Signatures of mutational processes in human cancer

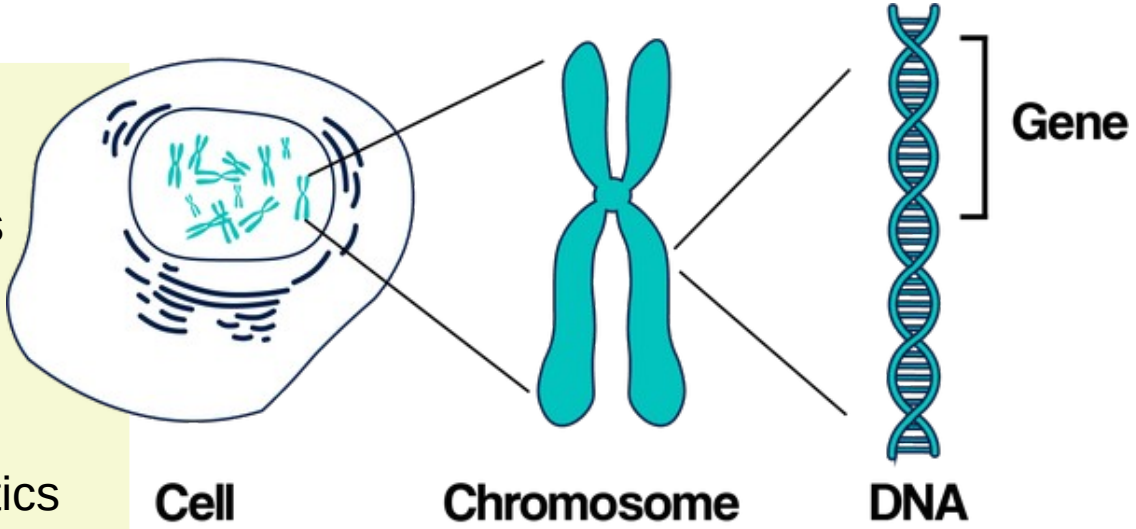
Noel László Plaszkó

Data science laboratory
Supervisor: Orsolya Pipek

Chromosomes, genes and mutations (for dummies...)

Chromosomes

- thread-like structures in cells
- 46 chromosomes (arranged in 2 sets of 23)
- one set from your mother, one from your father
- determine physical characteristics
- contain genes



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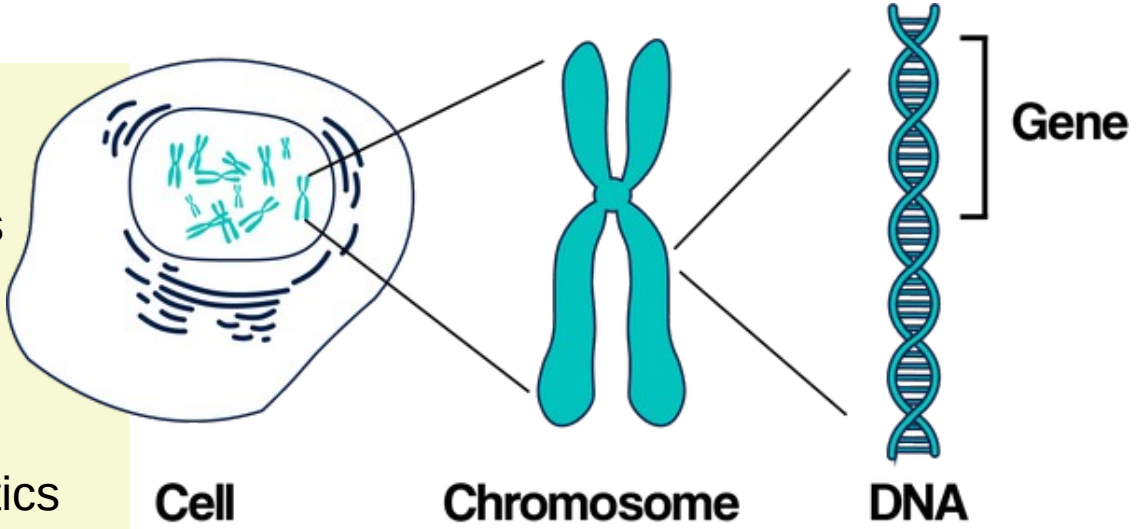

Genes

- the basic physical unit of inheritance
- control how your cells work by making proteins
- must have the correct instructions for making its protein
- allows the protein to perform the correct function for the cell

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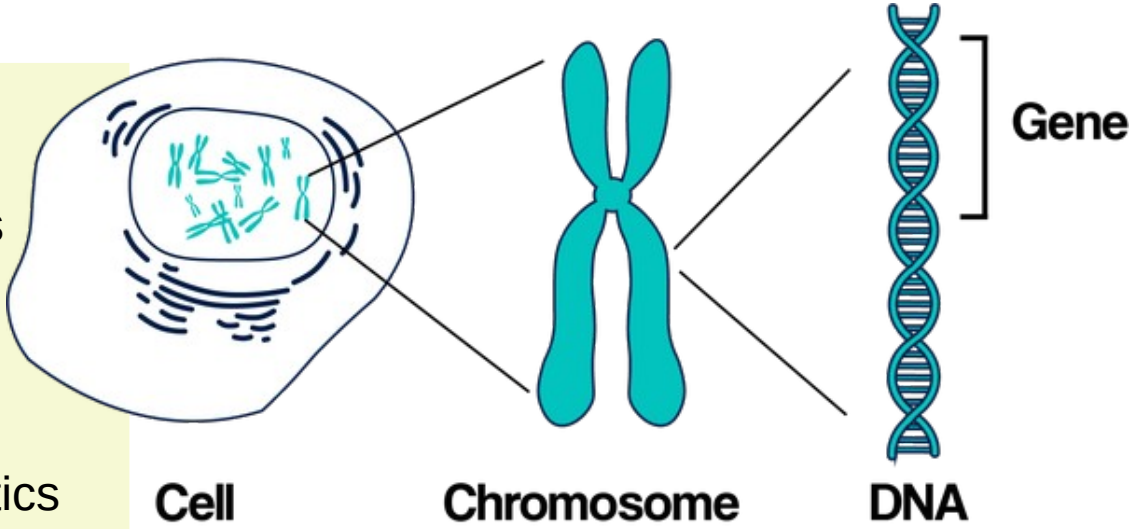

Genes

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Proteins

- act as messengers for the cell

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Chromosomes, genes and mutations (for dummies...)

- Genes in cells can mutate
- Due to mutation:
  - ➔ Abnormal protein is created
  - ➔ Or protein's formation is prevented

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Cancer is caused
by somatic mutations of the DNA in the tumor cells.

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DNA sequencing and mutations

DNA sequencing:

- determine the order of the four bases in DNA (adenine, guanine, cytosine, and thymine)

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Aim of the project

Investigation of somatic mutations (substitutions)
(somatic: occur from damage to genes in a particular cell)

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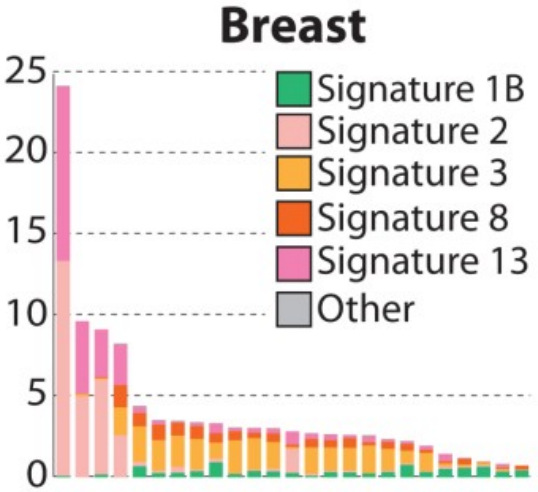

Decomposing the mutational spectra of each sample to a weighted combination of the operating mutational processes (signatures) in a specific disease

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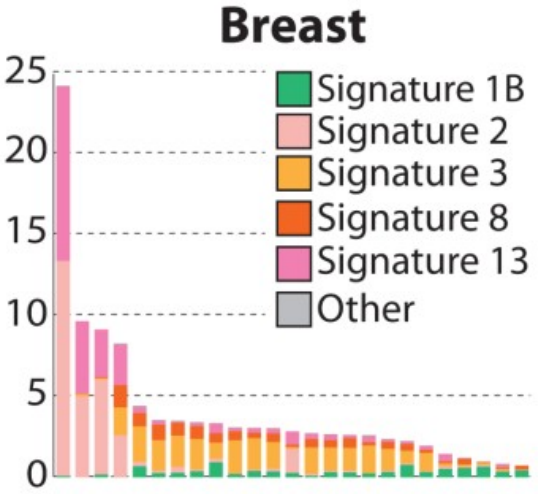
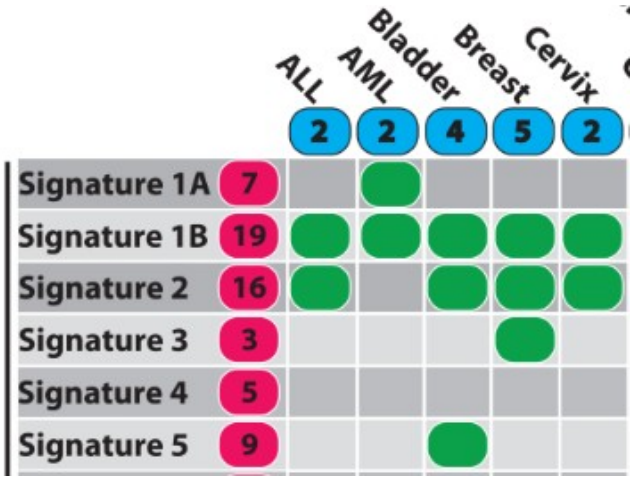


Decomposing the mutational spectra of each sample to a weighted combination of the operating mutational processes (signatures) in a specific disease

Clustering of these signatures across disease types



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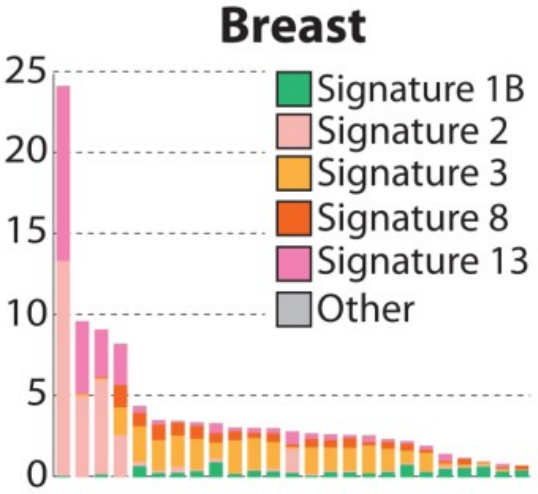

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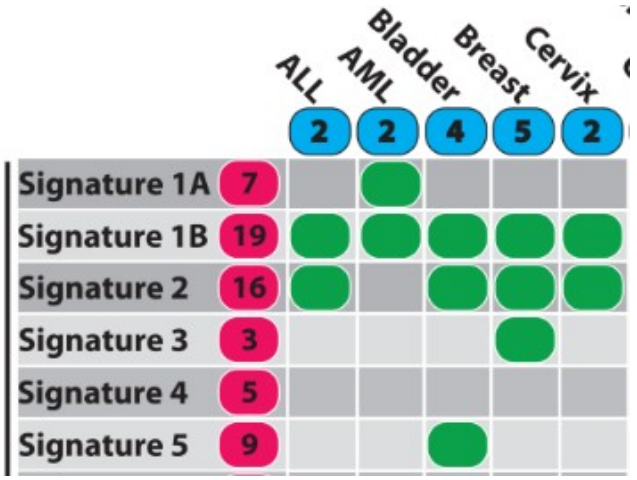

General task:

Perform the analysis described in [4] to identify
"mutational signatures"
in sample sets of different cancer types

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Datasets

1) Lists of somatic mutations for different cancer types

- LUAD (lung adenocarcinoma)
- LUSC (lung squamous cell carcinoma)
- KIRC (kidney renal clear cell carcinoma)
- OV (ovarian cancer)
- PRAD (prostate adenocarcinoma)

Task: understand mutational catalogs, Mutation Annotation Format (MAF) data structure
Source: https://github.com/sdam-elte/dslab2021/tree/main/projects/07-mutational_signatures_in_cancer

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Data storage:
- Not large (<300MB)
- Huge amount of rows
- Huge amount of character sequences

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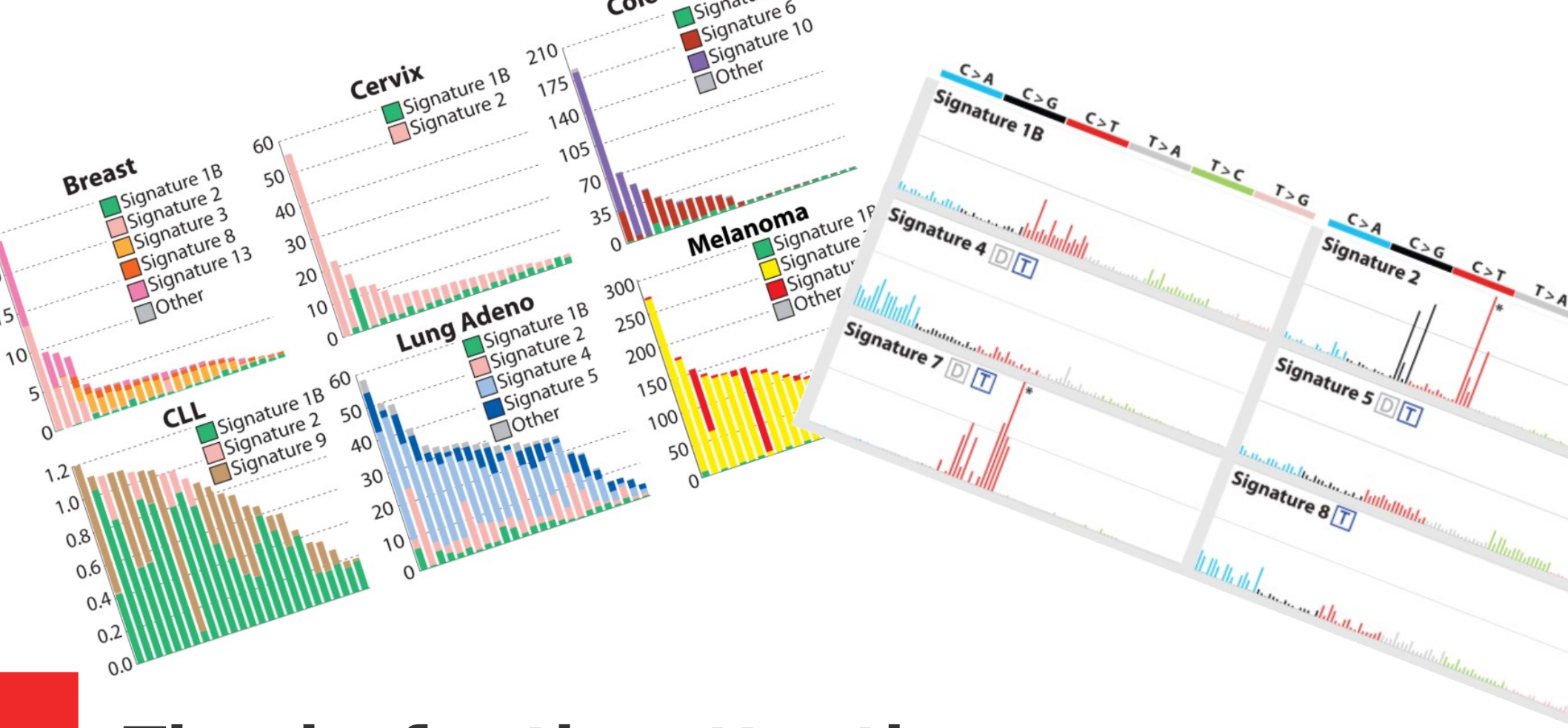
Tools:
Python, Pandas, sklearn (non-negative matrix factorization), Matplotlib/Seaborn/Bokeh/Plotly, numPy

sequences



Thanks for the attention