Hello World

Nadezda Volkova

17.08.2016

Who am I

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Nadia Volkova

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Nadia Volkova

- MSU - Cryptography
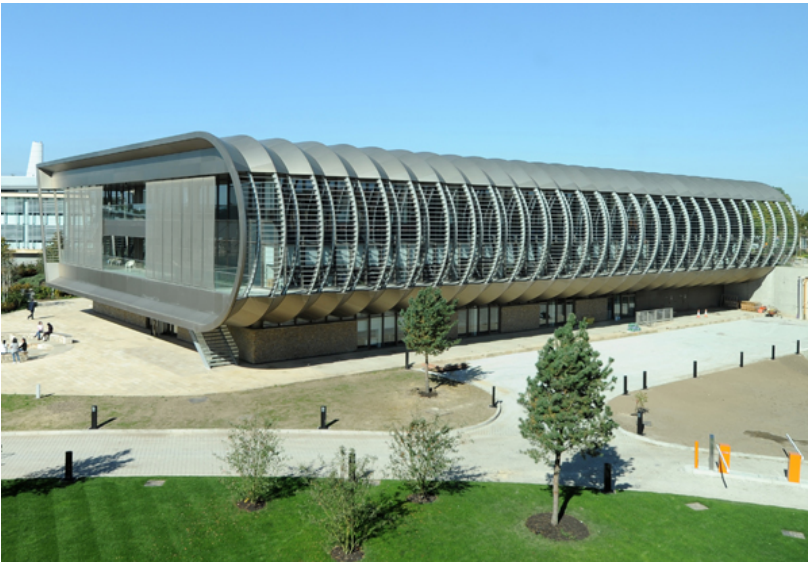
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- MSU - Cryptography

- TUM - Biostatistics

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- MSU - Cryptography

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- EBI – Cancer genomics

What do I do

- Programming for genomics: stats in R and python

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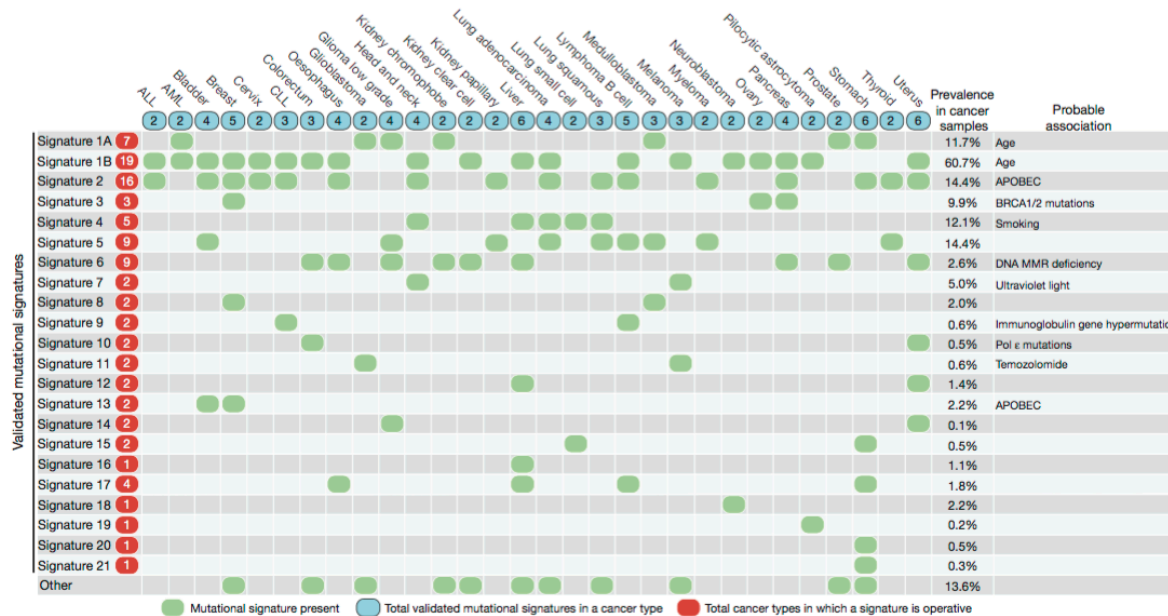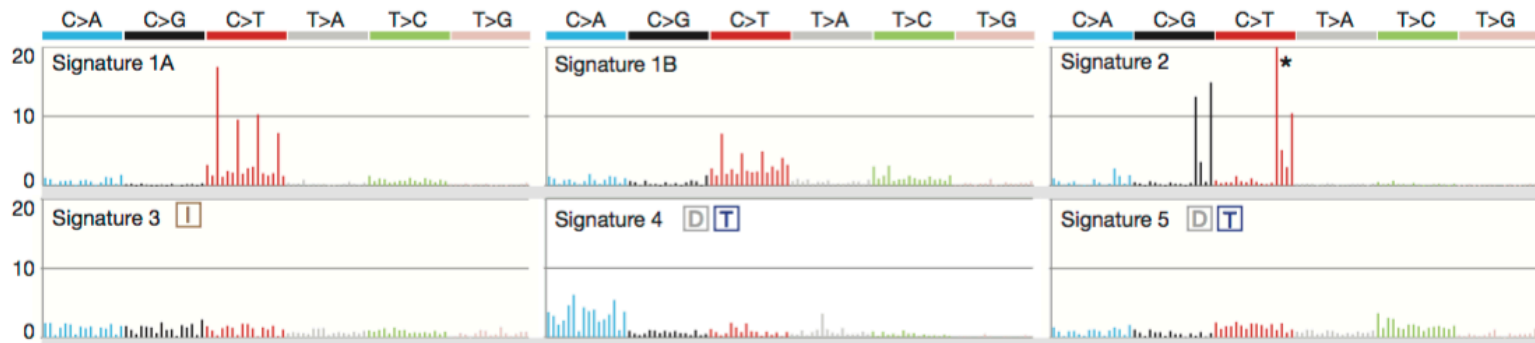- Little bit of biology

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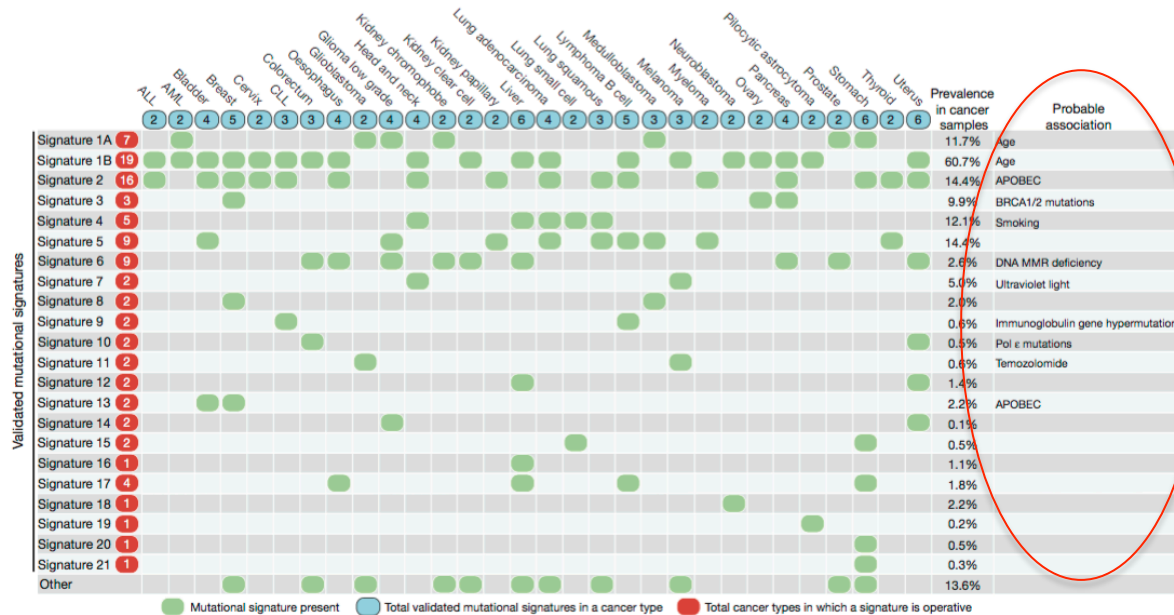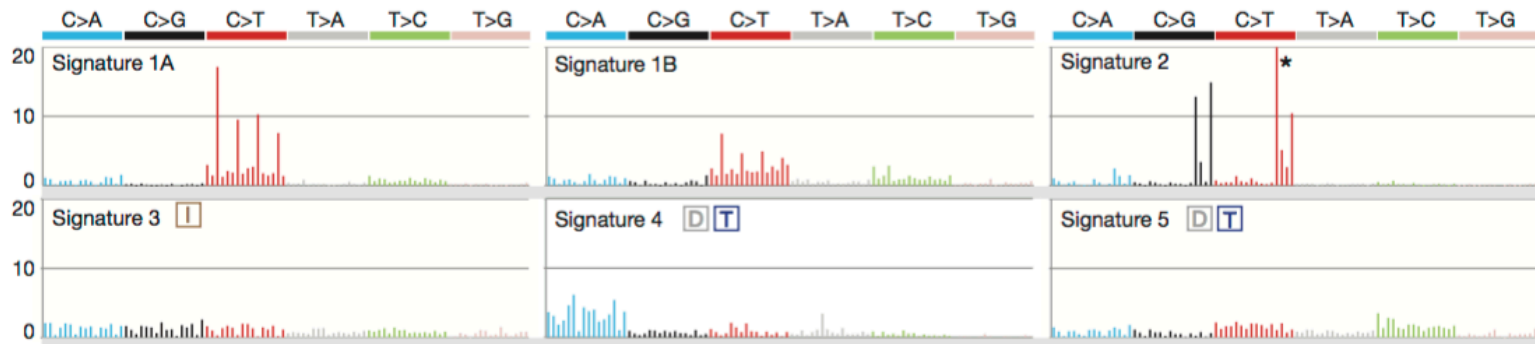- Little bit of biology
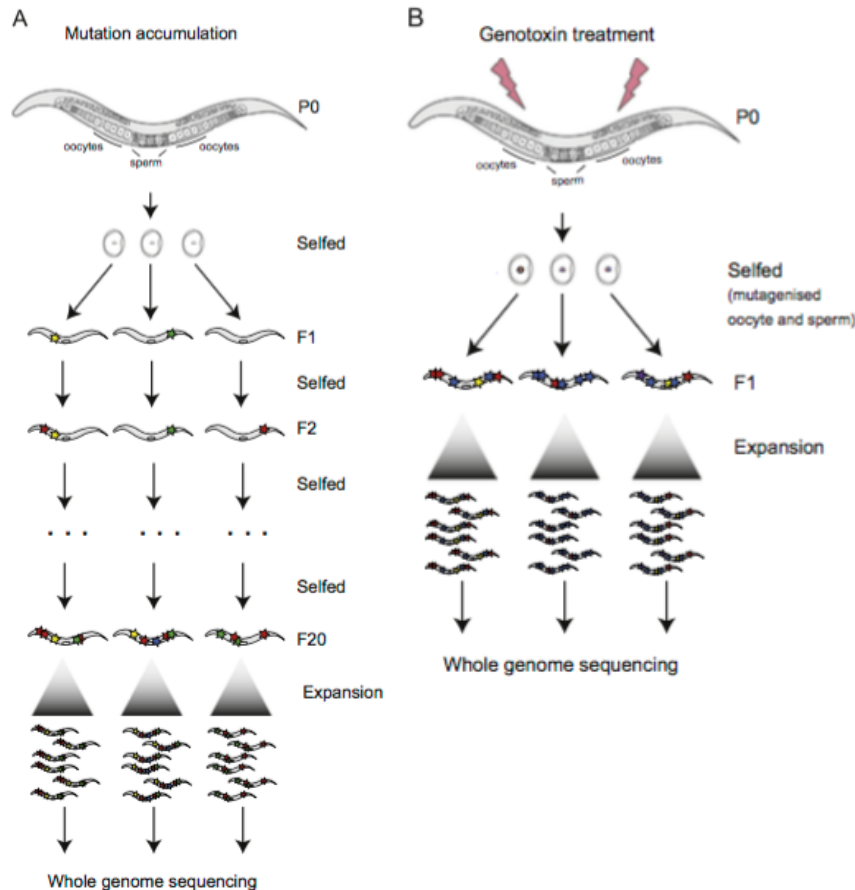
My work: Background

Cancer and mutational signatures

Alexandrov et al. 2013

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Cancer and mutational signatures
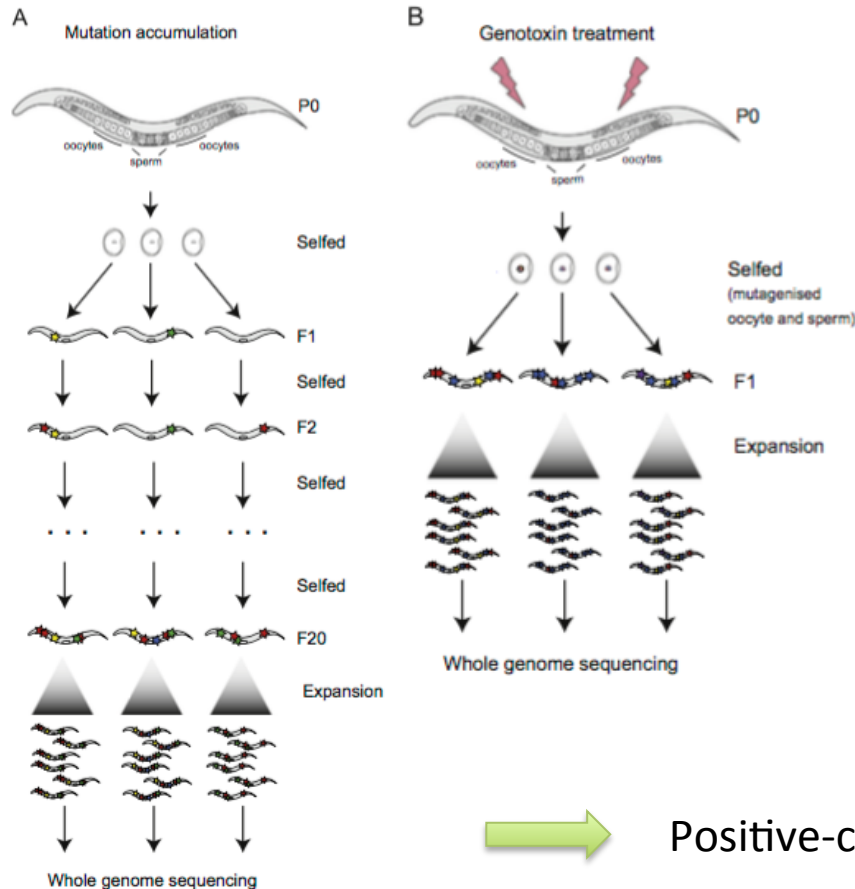

Alexandrov et al. 2013

Experiments and model

Some numbers:
- 2206 samples
- 592 experiments
- 9 genotoxins
- 58 genetic backgrounds
- 17 variant types
- 113 significant gene-mutagen interactions

Meier, Gartner 2014

Experiments and model

A Mutation accumulation

B Genotoxin treatment

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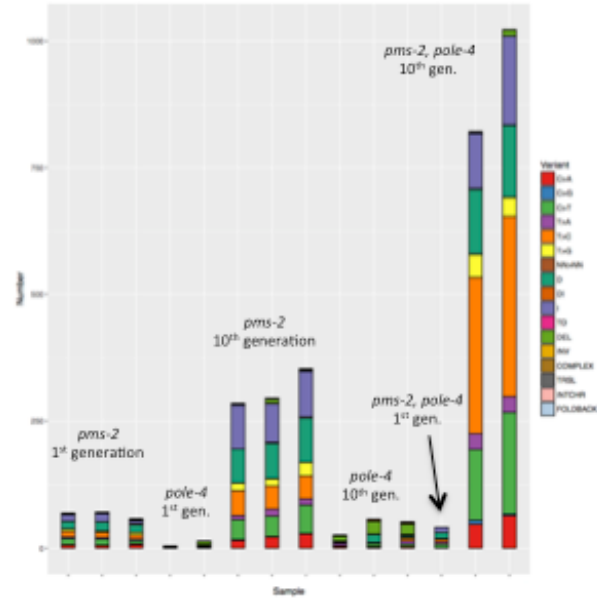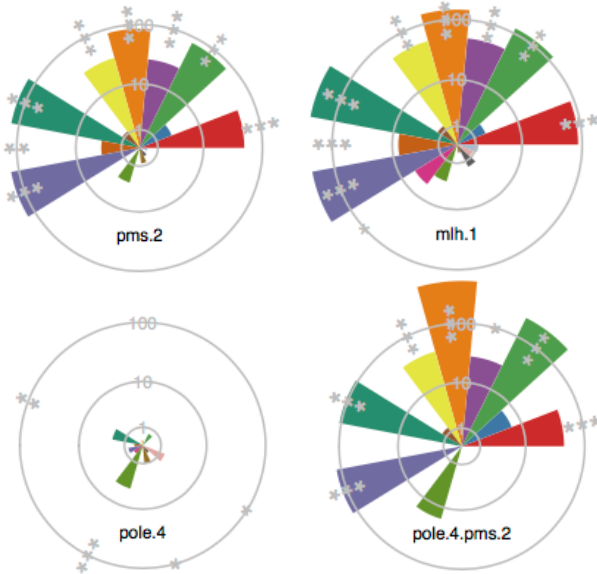- 17 variant types
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Positive-constrained additive Poisson model:

$$E[Y_j] = \lambda_j = X\beta_j^T = X_{gen}\beta_{j,gen}^T + X_{mut}\beta_{j,mut}^T + X_{int}\beta_{j,int}^T, \beta_j \in \mathbb{R}_k^+$$

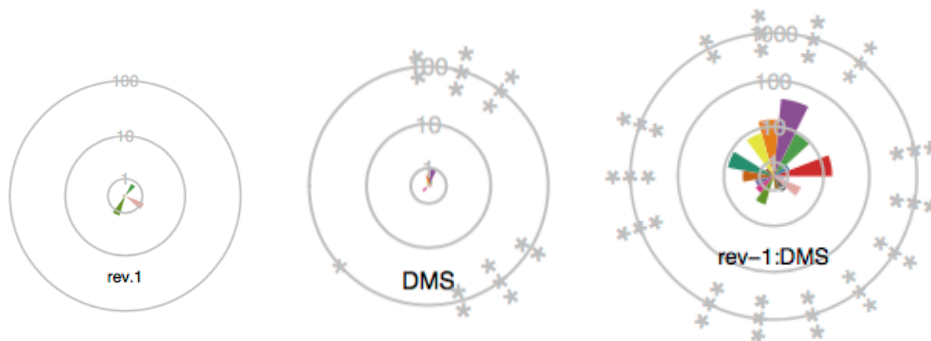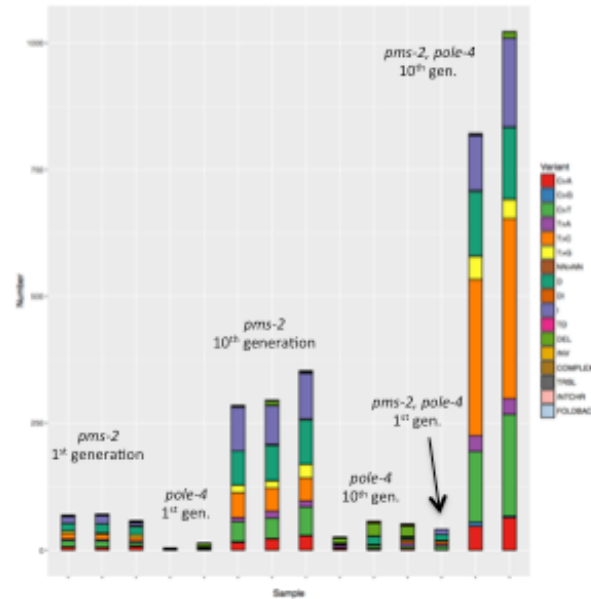Meier, Gartner 2014
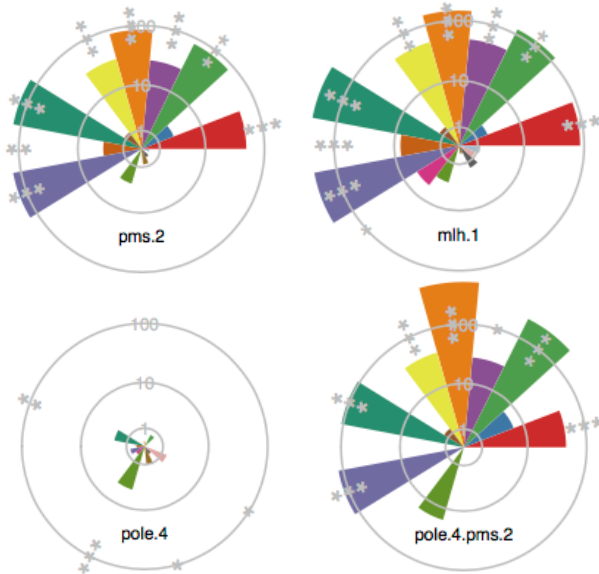
Beautiful pictures

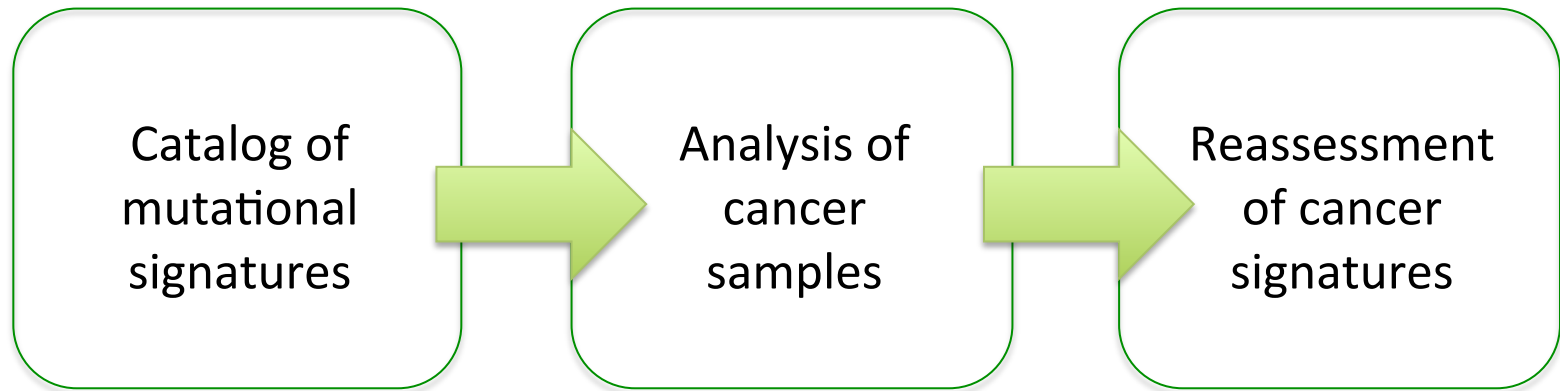# Beautiful pictures

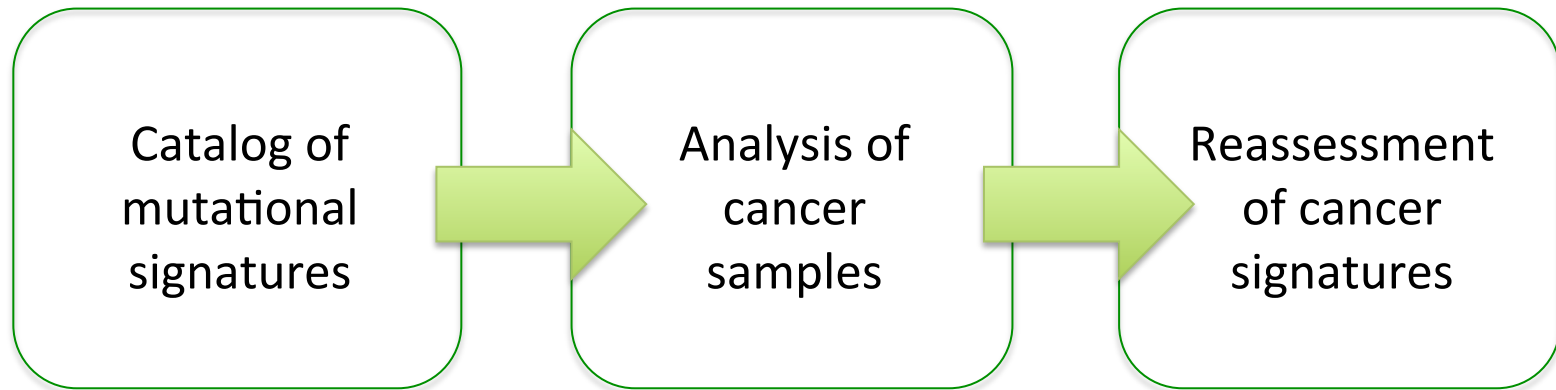Gene-gene interaction effect

Beautiful pictures

Gene-gene interaction effect

rev-1 – ortholog of human translesion REV1 polymerase

COMSIG: Consortium for Mutational Signatures

Catalog of mutational signatures → Analysis of cancer samples → Reassessment of cancer signatures

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Cancer Free

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Thank you for not shouting, throwing things at me or falling asleep ☺