SigProfilerAssignment

Presented by:

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Cancer Genome Analysis

12 – 16 September 2022 – Virtual course

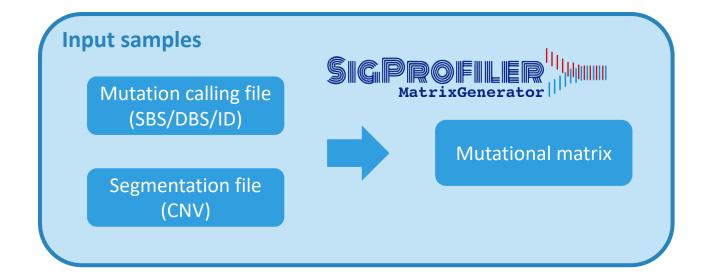




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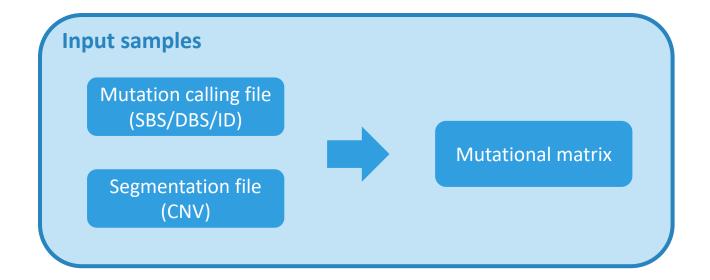
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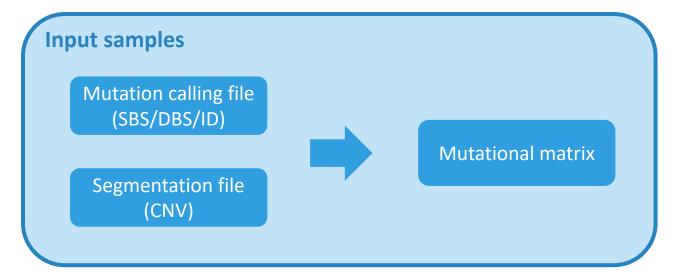


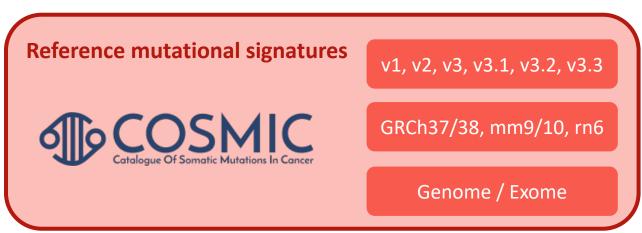








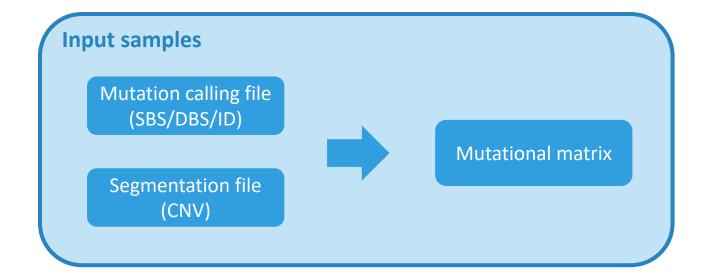




$$\mathbf{M} = \mathbf{S} \times \mathbf{A}$$

- t mutational contexts
- **n** samples
- **k** signatures







Reference mutational signatures

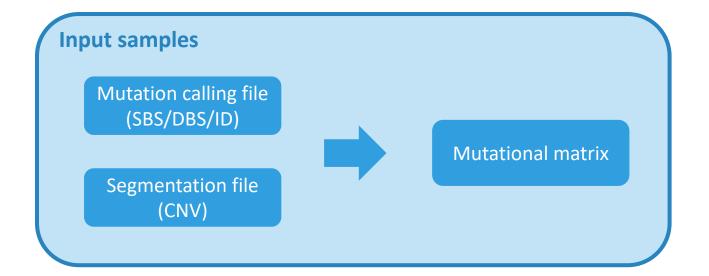
v1, v2, v3, v3.1, v3.2, v3.3

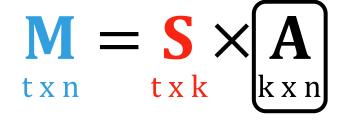
GRCh37/38, mm9/10, rn6

Genome / Exome

- t mutational contexts
- **n** samples
- **k** signatures







Reference mutational signatures

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v1, v2, v3, v3.1, v3.2, v3.3

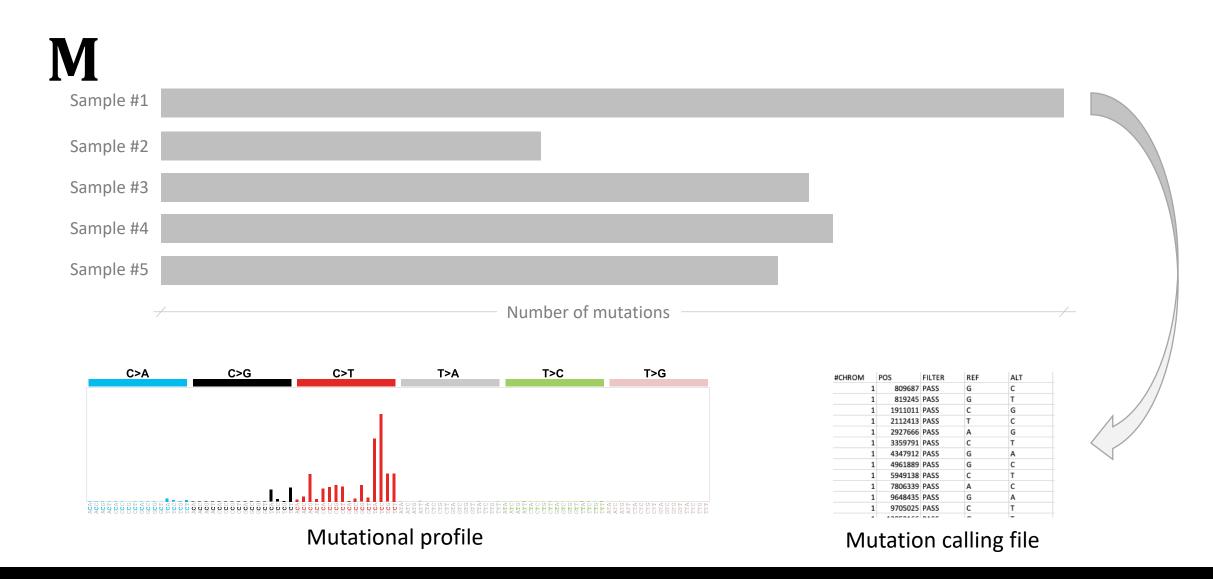
GRCh37/38, mm9/10, rn6

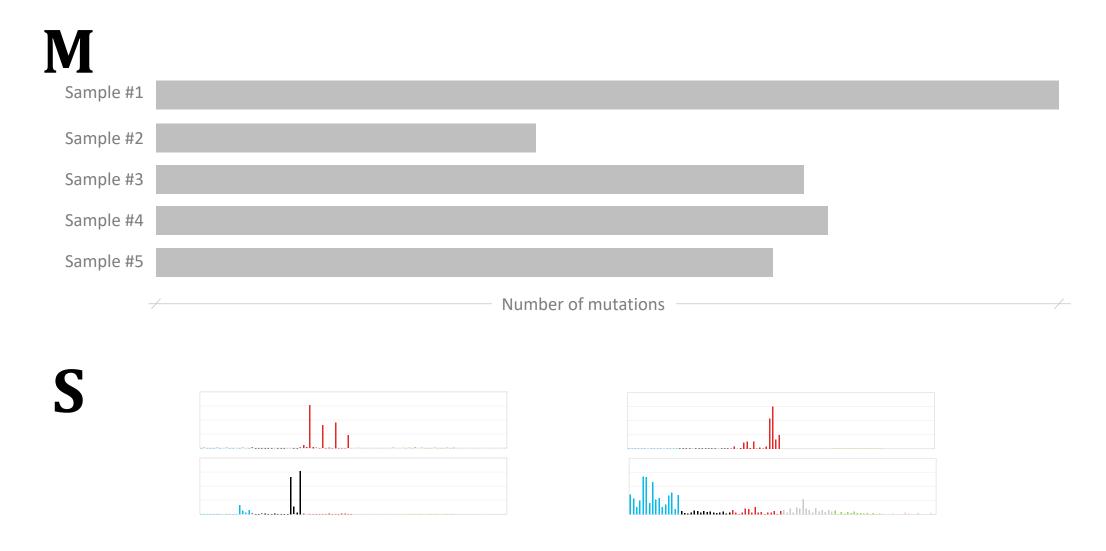
Genome / Exome

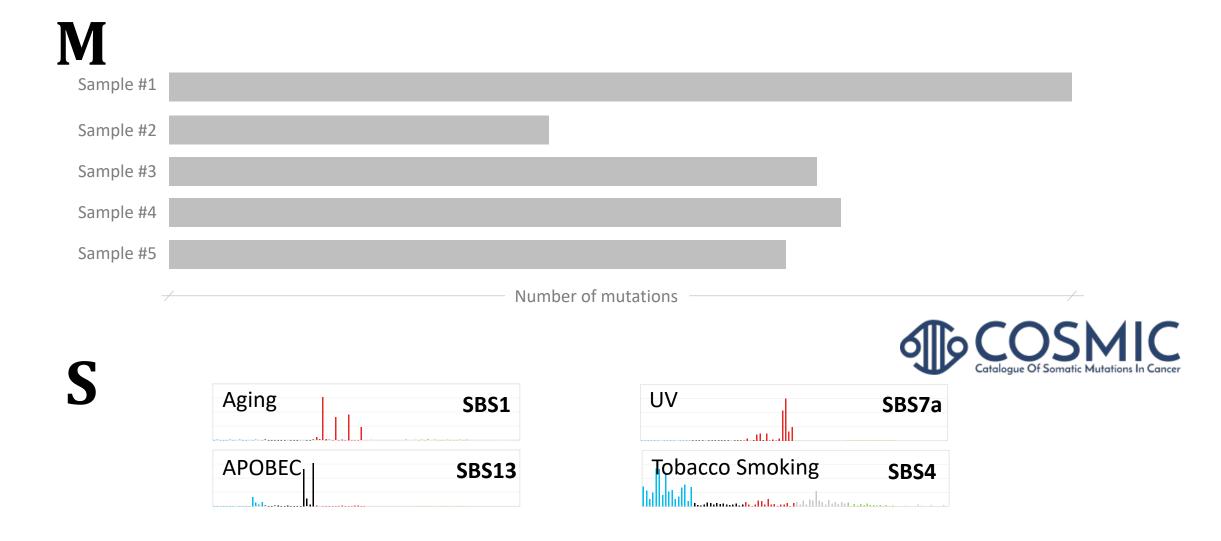
t mutational contexts

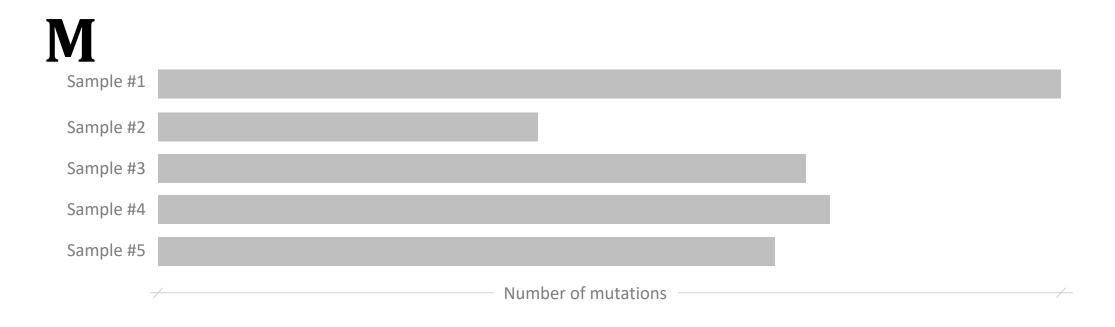
n samples

k signatures

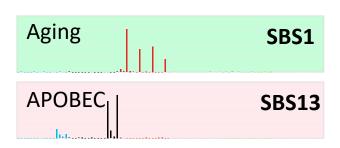


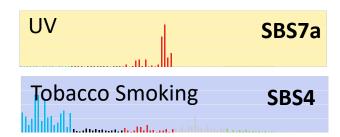


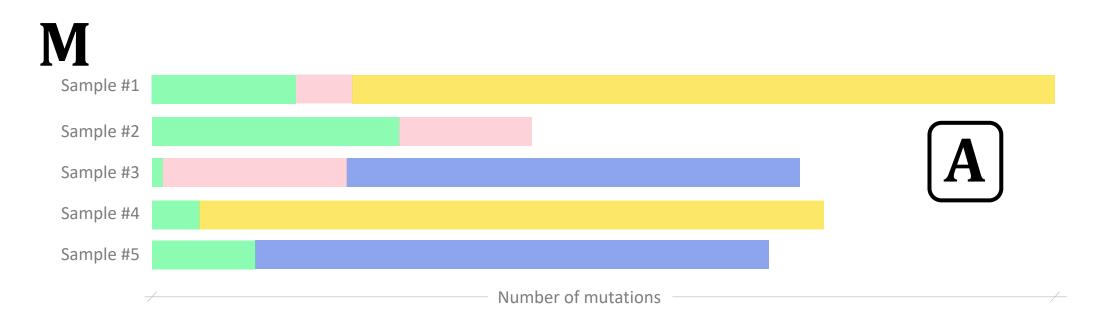


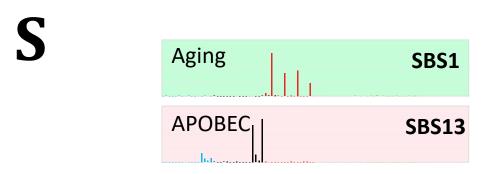














Useful links – SigProfilerAssignment

- GitHub repository
 https://github.com/AlexandrovLab/SigProfilerAssignment
- Python package (PyPI)
 https://pypi.org/project/SigProfilerAssignment/
- COSMIC Mutational Signatures website https://cancer.sanger.ac.uk/signatures/