **Shiraishi et al** [3] describes probabilistic mutational signatures in analogy to the way we model transcription factor binding motifs, i.e., considering the single bases of the motif as independent (much fewer parameters).

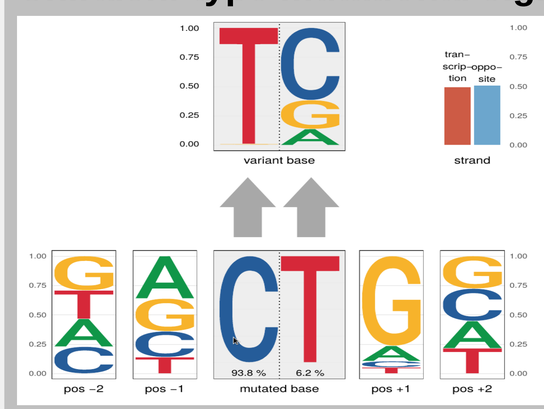
We developed a user-friendly R package, called **decompTumor2Sig** [4], that can be used to evaluate the contributions ("exposures") of both Alexandrov- and Shiraishi-type signatures to the somatic mutations found in an individual tumor.

Alexandrov-type mutational signatures



Figure from Alexandrov et al. (Nature 500:415-421, 2013; https://cancer.sanger.ac.uk/cosmic/signatures)

Shiraishi-type mutational signatures



Nucleotide change (central base)

C>A	C>G	C>T	T>A	T>C	T>G
0.004	0.006	0.928	0.009	0.038	0.015

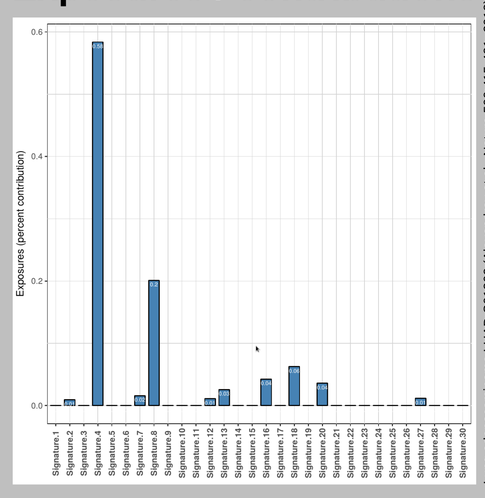
Flanking bases

Position	A	C	G	T
-2	0.237	0.228	0.293	0.242
-1	0.362	0.220	0.279	0.139
+1	0.131	0.053	0.764	0.052
+2	0.232	0.277	0.277	0.214

Transcription strand

plus strand	minus strand
0.493	0.507

Exposures / contributions



Lung adenocarcinoma LUAD-S01302 (Alexandrov et al., Nature 500:415-421, 2013)
Alexandrov / COSMIC signature 4 = smoking; signature 8 = unknown aetiology

Cross validation of predicted exposures with two datasets

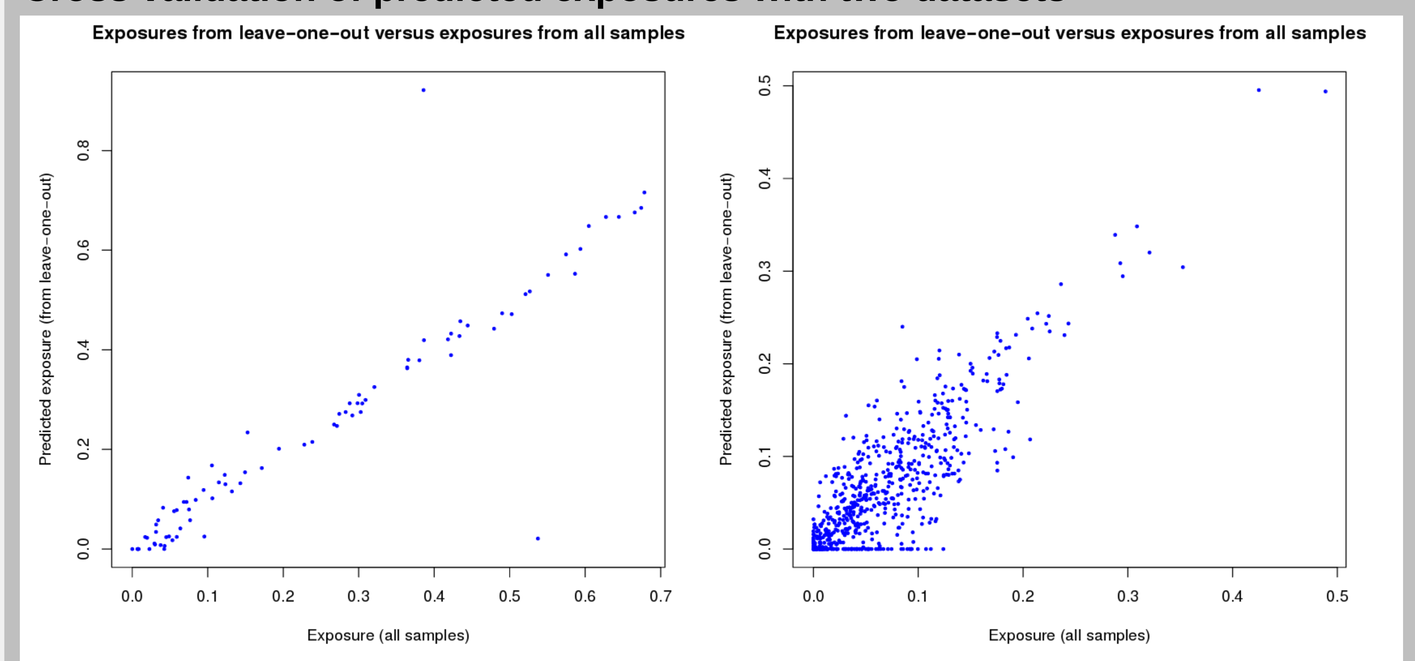


Figure 2: Comparison of contributions/weights ("exposures") predicted for individual tumors (`decompTumor2Sig`; y-axis) and collectively computed (`pmsignature`; x-axis). Left: leave-one-out test on 21 breast cancers ($r = 0.923$). Right: test set of 44 out of 435 tumors ($r = 0.807$).

Usage example

```
### decompTumor2Sig example for Shiraishi signatures ###

library(decompTumor2Sig)

# load signatures (or convert from pmsignature)
signatures <- loadShiraishiSignatures(sigfiles)

# load reference genome and transcript annotation
rG <- BSgenome.Hsapiens.UCSC.hg19:: [...]
tA <- TxDb.Hsapiens.UCSC.hg19.knownGene:: [...]

# read mutations of the individual tumor(s)
genomes <- loadGenomesFromVCF("tumor.vcf", numBases=5,
                      type="Shiraishi", trDir=TRUE,
                      refGenome=rG, transcriptAnno=tA)

# predict exposures for tumor(s)
exposures <- decomposeTumorGenomes(genomes, signatures)

exposures
#$PD4072a
#[1] 0.41464965 0.52231228 0.06303806 0.00000000
```

Mathematical approach to compute exposures (=weights, vector *w*) to signatures (matrix ***S***) for tumor genome (vector *g*):

The approach is based on classical quadratic programming because we can solve the following problem:

$$\text{minimize} \quad (g - \mathbf{S}w)^T(g - \mathbf{S}w) = g^Tg - g^T\mathbf{S}w - (\mathbf{S}w)^Tg + (\mathbf{S}w)^T\mathbf{S}w$$
$$\text{subject to} \sum_{s=1}^{K} w_s = 1, w_s \geq 0$$

or simplified:

$$\text{minimize} \quad -g^T\mathbf{S}w + \tfrac{1}{2}w^T\mathbf{S}^T\mathbf{S}w \qquad \text{subject to} \quad \sum_{s=1}^{K} w_s = 1, w_s \geq 0$$

[1] Alexandrov et al. (2013) Deciphering signatures of mutational processes operative in human cancer. *Cell Rep* **3**(1):246-259.
[2] Alexandrov et al. (2013) Signatures of mutational processes in human cancer. *Nature* **500**:415-421.
[3] Shiraishi et al. (2015) A simple model-based approach to inferring and visualizing cancer mutation signatures. *PLoS Genet* **11**(12):1005657.
[4] Krüger, Piro (2019) decompTumor2Sig: Identification of mutational signatures active in individual tumors. *BMC Bioinformatics* **20**(Suppl 4):152.

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