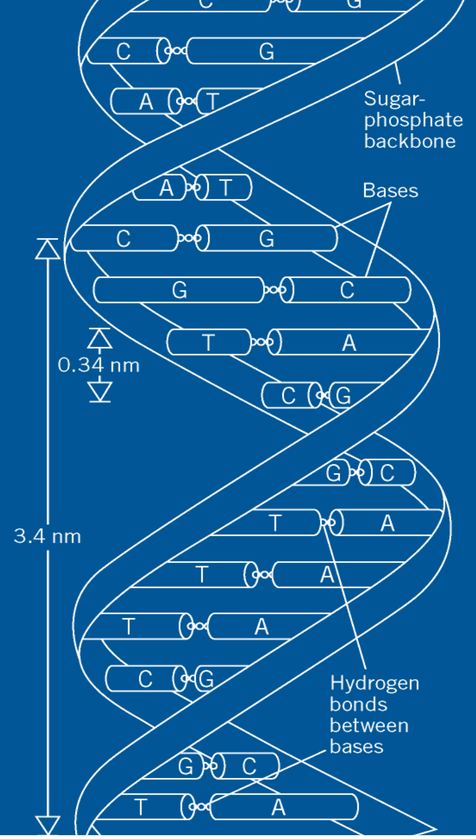


Facilitating the collaborative pursuit of scientific discovery with The FacileData Ecosystem

Steve Lianoglou
Computational Biologist
Cancer Immunology
Genentech

@slianoglou
@lianos
@faciledata

These tools will be open sourced

https://github.com/faciledata

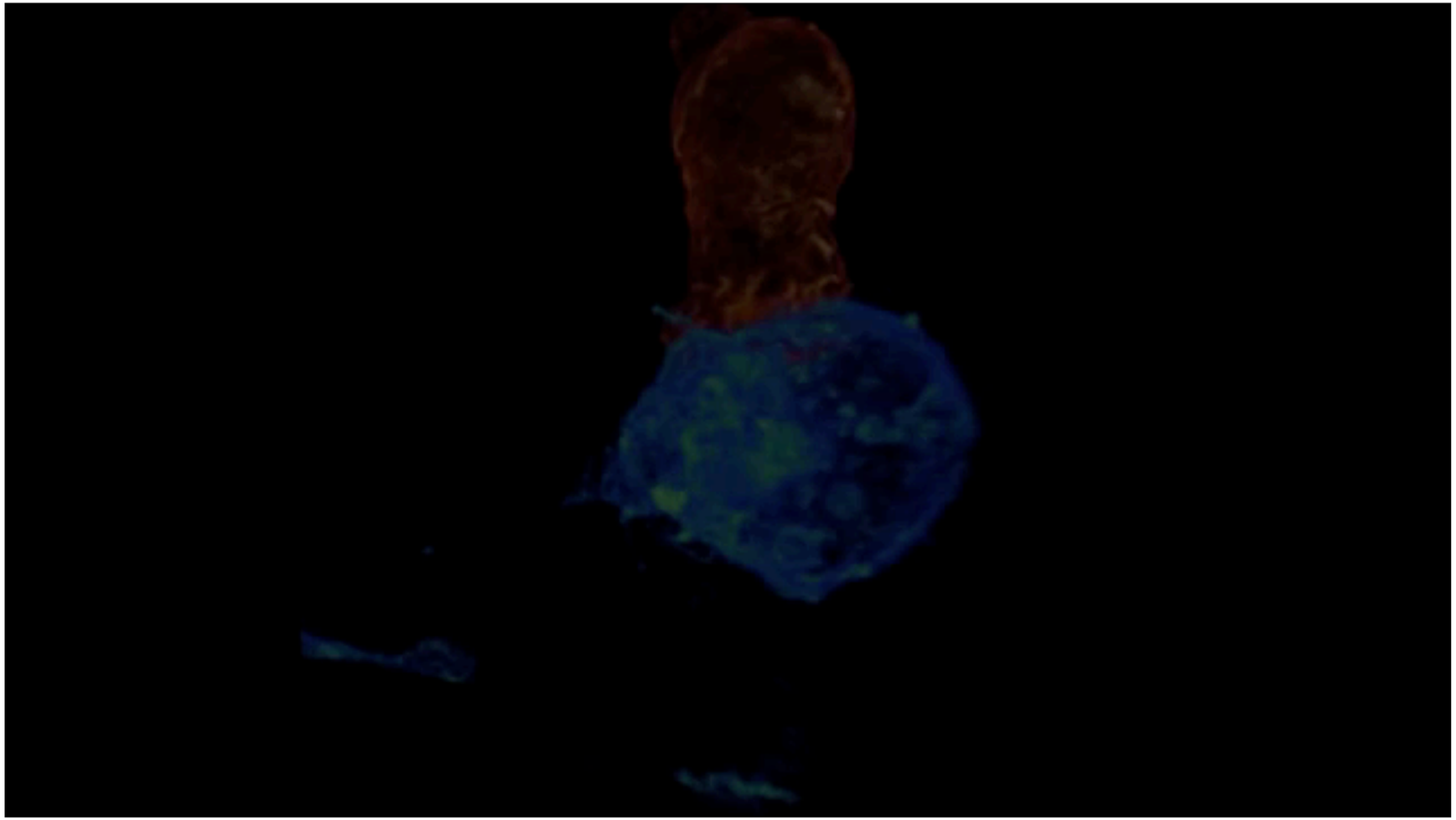
Slides and code used for presentation

https://github.com/faciledata/talks/2017-plotcon

★ star `faciledata/talks` repository to be updated ★

when tools are released

Cancer Immunology: the immune system can combat cancer



Alex Ritter

We can read DNA at scale

Illumina HiSeq

In a single run (4 days)*
12 Genomes
100 Transcriptomes

* https://www.illumina.com/systems/sequencing-platforms/hiseq-3000-4000/specifications.html

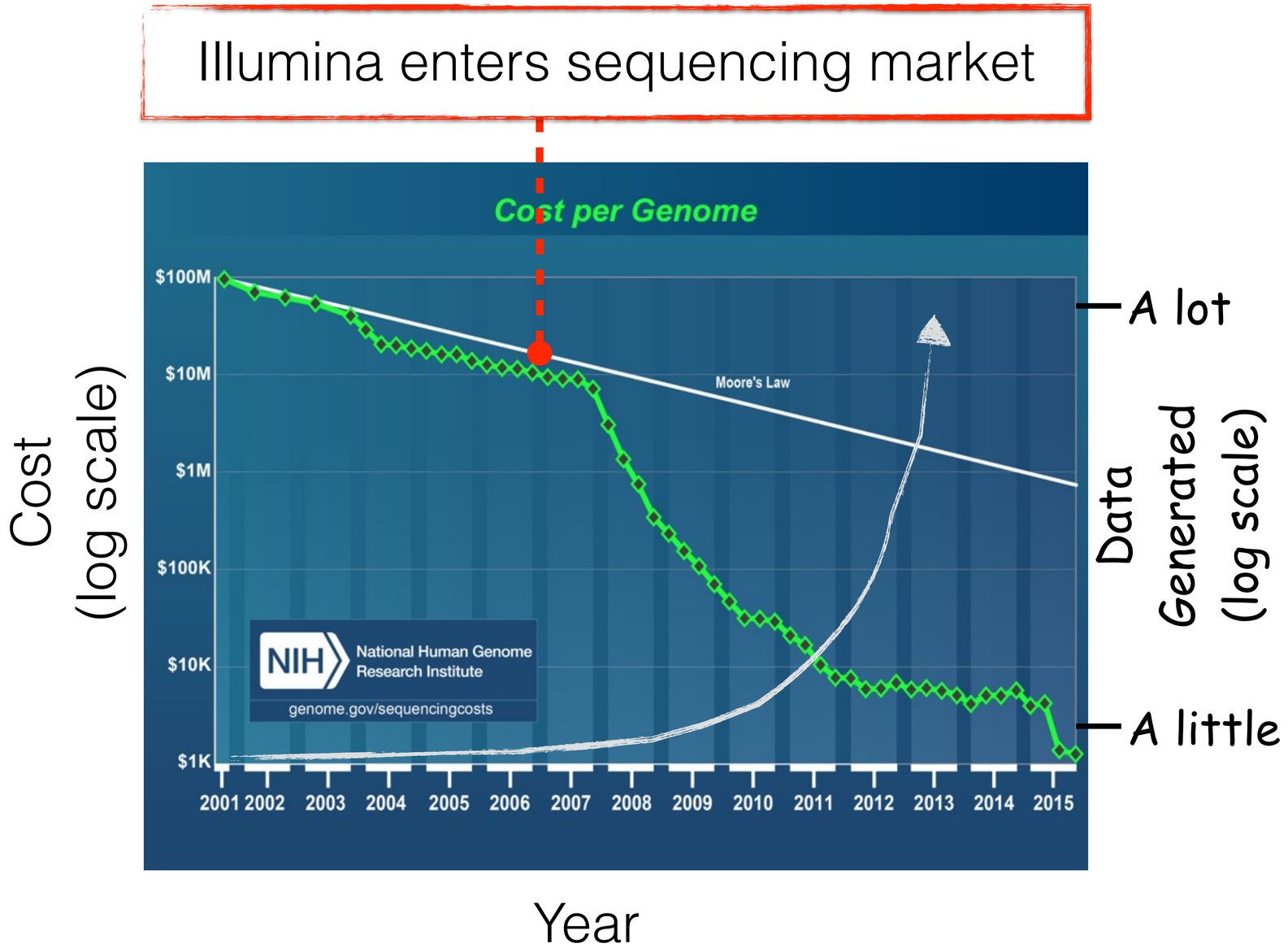
Fast and accurate DNA sequencing revolutionized study of biology

- **Genome sequencing**: identifies alterations in DNA
  - Mutations
  - Insertions, Deletions, Amplifications
  - Rearrangements
- **Transcriptome sequencing**: characterizes the identify and abundance of genes (RNA) expressed in a tissue or cell
  - Understand the mechanisms by which the cell performs its function
  - Understand what makes a tumor different than normal tissue
  - Understand why a tumor responds (or not) to a particular treatment

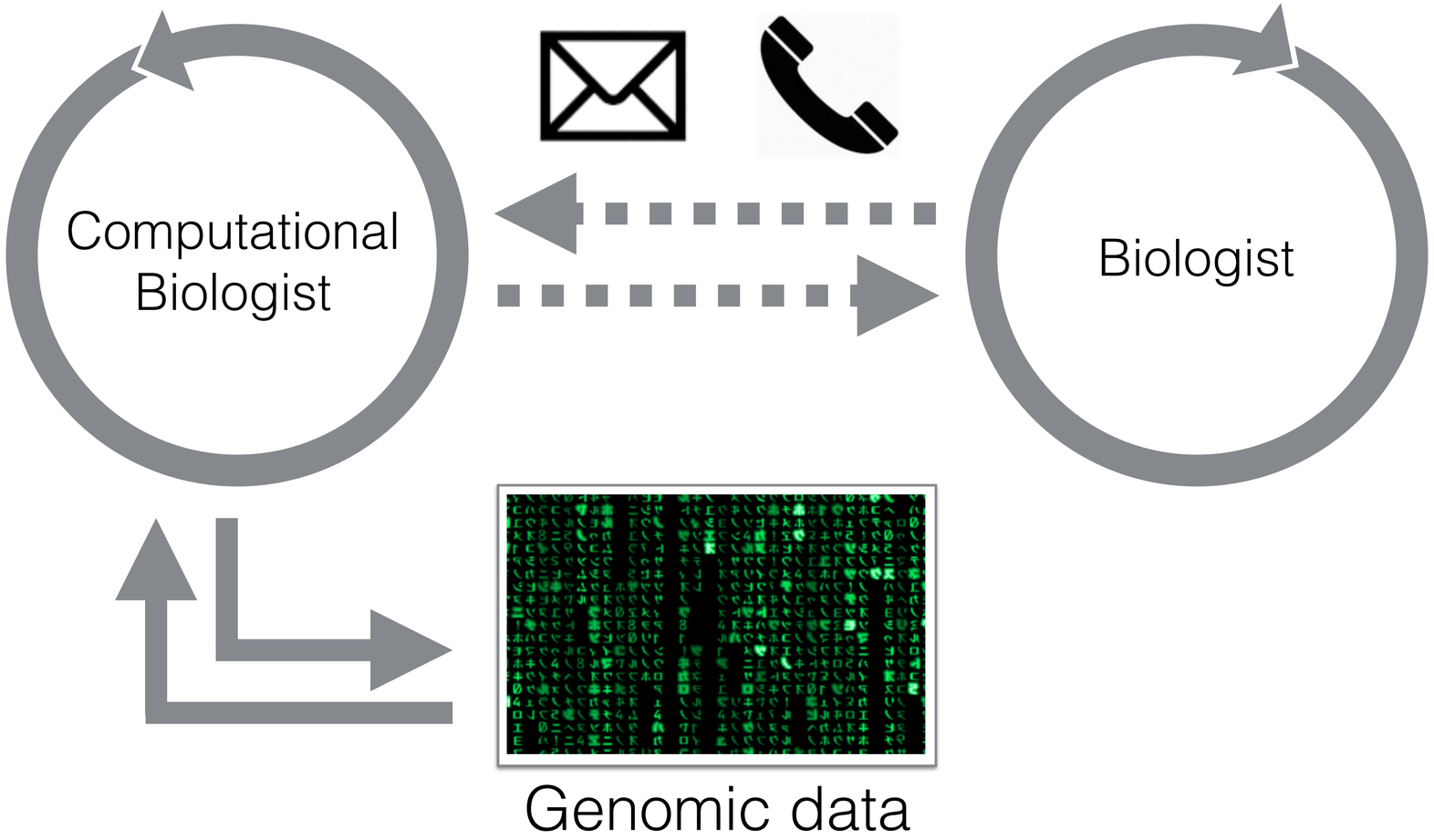
The universe of things the genome can do

The thing the genome is doing right now

Biology has been transformed into a data driven science

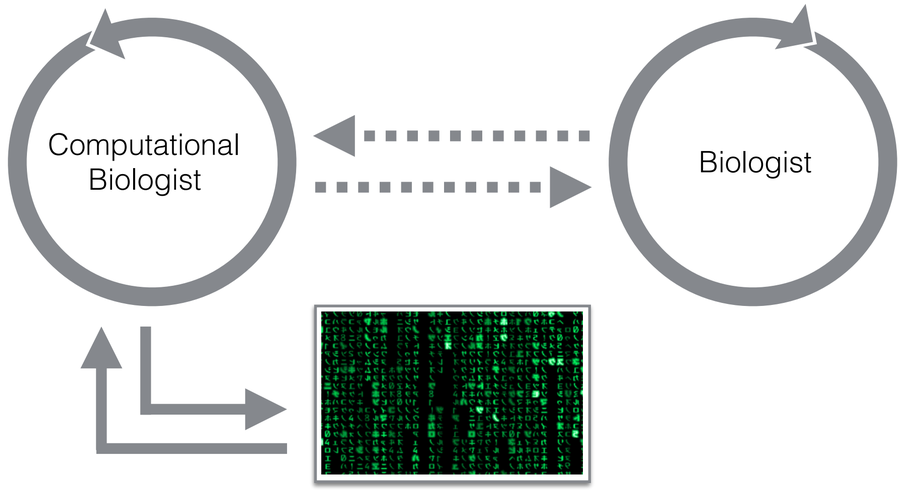


The state of data driven exploration and discovery



Problems with current state of data driven exploration

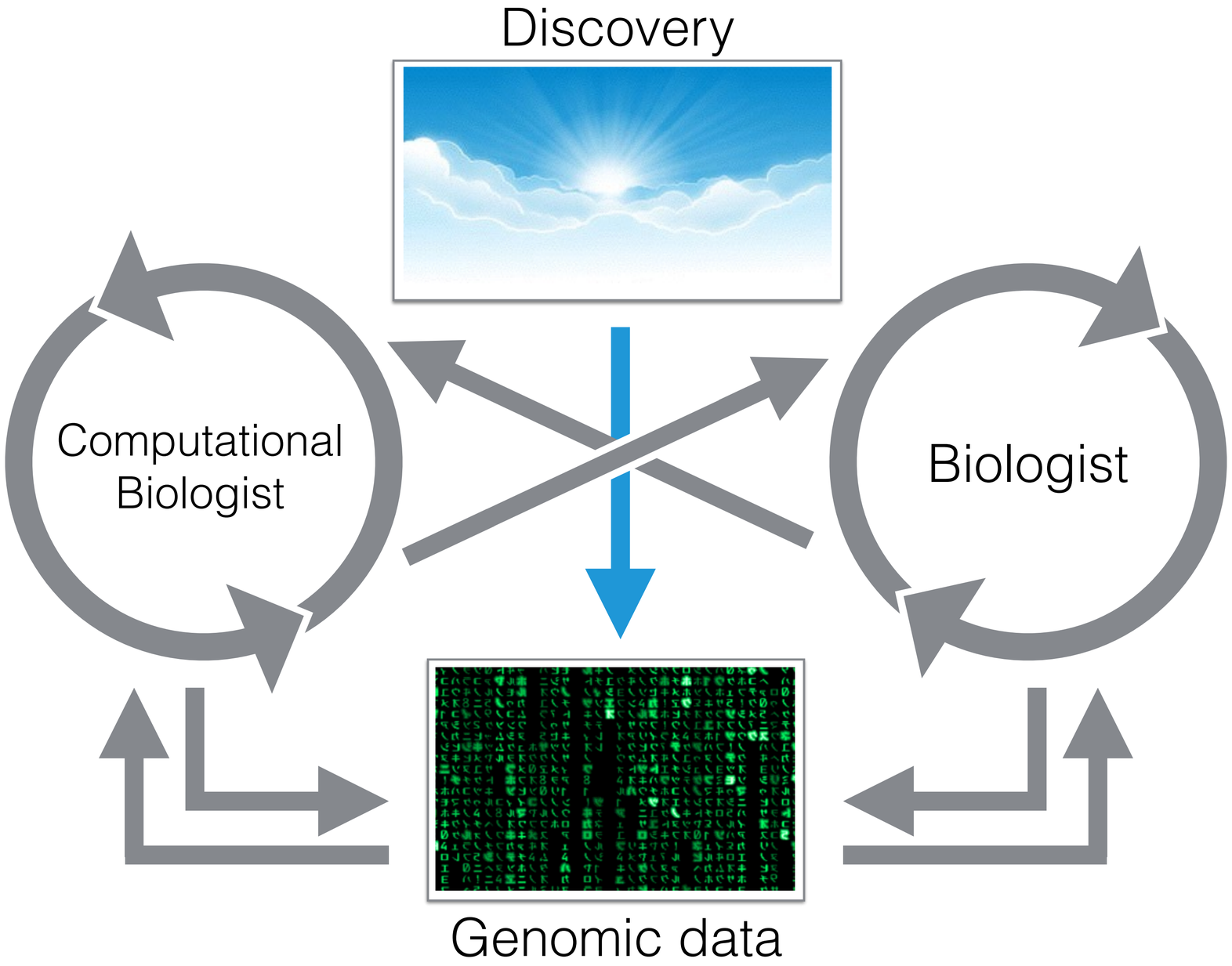
- Biologist has limited ways to meaningfully interact directly with the data.
  - Relies on computational biologist for even most simple of EDA
  - Long turn around times (Colin Ware: "delay creates a universe of ideas lost")
  - Context switches and broken *flow* for all



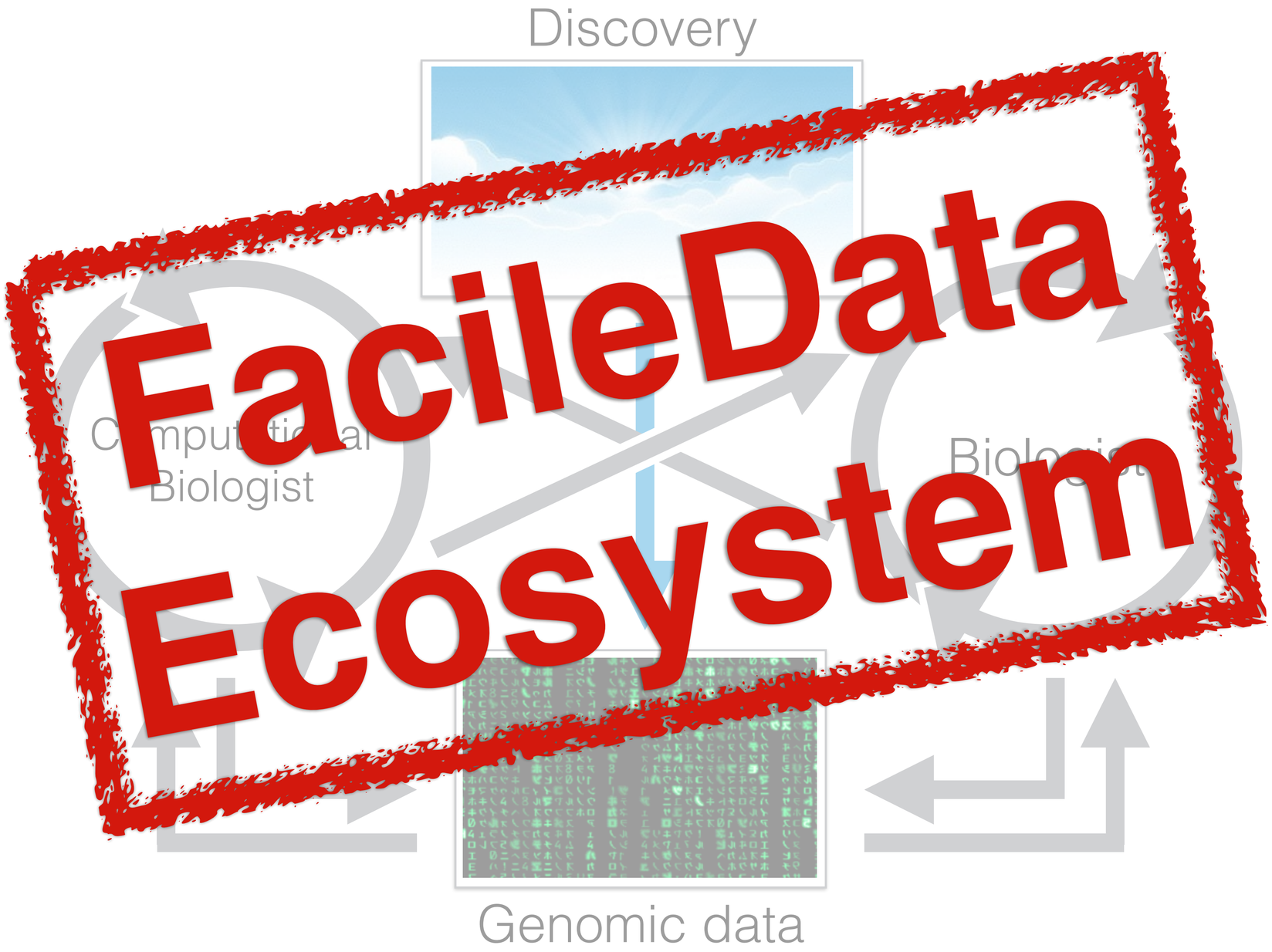
- The units of "knowledge transfer" are emails, tables of statistics, and figures **divorced from the data** (even if using Rmarkdown)
  - Makes it hard to iterate on EDA between collaborators

This is a *service model* not a *collaborative model*

A model for collaborative data driven exploration and discovery



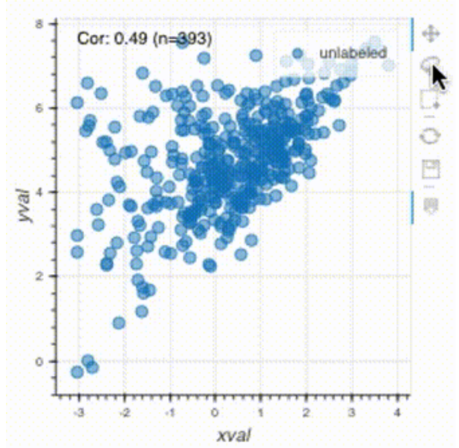
A model for collaborative data driven exploration and discovery



Tools to facilitate collaborative exploration

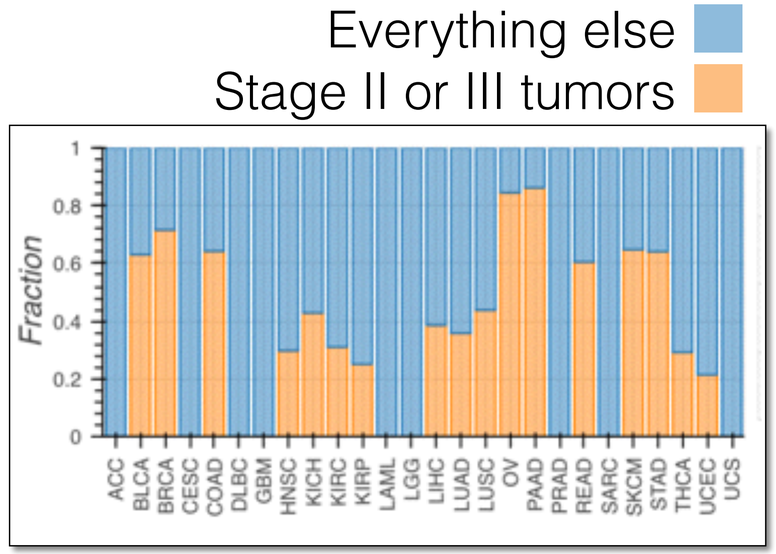
The FacileData Frontend (FacileExplorer)

- Designed to enable **sustained and independent** interactive data exploration by non-informaticians
- Empowers users to compute over data via its GUI
- Provides ability to hand off analyses "in flight", not just results



The FacileData Backend (FacileDataSet)

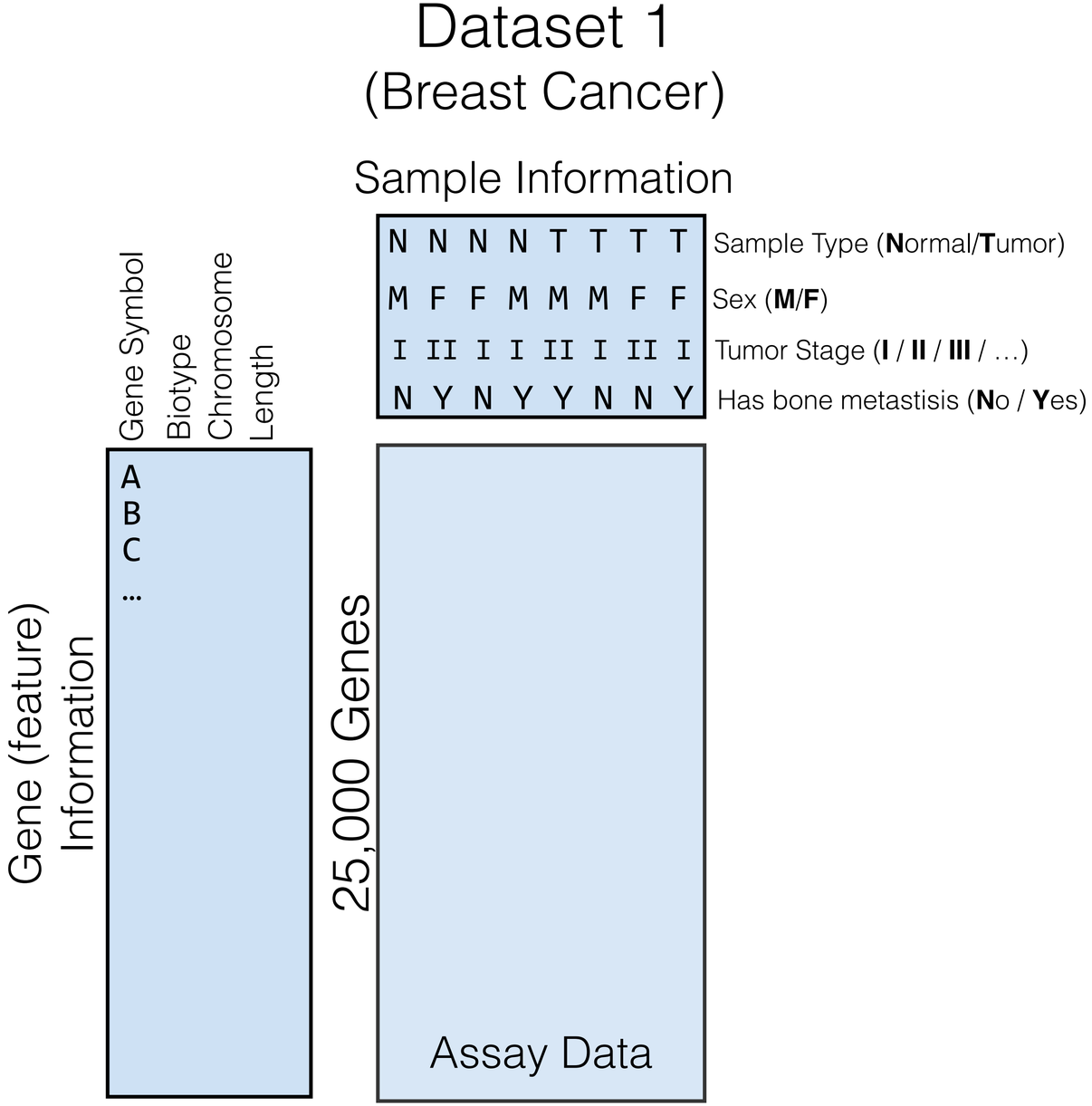
- Consolidates different high-throughput genomics datasets behind a single point of access
- Fast and efficient query and retrieval of **arbitrary data subsets** (features and samples) across datasets.
- Provides a **covariate-centric view** over these data
- Provides a data access API conducive to exploratory data analysis via code or GUI (dplyr/tidy-*ish*)



3321 / 8024 TCGA samples

The FacileData Backend (FacileDataSet)

High-throughput genomics data is large and complex



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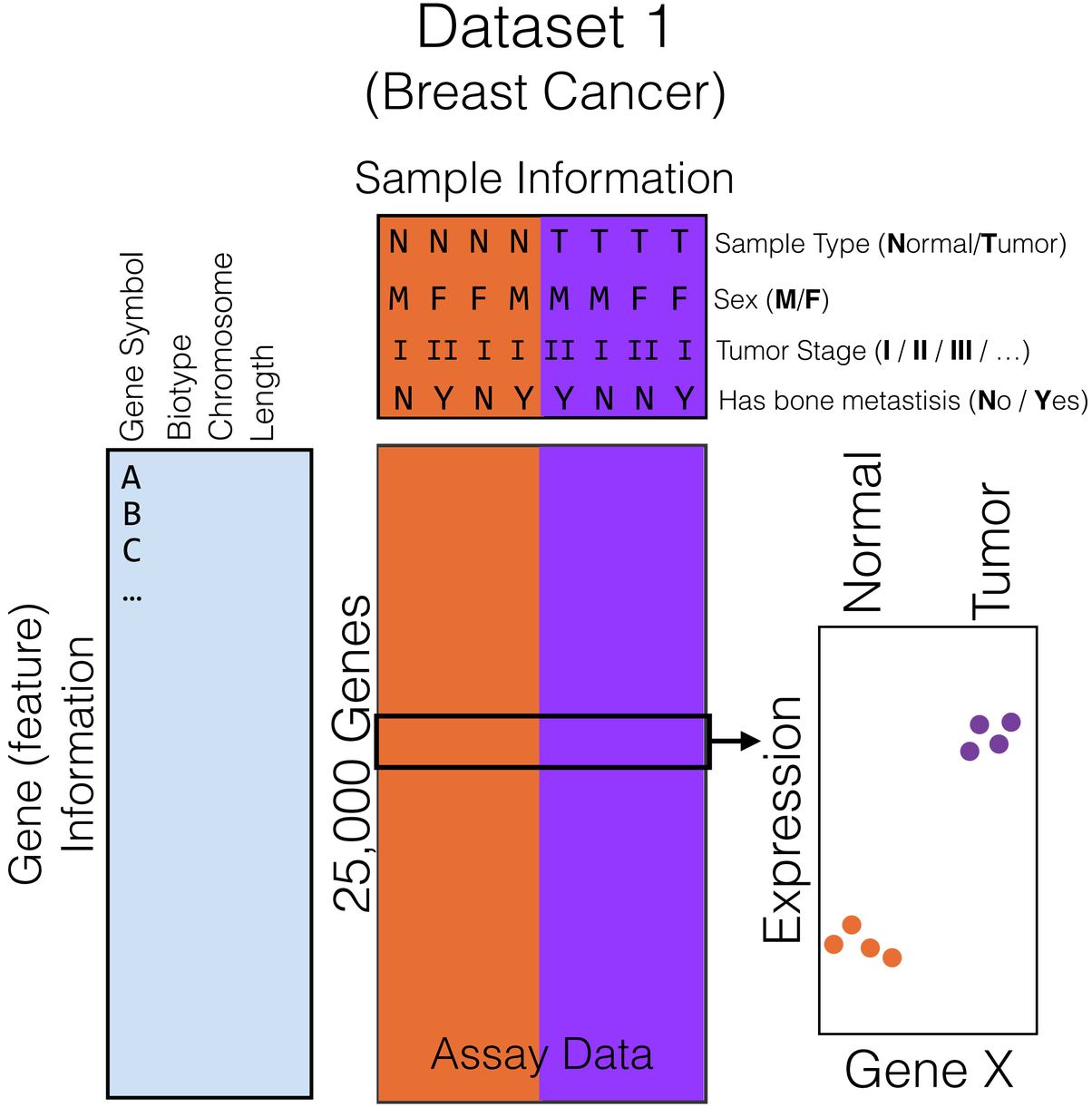
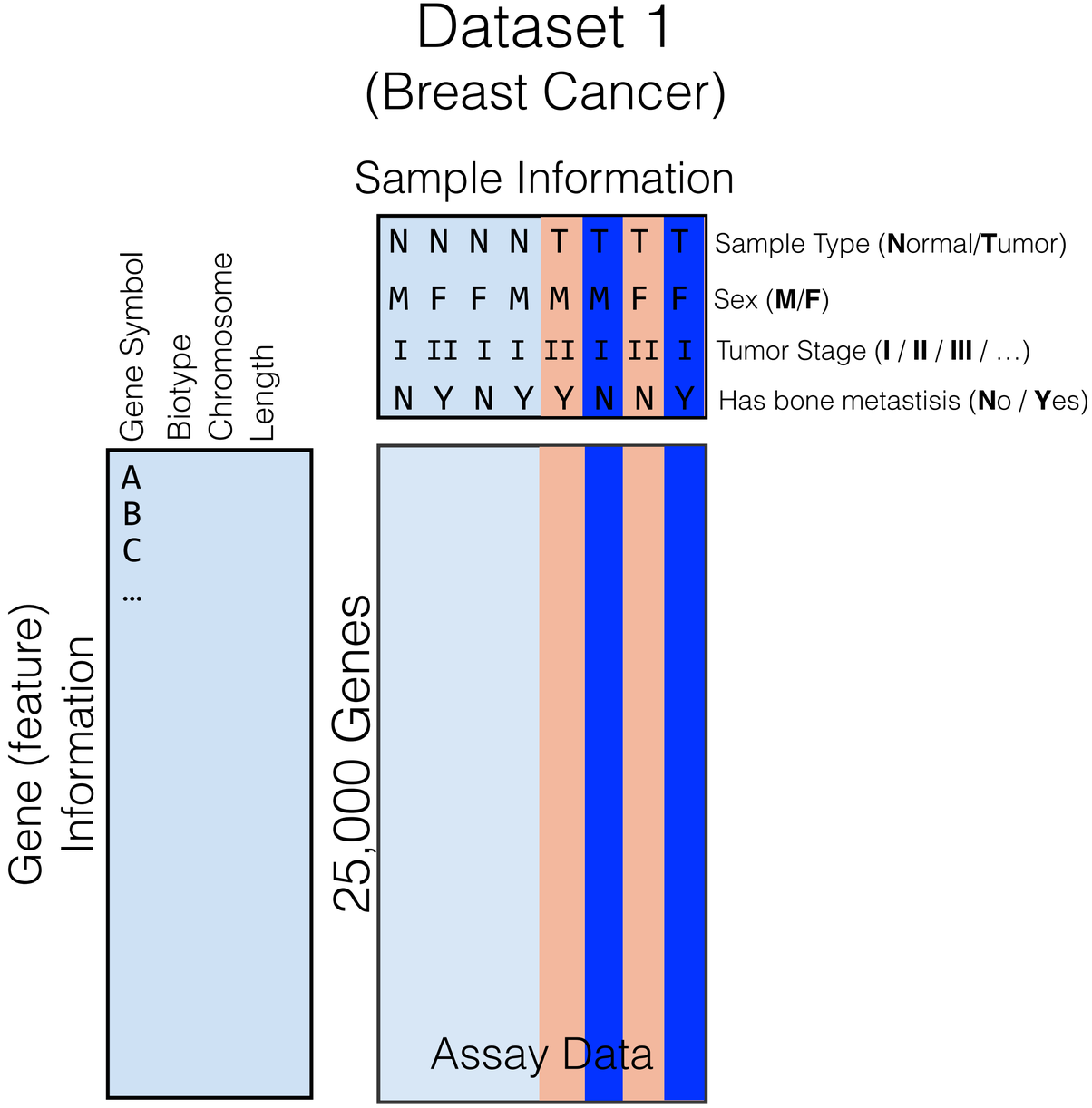


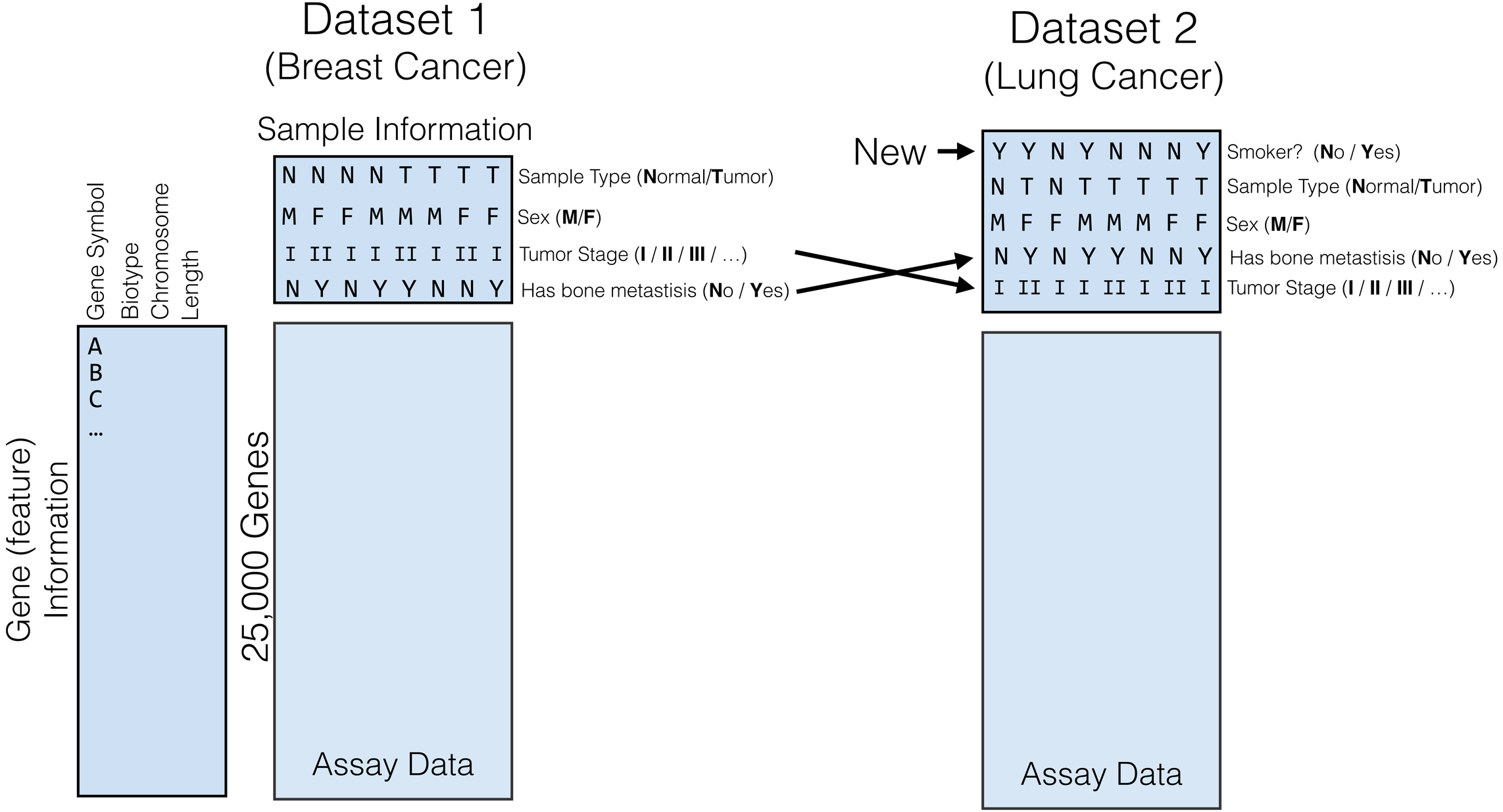
Normals vs Tumors

High-throughput genomics data is large and complex

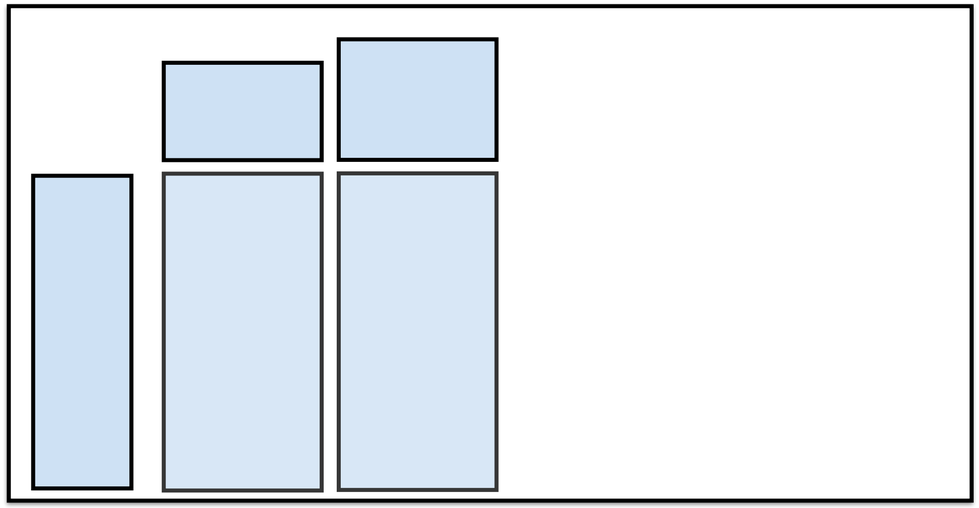


Stage I vs Stage II

High-throughput genomics data is large and complex



FacileDataSet provides single point of access across multiple datasets



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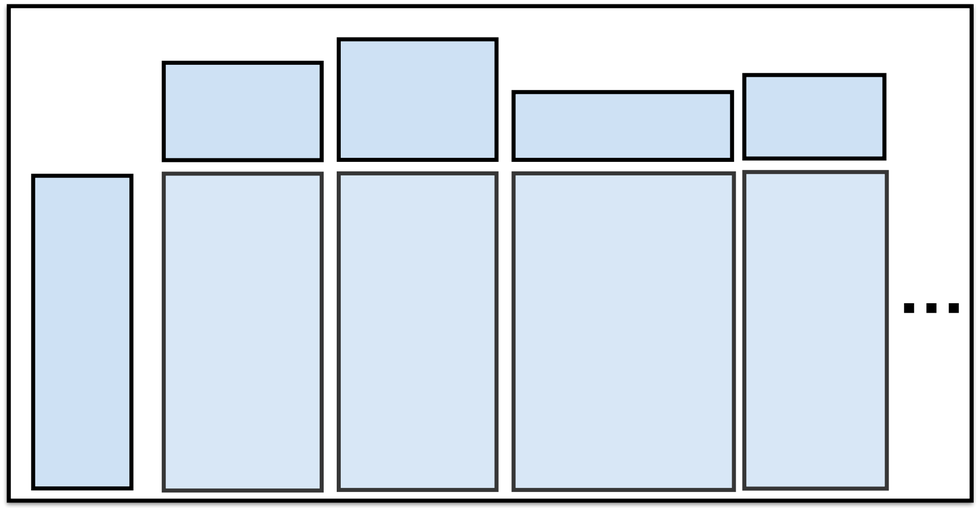
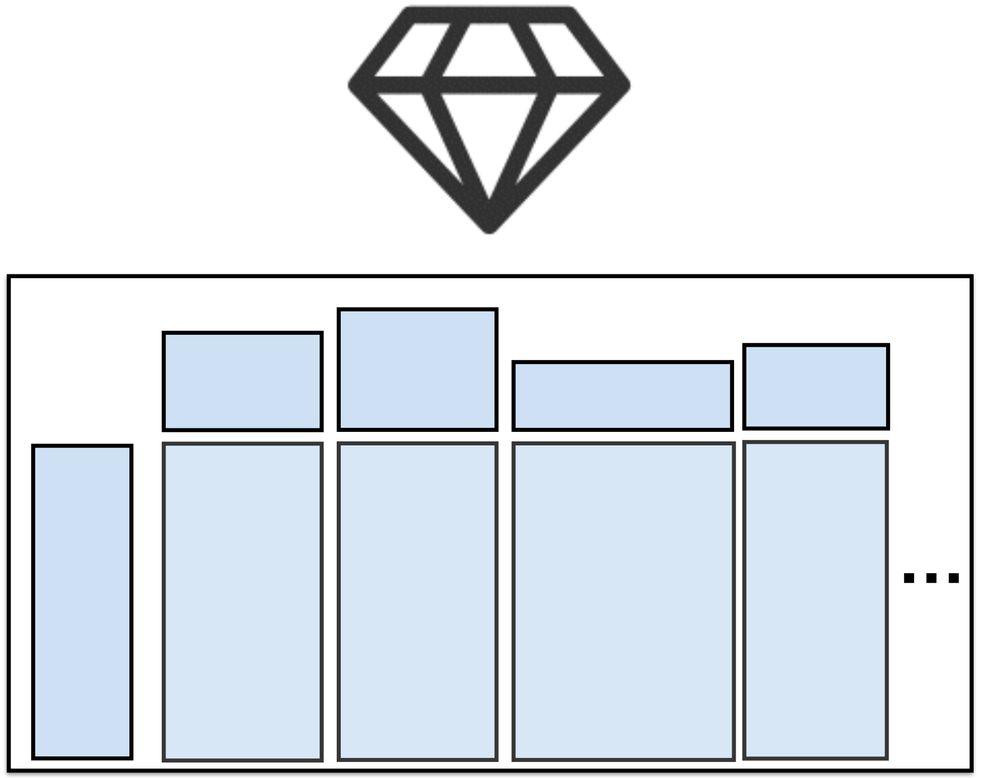


FacileDataSet

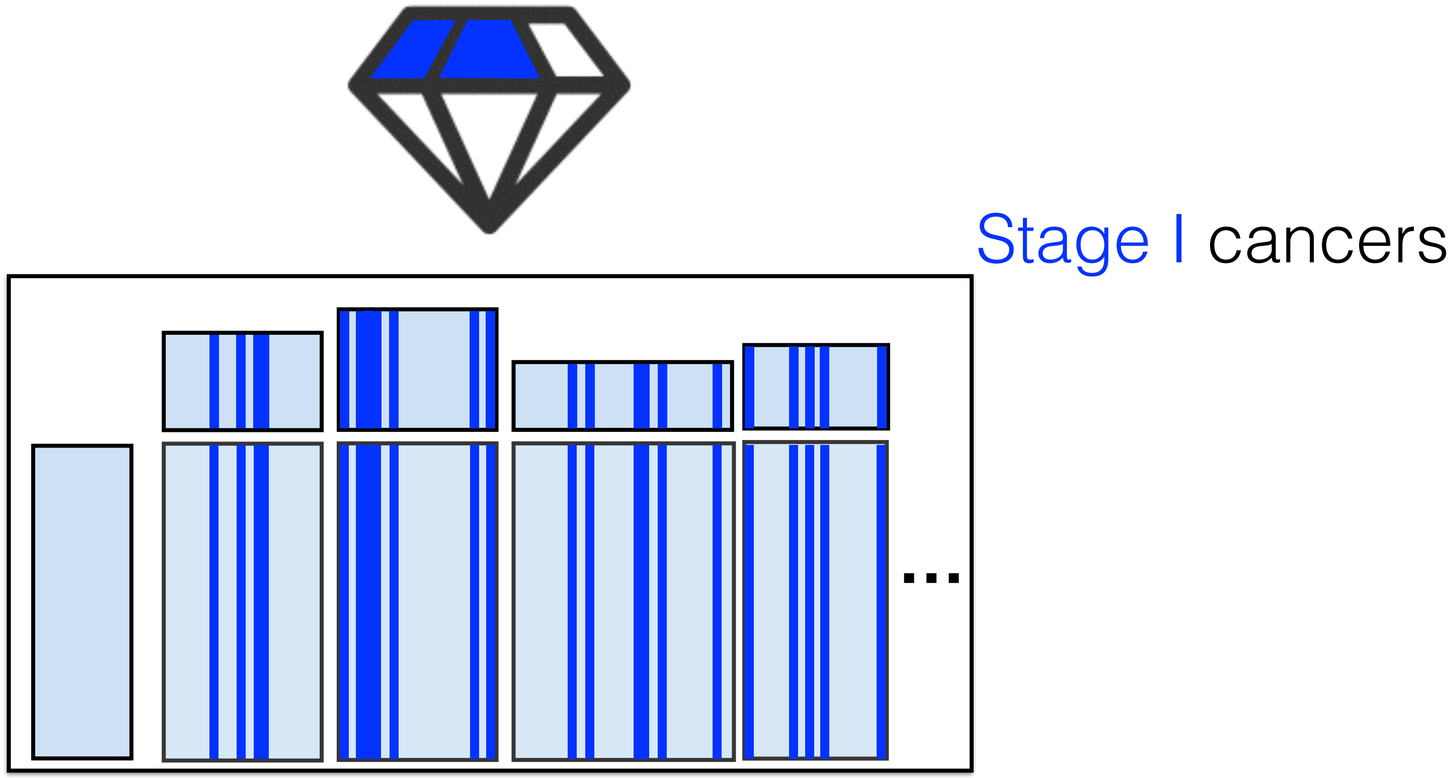
FacileDataSet provides a covariate-centric interface to assay data across multiple datasets



FacileDataSet

Think of data as a multi-faceted diamond

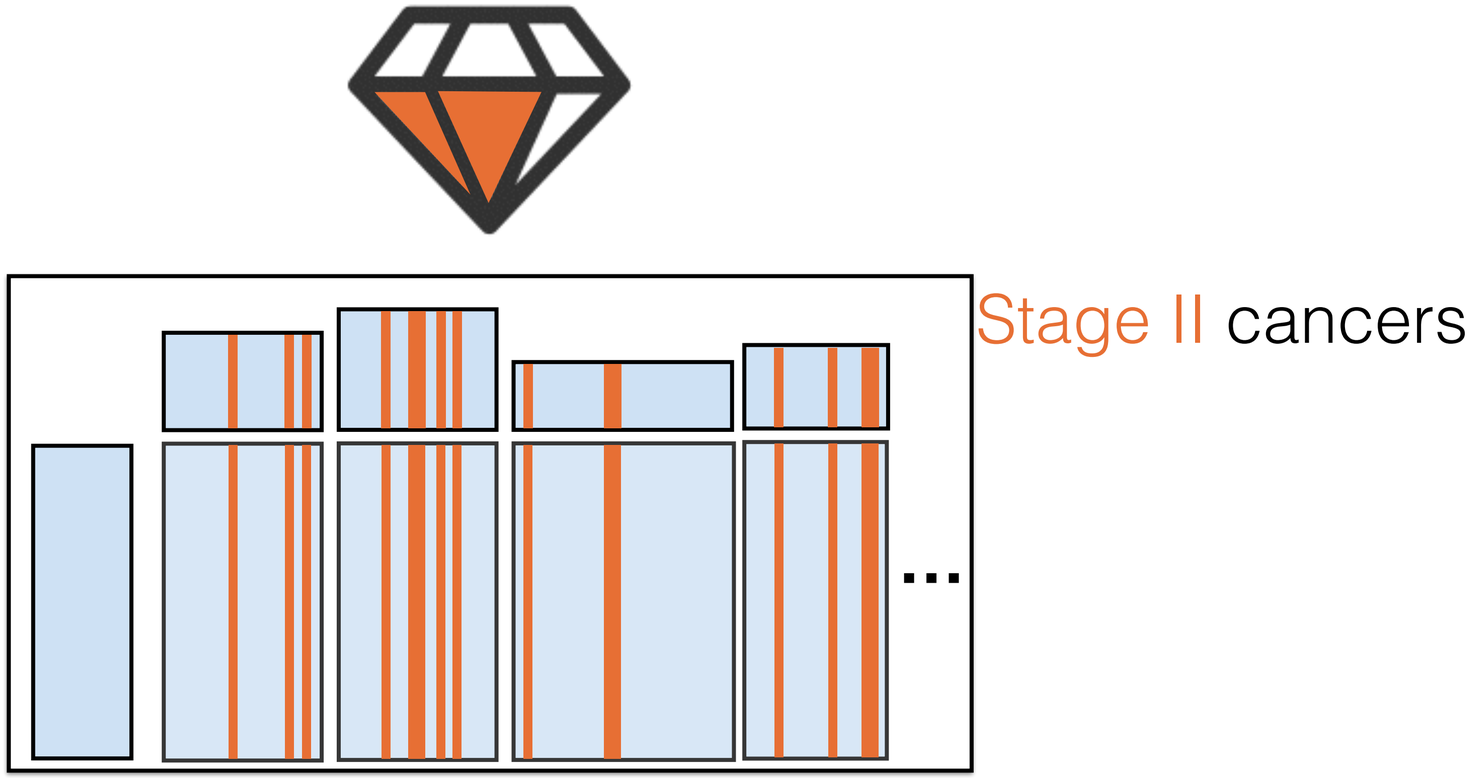
FacileDataSet provides a covariate-centric interface to assay data across multiple datasets



FacileDataSet

Think of data as a multi-faceted diamond
Facets are defined by combinations of covariates

FacileDataSet provides a covariate-centric interface to assay data across multiple datasets



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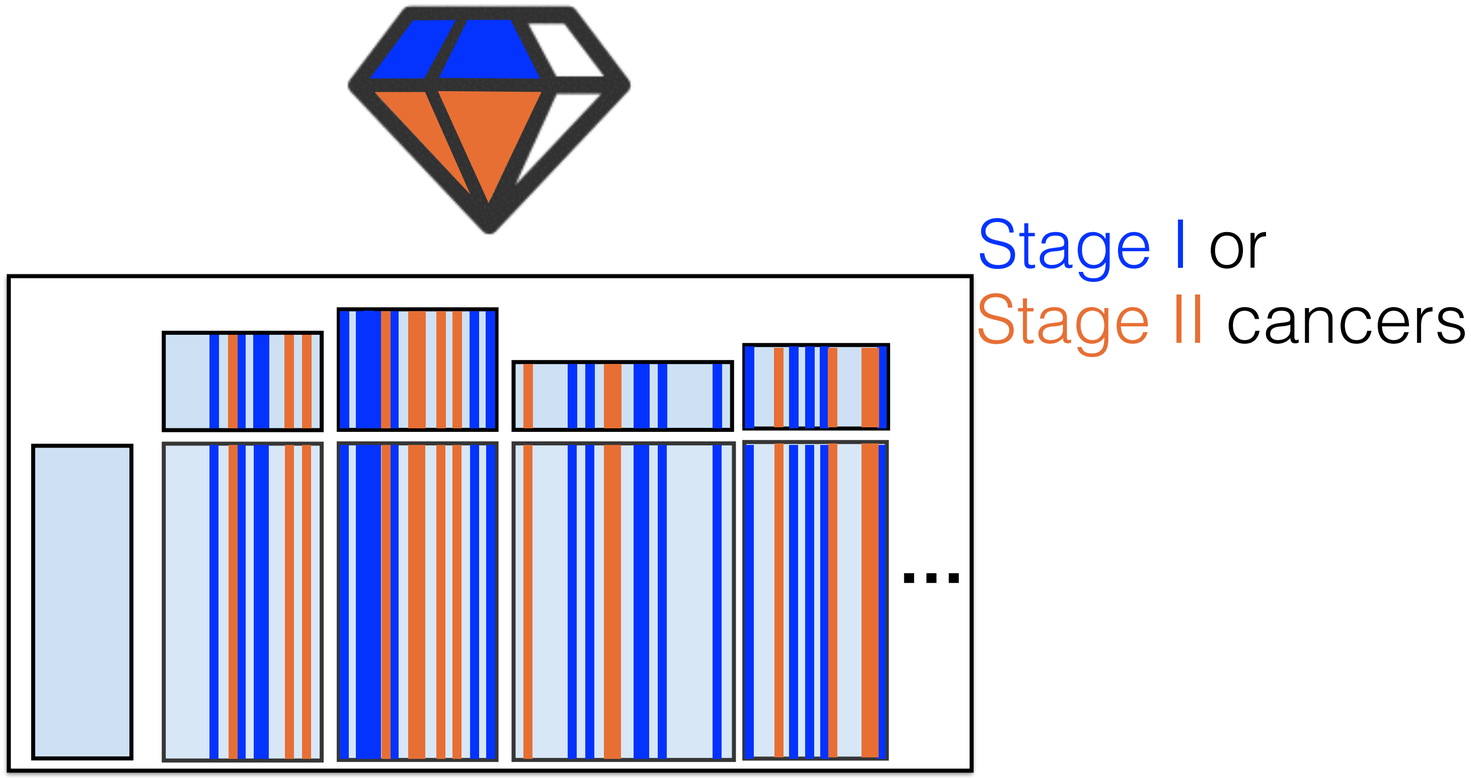

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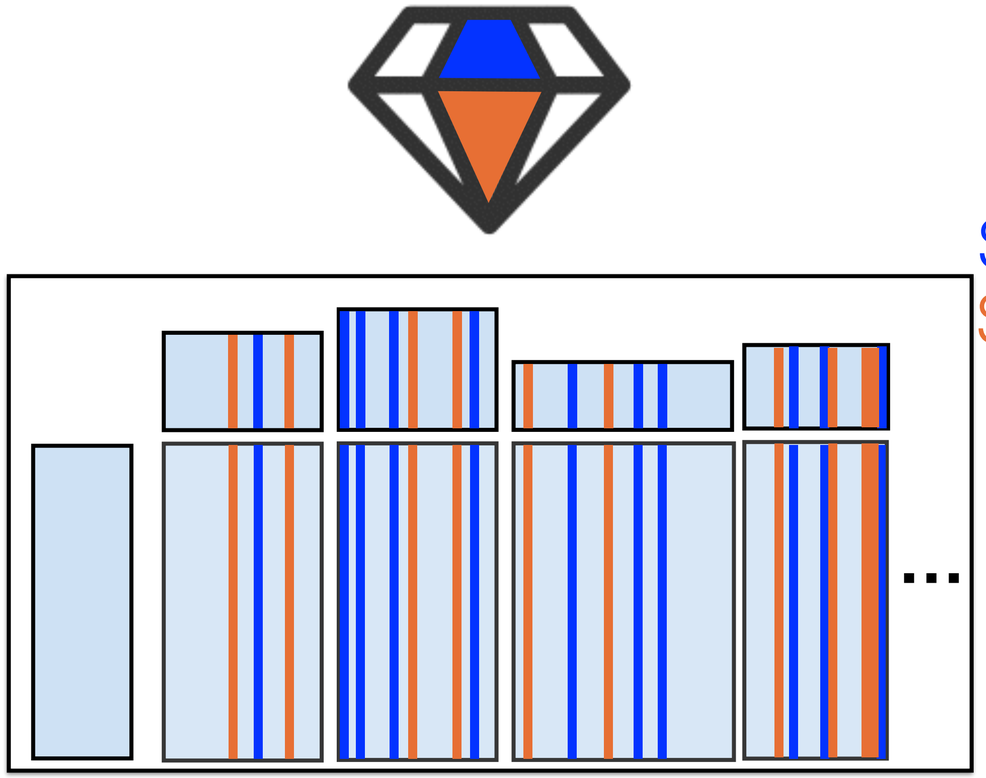


Stage I or
Stage II cancers

… that respond to treatment X

FacileDataSet

The FacileData Frontend (FacileExplorer)

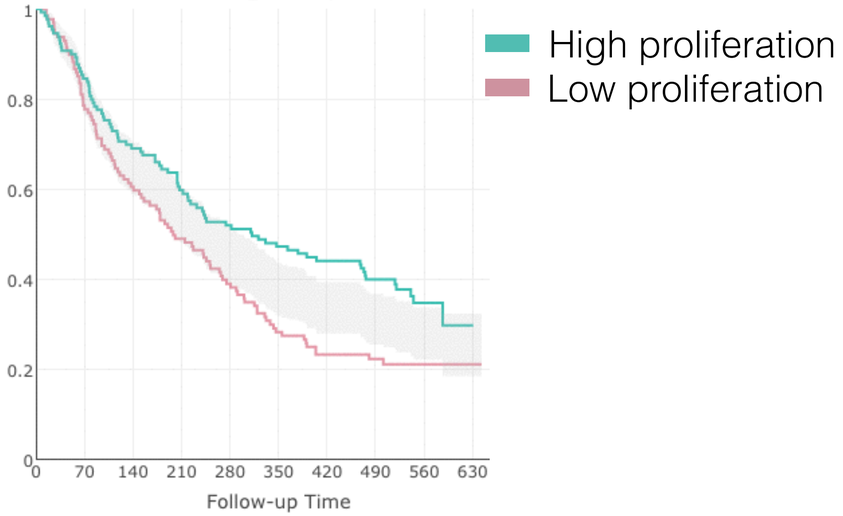
Anatomy of a Facile Survival Analysis

These results are hypothetical

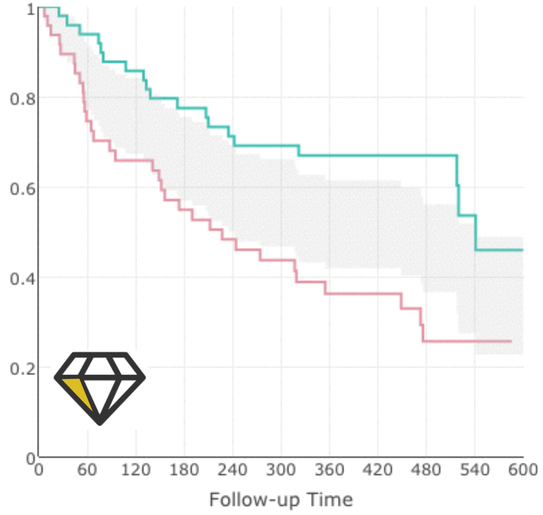
- User decides to analyze lung squamous tumors in TCGA FacileDataSet
- User asks if gene signature for proliferation is prognostic biomarker for overall survival
- User "one-clicks" an *Iterative Faceted Analysis* to identify other facets of data this result generalizes to

TCGA

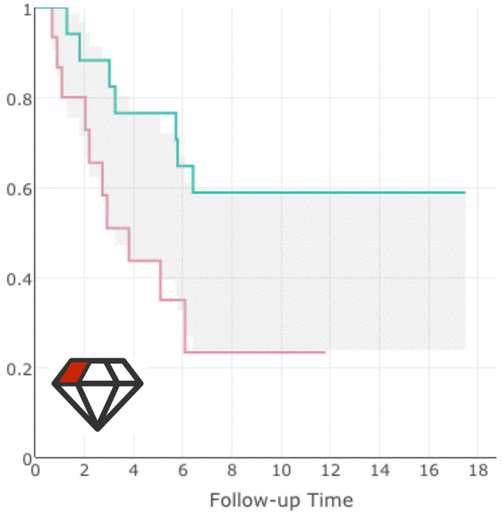
TCGA Lung Squamous



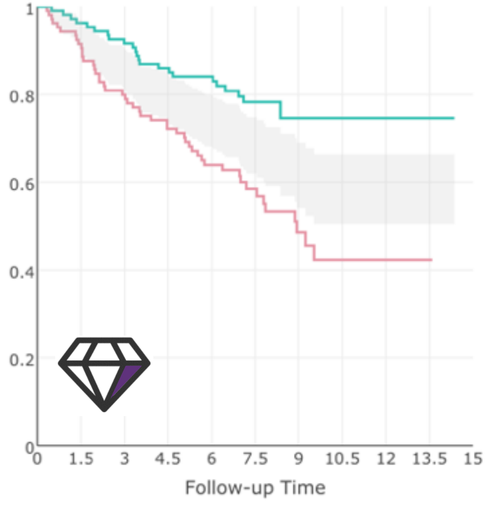
TCGA Lung Adenosarcoma



TCGA: ER+ Breast



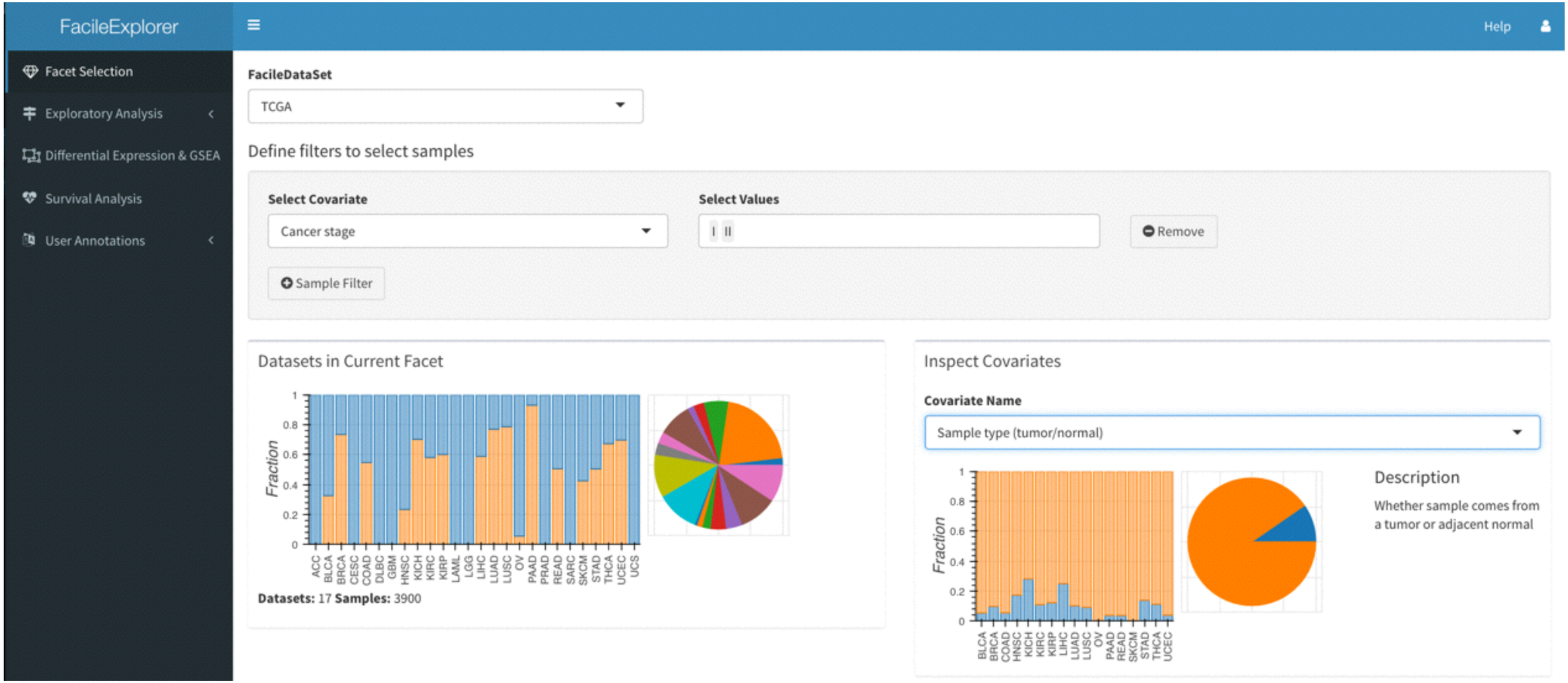
TCGA: Bladder



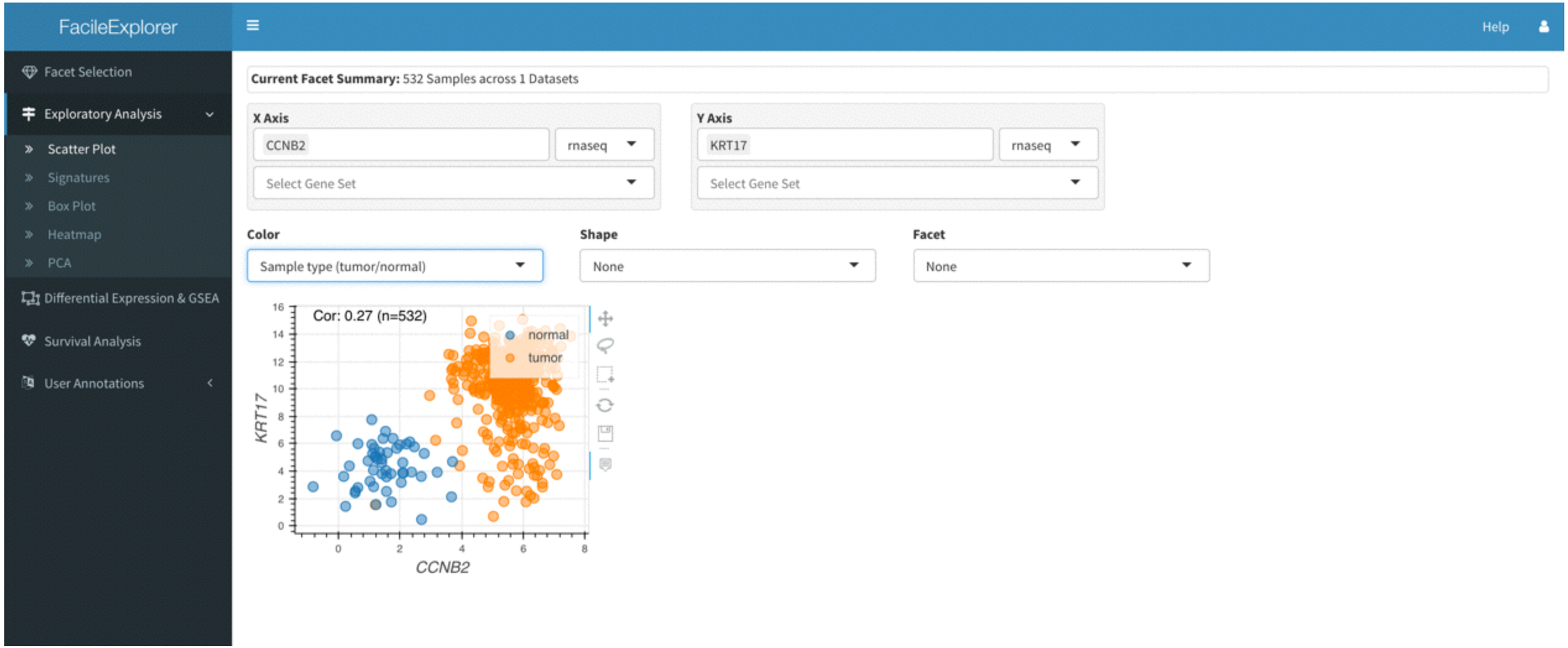
Live demo of FacileExplorer

GUI → Analyst → GUI

Live Demo: Exploring Facets of TCGA



Live Demo: Single gene markers of Proliferation vs P53 response in TCGA Lung Squamous (tumors and normals)



Live Demo: Recover brushed annotations and generate graph via code


```
library(FacileExplorer)
library(FacileTCGADataSet)
tcga <- FacileTCGADataSet()

samples <- tcga %>%
  filter_samples(indication == "LUSC")

features <- tcga %>%
  filter_features(name %in% c("CCNB2", "KRT17")) %>%
  mutate(assay="rnaseq")

dat <- samples %>%
  with_sample_covariates('sample_type') %>%
  with_assay_data(features, normalized=TRUE, spread="name")

ggplot(dat, aes(CCNB2, KRT17, color=sample_type)) +
  geom_point() +
  theme(legend.position="bottom")
```

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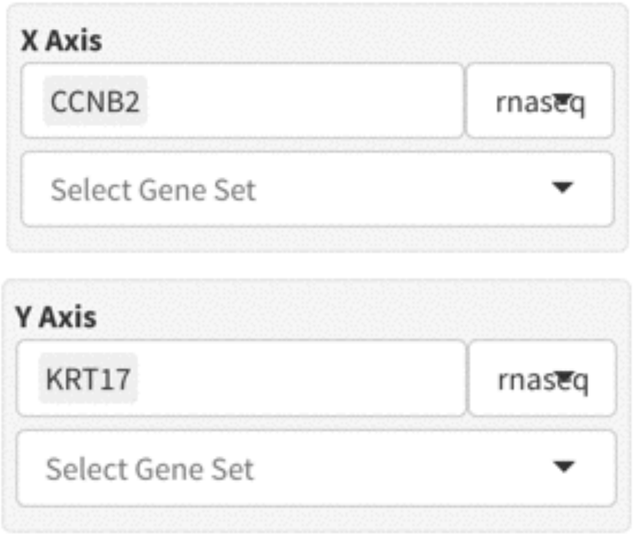

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  theme(legend.position="botto
```

dataset	sample_id	CCNB2	KRT17	sample_type
LUSC	TCGA-18-3406-01A-01R-0980-07	5.0915656	13.758303	tumor
LUSC	TCGA-18-3407-01A-01R-0980-07	4.7749408	12.631085	tumor
LUSC	TCGA-18-3408-01A-01R-0980-07	5.2399864	9.227850	tumor
LUSC	TCGA-18-3409-01A-01R-0980-07	4.6457598	12.166467	tumor
LUSC	TCGA-18-3410-01A-01R-0980-07	7.1772091	7.319666	tumor
LUSC	TCGA-18-3411-01A-01R-0980-07	6.3701353	12.286020	tumor
LUSC	TCGA-18-3412-01A-01R-0980-07	6.2838198	12.437087	tumor
LUSC	TCGA-18-3414-01A-01R-0980-07	6.1370424	11.362722	tumor
LUSC	TCGA-18-3415-01A-01R-0980-07	6.5267915	12.290913	tumor
LUSC	TCGA-18-3416-01A-01R-0980-07	5.5907905	8.691251	tumor

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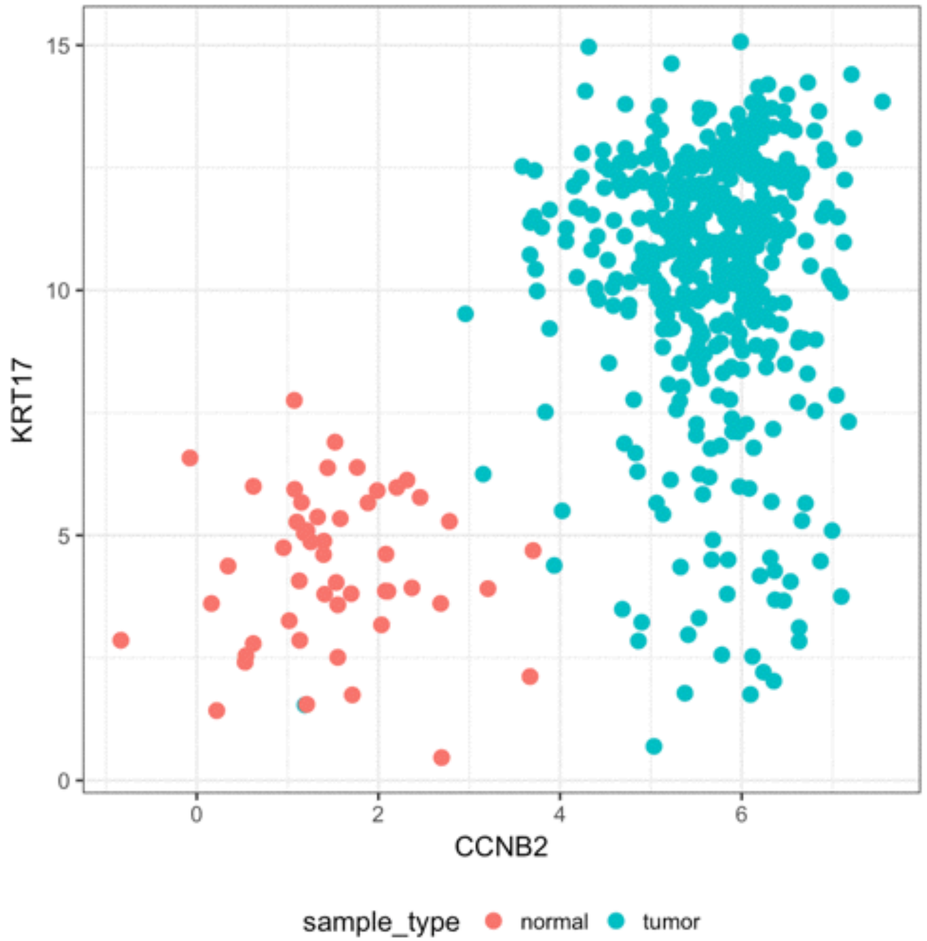


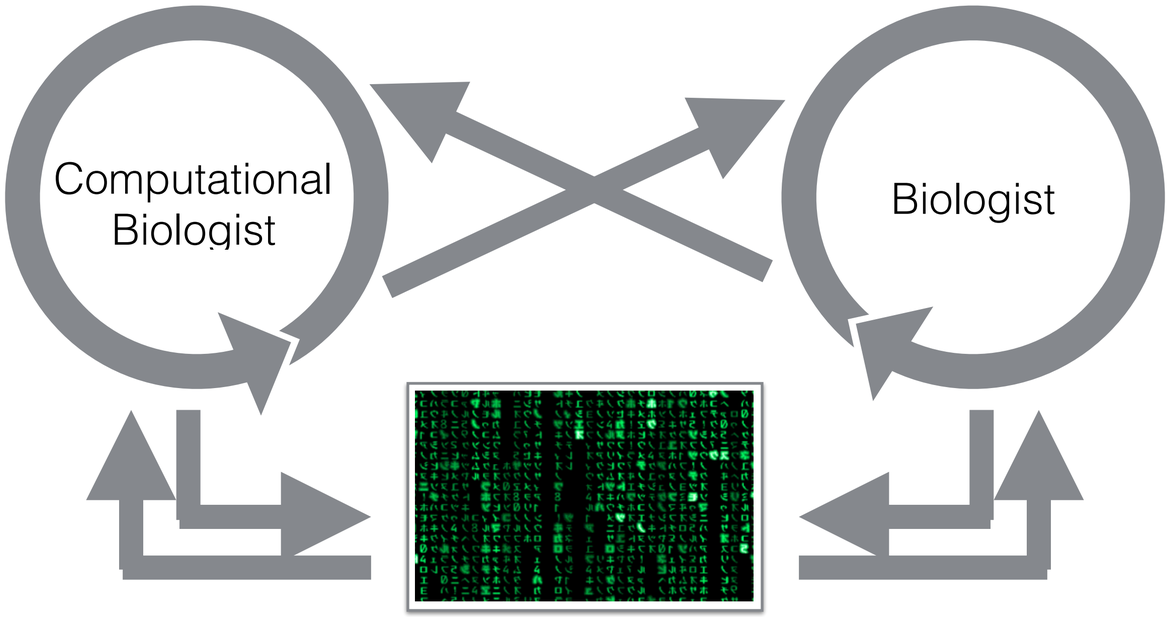
Long Term Goal

- Exploit modular design of analysis components to enable dynamic Rmarkdown report generation within the FacileExplorer.
  - Individual module result (scatter plot, survival, heatmap, etc) can be exported with prose to a growing report (thanks to Michael Lawrence for idea).
  - These reports maintain connection to data backend
- Analyst can consume URL of report in local workspace to re-instantiate the state of analysis for any module embedded in the report (baton passed).

```
state <- restore("http://facilereports/d04be94#prolif-scatter")
```

Summary

- FacileData Ecosystem provides tools to make collaborative science more efficient
  - Empowers sustained, independent, and interactive exploration
  - Enables each scientist to bring their expertise to bear on problem
  - Provides means to "hand off" analyses for further exploration by keeping results connected to their data



Acknowledgements

The FacileData Working Group


Matthew Albert


Marcia Belvin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Haiyin Chen


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Genentech

Michael Lawrence
Luciana Molinero
Yulei Wang
Christine Moussion
Pete Haverty
Gabe Becker
Dorothee Nickles
Ben Shaibe
Matt Buechler
Sascha Rutz
Tess Delfino
Shannon Turley

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