

# **Discovering Cancer Signatures via Non-Negative Matrix Factorization**

---

Nima Hejazi, Amanda Mok, Courtney Schiffman

2018-10-03

# Introduction

---

## Overview and Motivations

- Cancer biology is an extremely active area of research on all fronts, from molecular biology and bioinformatics to translational medicine.
- Statistical learning methods have met with great success when applied to complex and richly structured data, including images and text.
- Unsupervised clustering (e.g., matrix factorization) may help to learn about or discover fundamental common properties of various cancers.
- We review the key mathematical details of and explore the uses of matrix factorization (in particular, NMF) in cancer biology.

# Overview of Matrix Factorization

- Matrix factorization as unsupervised learning
- What can we learn about objects by matrix factorization?
- A general formulation of matrix factorization
- Various forms of matrix factorization: NMF, PCA, VQ
- Applications of matrix factorization: images
- Biological applications of matrix factorization

# Non-Negative Matrix Factorization

---

## What is Matrix Factorization?

- Suppose we have a *data matrix*  $V$  of dimension  $n \times m$ , each column of which is an  $n$ -vector of observations.
- A factorization of  $V$  produces two matrices  $\{W, H\}$  that approximately capture the information present in  $V$ .
- From linear algebra, we have  $V_{ij} \approx (WH)_{ij} = \sum_{a=1}^r W_{ia}H_{aj}$ .
- The dimensionality of the induced matrix factors is reduced wrt  $V$  – that is, let  $W$  be  $n \times r$  and  $H$  be  $r \times m$ .
- This can be viewed as a form of data compression when the rank  $r$  is small in comparison to  $n$  and  $m$ .
  - In particular,  $r$  is often chosen such that  $(n + m)r \leq nm$ .
  - Since we control  $r$ , we control the degree of data compression.

# What is Matrix Factorization?

- With the factorization  $V_{ij} \approx \sum_{a=1}^r W_{ia} H_{aj}$ , the matrix factors  $W$  and  $H$  each pick up different important aspects of  $V$ .
- When  $V$  is a  $n \times m$  matrix of images of faces, where each row corresponds to a pixel and each column an image:
  - the  $r$  columns of  $W$  may be thought of as basis images,
  - and each of the  $j$  columns of  $H$  is termed an encoding (coefficients to be applied to basis images).
- Various forms of matrix factorization place different types of constraints on the manner in which  $W$  and  $H$  are generated.

## Vector Quantization (VQ)

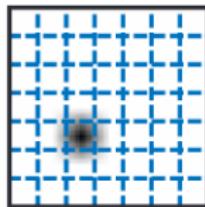
- **Constraint:** each column of  $H$  has a single entry equal to unity, with all other entries being set to zero.
- Since this is a constraint on the *encoding* columns, this results in each column of  $W$  being a distortion of the target image.
- Equivalently, each column of  $V$  is approximated by a single basis (column of  $W$ ).
- In terms of image processing/learning, VQ constraint is responsible for the decomposition learning *prototypical* faces.

# VQ: Prototypical Faces

VQ



X



=

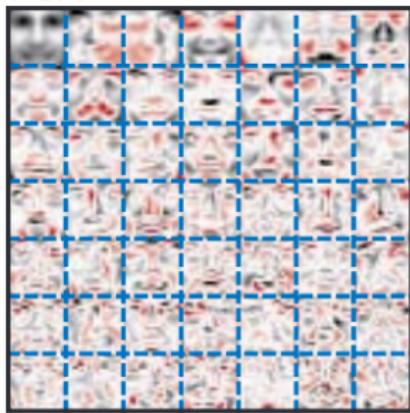


# Principal Components Analysis (PCA)

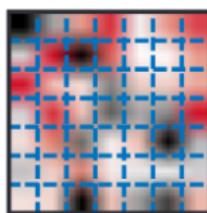
- **Constraint:** columns of  $W$  are set to be orthonormal; rows of  $H$  are set to be orthogonal to one another.
- Relaxation of VQ constraint: each face in our data set may be represented by a linear combination of basis images in  $W$ .
- This results in a distributed encoding of each of the face images in  $V$ ; basis images have been termed *eigenfaces*.
- Statistical interpretation: each eigenface represents the direction of largest variance within the sample data.
- Intuitive interpretation: ??? (Complex cancellations make eigenfaces very difficult to interpret.)

## PCA: *Eigenfaces*

PCA



X

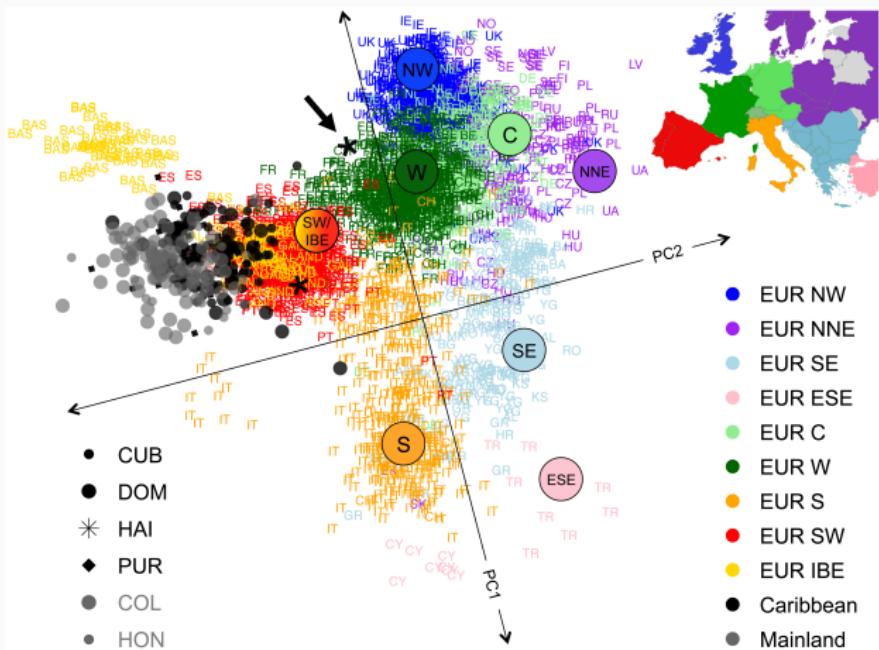


=



# PCA in Biology: Population Genetics in Europe

- Obligatory example: Novembre et al. (2008), "Genes mirror geography within Europe", *Nature*.



## What is NMF?

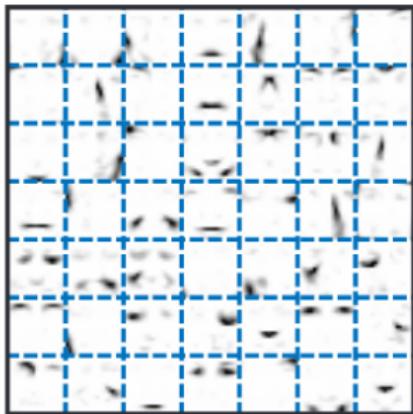
- **Constraint:** decomposition into matrix factors  $W$  and  $H$ , wherein any nonzero entries in  $W$  and  $H$  must be *positive*.
- Since there are no cancellations (unlike in PCA), multiple basis images may be used to reconstruct a face by additive linear combination.
- Since basis images and encodings are all positive, each basis image may be thought of as picking up a *part of a face*.

## What does non-negativity buy us?

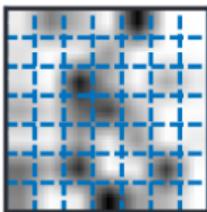
- In practice, NMF produces sparse basis and encoding matrices.
- The basis images are *non-global* – that is, groups of basis images pick up variation in a part of a face (e.g., eyes, mouth).
- The encodings are also sparse, since not all basis images are used in reconstituting any given face image.
- Thus, encodings are *sparsely distributed*, unlike the fully distributed encodings of PCA and the unary encodings of VQ.

## NMF: Parts of Faces

NMF



X



=



Original

## Overview of NMF

- Generally, NMF may be viewed as a generative model (neural network) for how the directly observable variables  $V$  arise from hidden variables  $H$ .
- Each hidden variable (in  $H$ ) may be thought of as co-activating a subset of the visible variables to reconstruct an example.
- In particular, a large and varied group of hidden variables may be combined additively to generate a whole example.

# Implementing NMF

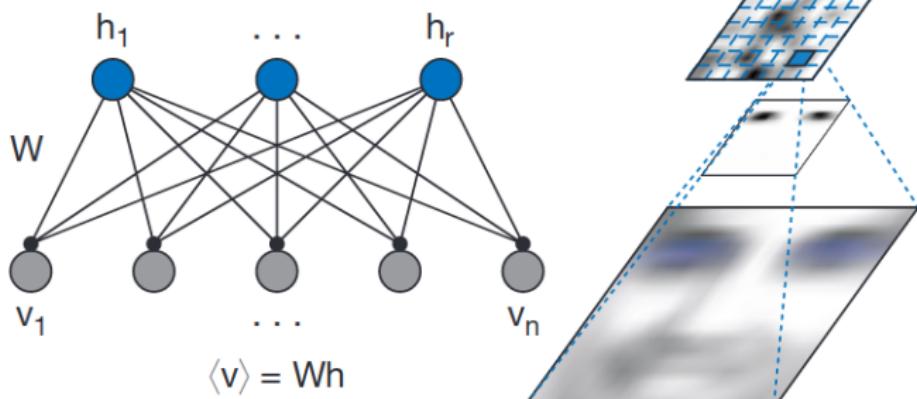
- Lee and Seung (1999) combine a set of update rules with an objective function

$$F = \sum_{i=1}^n \sum_{\mu=1}^m V_{i\mu} \log(WH)_{i\mu} - (WH)_{i\mu},$$

which converges to a local maximum with iterative updates under the given rules.

- Update rules:
  - $W_{ia} \leftarrow W_{ia} \sum_{\mu} \frac{V_{i\mu}}{(WH)_{i\mu}} H_{a\mu}$
  - $W_{ia} \leftarrow \frac{W_{ia}}{\sum_j W_{ja}}$
  - $H_{a\mu} \leftarrow H_{a\mu} \sum_i W_{ia} \frac{V_{i\mu}}{(WH)_{i\mu}}$
- Exact form of objective function is not too important – could also simply use a squared error objective function.

# NMF as a neural network



## NMF as a neural network

- Visible variables  $V$  generated by excitatory connections between hidden variables  $H$ .
- To learn values of the hidden variables  $H$ , an additional set of inhibitory feedback connections is required.
- The non-negativity constraints that define NMF capture intuitive biological notions of how neurons work, suggesting that NMFs may present a simplified model of how the brain learns parts of objects in perception.

## NMF in cancer biology

- So, we've now established that NMF finds *parts* of the input matrix through the non-negativity constraint it imposes on the matrix factors.
- This has important applications for exploring cancer biology; namely, applying NMF could help us detect *parts of tumors*.
- Interpretation is challenging: does this mean we're detecting subclonal populations?
- There's a whole lot more to come.

## A bit of biology (Amanda)

---

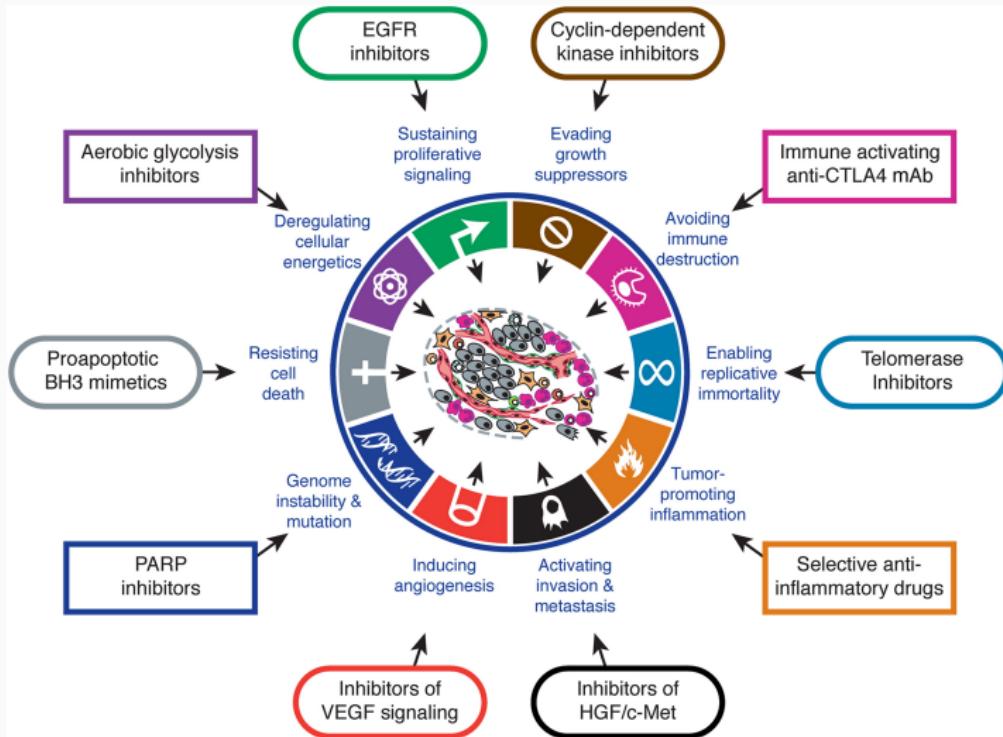
# What is cancer?

- Complex tissues with multiple cell types and interactions
- Characterized by unchecked somatic cell proliferation
- Normal cells acquire hallmark traits that enable them to become tumorigenic<sup>1</sup>

---

<sup>1</sup>Hanahan and Weinberg (2011)

# Hallmarks of Cancer



**Figure 1: Hallmarks of Cancer**

# Cancer is a genetic disease

- Germline mutations: inherited from parents
  - Mutations in tumor suppressor genes or oncogenes can predispose someone to develop cancer
- Somatic mutations: acquired over time in somatic cells
  - Endogenous: DNA damage as a result of metabolic byproducts
  - Exogenous: DNA damage as a result of mutagenic exposure
- Epigenetic modifications: no change to DNA sequence
  - DNA methylation
  - Histone modification
  - MicroRNA gene silencing

# Somatic mutations

- Rearrangements
- Copy number changes
- Indels
- Base substitutions
  - 6 types of substitutions (C>G, C>T, C>A, G>T, G>A, T>A)
  - 4 types of 5' base nucleotide
  - 4 types of 3' base nucleotide
  - Transcriptional strand

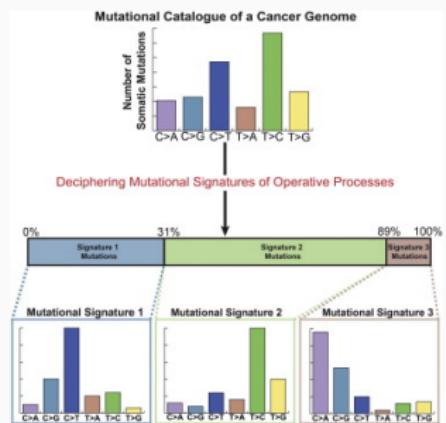
# Clonal evolution in cancer

## Applying NMF to mutational processes

---

# Alexandrov et al. (2013) characterize mutational processess as a blind source separation problem

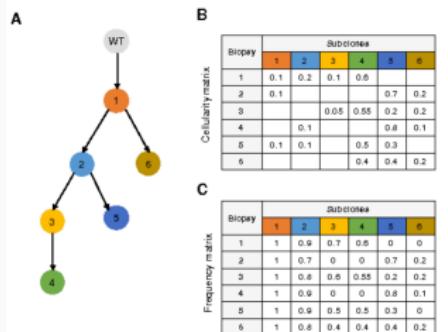
Mutational catalogs “are the cumulative result of all the somatic mutational mechanisms ...that have been operative during the cellular lineage starting from the fertilized egg...to the cancer cell.”



# How is the work of Alexandrov et al. (2013) related to inferring clonal evolution of tumors?

Goal: learn the “evolutionary history and population frequency of the subclonal lineages of tumor cells.”

- From SNV frequency measurements, try to infer the phylogeny and genotype of the major subclonal lineages.

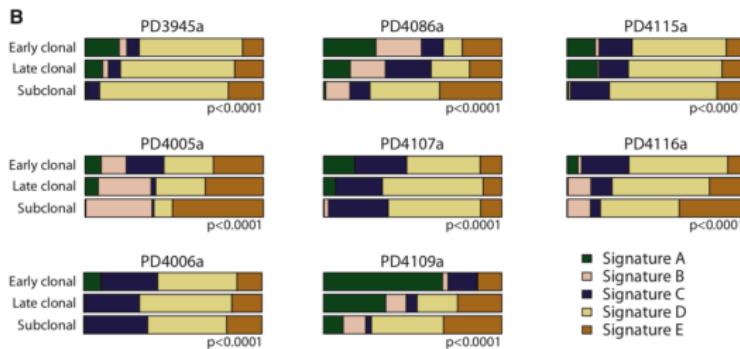


Shot 2018-10-01 at 8.18.04 PM.bb

# How is the work of Alexandrov et al. (2013). related to inferring clonal evolution of tumors?

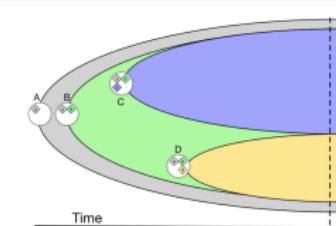
Different clonal mutations will have different signatures.

Shot 2018-10-01 at 8.19.57 PM.bb



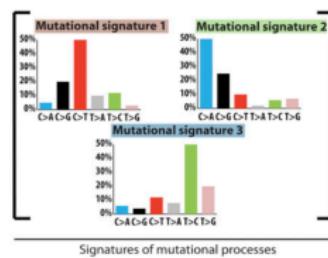
# Both works want to uncover driver mutations

Inferring clonal evolution of tumors



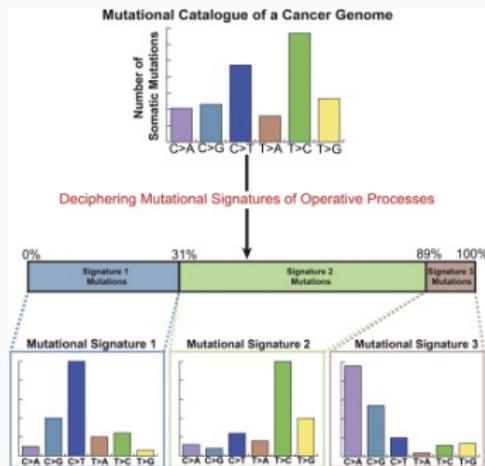
Shot 2018-10-01 at 8.46.46 PM.bb

Deciphering Signatures of mutational processes



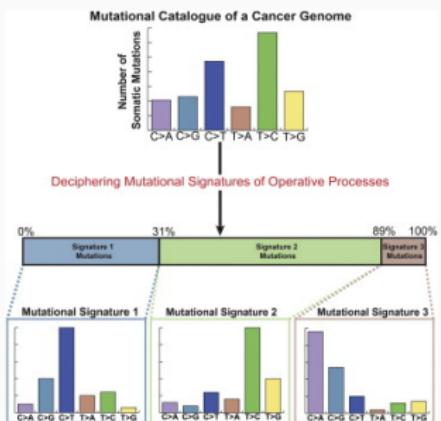
Shot 2018-10-01 at 8.48.29 PM.bb

Alexandrov et al. (2013) focus more on uncovering the cumulative mutational processes that make up a cancer genome, rather than the evolution of the tumor.



# NMF is a natural method for handling the BSS problem.

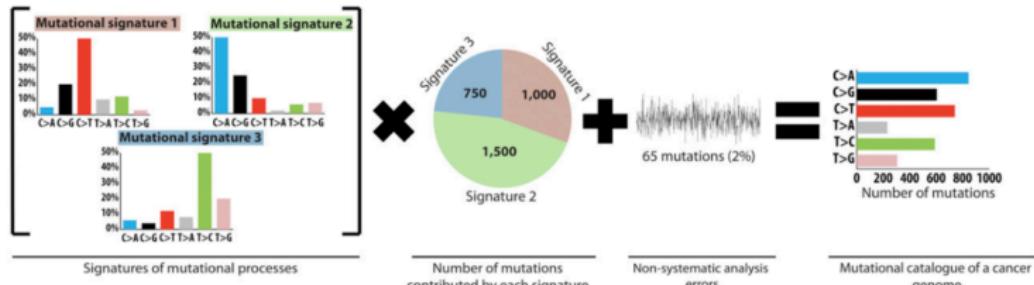
- Non-negative matrix entries.
- Want to learn the parts (mutational signatures of mutational processes) that add to the whole (mutational catalog).



# What are the basis vectors and encodings in the context of mutational processes?

Shot 2018-09-30 at 7.30.25 PM.bb

A



B

$$M \approx P \times E$$

$M$ ,  $K$  mutation types by  $G$  genomes

$P$ ,  $K$  mutation types by  $N$  mutation signatures

$E$ ,  $N$  mutation signatures by  $G$  genomes

# What are the basis vectors and encodings in the context of mutational processes?

Shot 2018-09-30 at 7.44.14 PM.bb

$$\begin{bmatrix} m_1^1 & m_2^1 & \cdots & m_{G-1}^1 & m_G^1 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ m_1^K & m_2^K & \cdots & m_{G-1}^K & m_G^K \end{bmatrix} \approx \begin{bmatrix} p_1^1 & p_2^1 & \cdots & p_{N-1}^1 & p_N^1 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ p_1^K & p_2^K & \cdots & p_{N-1}^K & p_N^K \end{bmatrix}$$

$$\times \begin{bmatrix} e_1^1 & e_2^1 & \cdots & e_{G-1}^1 & e_G^1 \\ \vdots & \vdots & \ddots & \vdots & \vdots \\ e_1^N & e_2^N & \cdots & e_{G-1}^N & e_G^N \end{bmatrix}$$

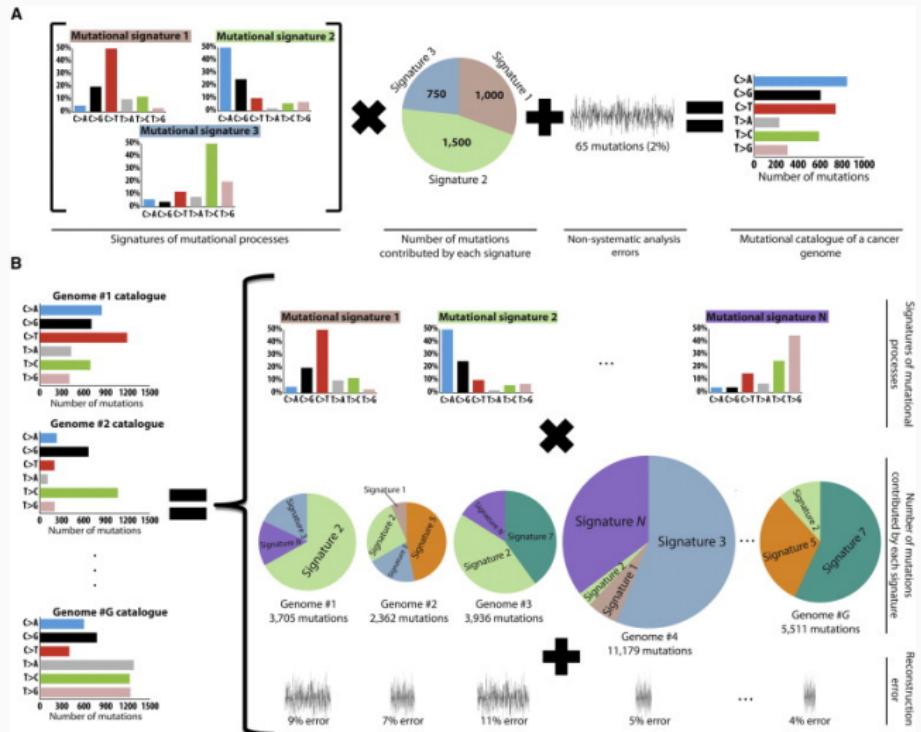
Shot 2018-10-01 at 8.25.26

$$m_g^i \approx \sum_{n=1}^N p_n^i e_g^n.$$

AM.bb

- $K$  = number of mutation types.
- $N$  = number of signatures.
- $G$  = number of genomes.

# The parts that make up the whole in mutational processes.



## Method for deciphering signatures of mutational processes

1. Input matrix  $M$  of dimension  $K$  (mutation types) by  $G$  (genomes).
2. Remove rare mutations ( $\leq 1\%$ ).
3. Monte Carlo bootstrap resampling.

## Method for deciphering signatures of mutational processes.

4. Apply the multiplicative update algorithm until convergence.

- Repeat steps 3 and 4  $I$  times, each time storing  $P$  and  $E$ .
- Typical values  $I = 400 - 500$

Shot 2018-09-28 at 8.35.41 AM.bb

$$\min_{P \in \mathbf{M}_{\mathbf{R}_+}^{(K,N)}, E \in \mathbf{M}_{\mathbf{R}_+}^{(N,G)}} \|\breve{M} - P \times E\|_F^2$$

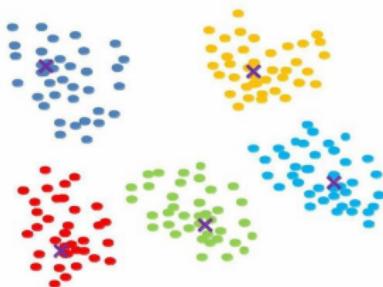
$$e_G^N \leftarrow e_G^N \frac{[P^T \breve{M}]_{N,G}}{[P^T P E]_{N,G}}$$

$$p_N^K \leftarrow p_N^K \frac{[\breve{M} E^T]_{K,N}}{[P E E^T]_{K,N}}$$

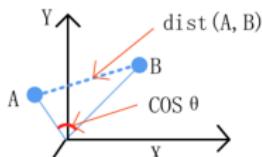
Shot 2018-09-28 at 8.35.52 AM.bb

## Method for deciphering signatures of mutational processes

5. Cluster the signatures (columns of  $P$  matrix) from the  $I$  iterations into  $N$  clusters, one signature per cluster for each of the  $I$  matrices.
  - This automatically clusters the exposures.
  - Use cosine similarity for clustering.

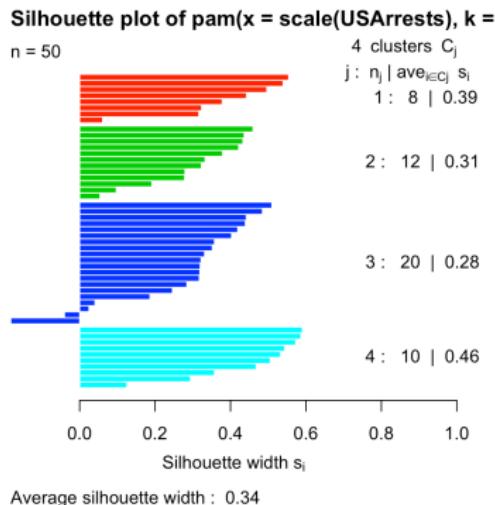


Shot 2018-10-02 at 8.12.01 AM.bb



# Method for deciphering signatures of mutational processes

6. Create the iteration averaged centroid matrix,  $\bar{P}$ , by averaging the signatures within each cluster.
7. Evaluate the reproducibility of the signatures by calculating the average silhouette width over the  $N$  clusters.



# Method for deciphering signatures of mutational processes

8. Evaluate the accuracy of the approximation of  $M$  by calculating the Frobenius reconstruction errors.

$$\min_{P \in \mathbf{M}_{\mathbb{R}_+}^{(K,N)}, E \in \mathbf{M}_{\mathbb{R}_+}^{(N,G)}} \|\tilde{M} - P \times E\|_F^2$$

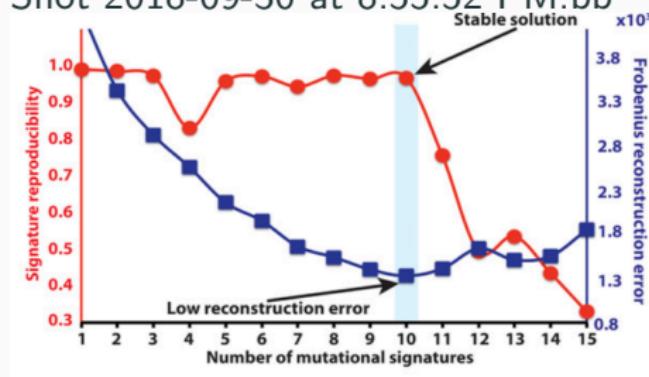
Shot 2018-09-28 at 8.35.41 AM.bb

9. Repeat steps 1-8 for different values of  $N = 1, \dots, \min(K, G) - 1$ .

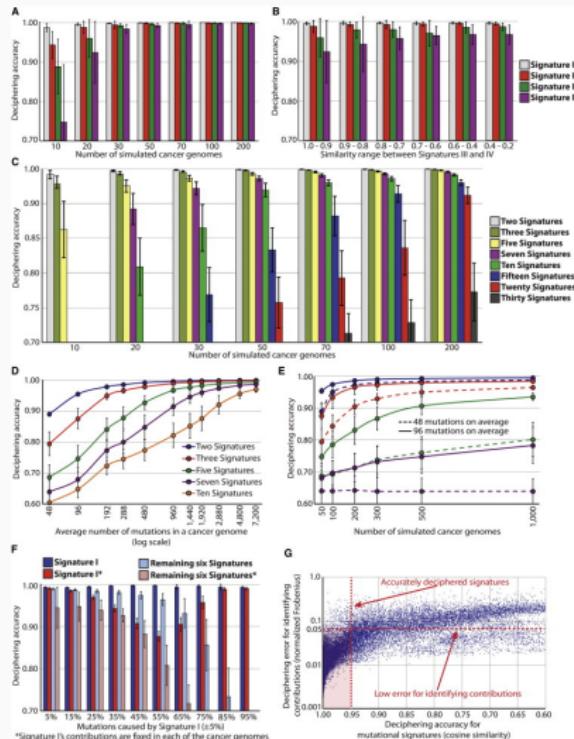
# Method for deciphering signatures of mutational processes

10. Choose an  $N$  corresponding to highly reproducible mutational signatures and low reconstruction error.

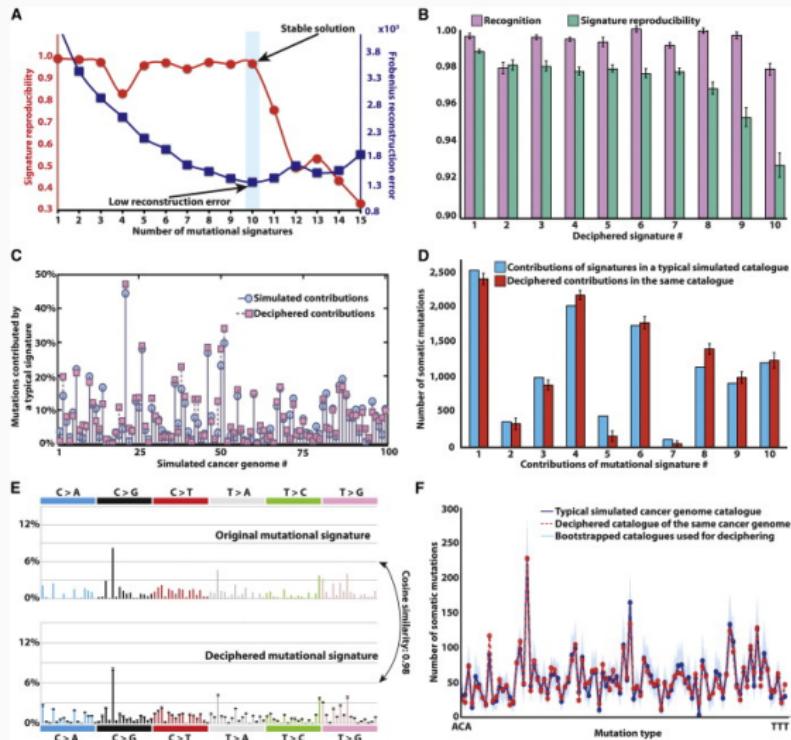
Shot 2018-09-30 at 8.55.52 PM.bb



# The method is affected by the number of genomes, uniqueness of signatures, and number of mutations



# The method recovers 10 signatures in a simulated cancer genome dataset



## Findings (Amanda)

- ...
- ...
- ...

We've talked enough (Amanda)

---

# Discussion

- ...
- ...
- ...

## References

- Alexandrov, Ludmil B, Serena Nik-Zainal, David C Wedge, Peter J Campbell, and Michael R Stratton. 2013. "Deciphering Signatures of Mutational Processes Operative in Human Cancer." *Cell Reports* 3 (1). Elsevier: 246–59.
- Hanahan, Douglas, and Robert A Weinberg. 2011. "Hallmarks of Cancer: The Next Generation." *Cell* 144 (5). Elsevier: 646–74.
- Lee, Daniel D, and H Sebastian Seung. 1999. "Learning the Parts of Objects by Non-Negative Matrix Factorization." *Nature* 401 (6755). Nature Publishing Group: 788.
- Novembre, John, Toby Johnson, Katarzyna Bryc, Zoltán Kutalik, Adam R Boyko, Adam Auton, Amit Indap, et al. 2008. "Genes Mirror Geography Within Europe." *Nature* 456 (7218). Nature Publishing Group: 98.