

# Data Analysis Projects

## MoBi 4. FS - SS2019



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# Concept

- **Project-oriented teaching:** provide hands-on experience with data analysis and programming
- **Goals**
  - experience data analysis challenges on real datasets related to research question
  - experience team work, also outside of your team!
  - learn to use modern data analysis tools: R / Python / markdown / notebooks / github

# Research topics / projects



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- **5 research projects** have been defined
- Each topic has up to **5 sub-projects**
- Each project will be worked out by **groups of 4 students**
- **one supervisor and master tutor per project**
- **Role of the master tutors:**
  - weekly meetings with groups working on project (Wednesday 10am-1pm)
- Meeting rooms: BioQuant SR42/43 + IPMB meeting room 5th floor  
2 other meeting places must be found (lounge corner at BioQuant?...)
- Tutors:  
Valentina Giunchiglia; Julia Rühle; David Schwarzenbacher; Nicolas Peschke; Alexander Mattausch

# Timeline



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*We do...*

*You do...*

**17/04**

Presentation of the projects

**24/04**

Presentation of R markdown  
and github

**15/05**

selection of projects  
and teams;  
registration

Presentation of  
project proposal  
(10 + 10 min)

**24/07**

**(25/07 for Project 03)**

Final presentation  
(15+10 minutes)

# Project proposal (15/05)

- During the project proposal presentation, you should
  - review some of the references given in the project description
  - explain what the questions / challenges are
  - describe which of these questions you want to adress in your project
  - indicate a approximate timeline
    - ▶ milestones = important steps in the analysis
    - ▶ when these milestones should be achieved
- Presentation in front of the project supervisors
  - 10 minutes presentation
  - 10 minutes discussion / questions
- *All team members are expected to contribute!*

# Projects / sub-projects



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- **Project 01: *Genetic interactions in cancer***

(Ashwini Sharma / Carl Herrmann)

- Data types: gene expression / gene mutations / gene knockdown / CNV

- **Project 02: *Cellular response to drug perturbation***

(Nicolas Palacio / Javier Perales)

- Data types: gene expression treated / untreated / mutations / metadata

- **Project 03: *Biomedical image analysis***

(Karl Rohr / Christian Ritter)

- Data types: MNIST images / cell nuclei images

- **Project 04: *Programming k-means***

(Thorsten Beier)

- Data types: scRNA-seq

- **Project 05: *Cancer DNA Methylation***

(Matthias Schlesner / Christian Heyer)

- Data types: DNA methylation WGBS

# Project selection / registration



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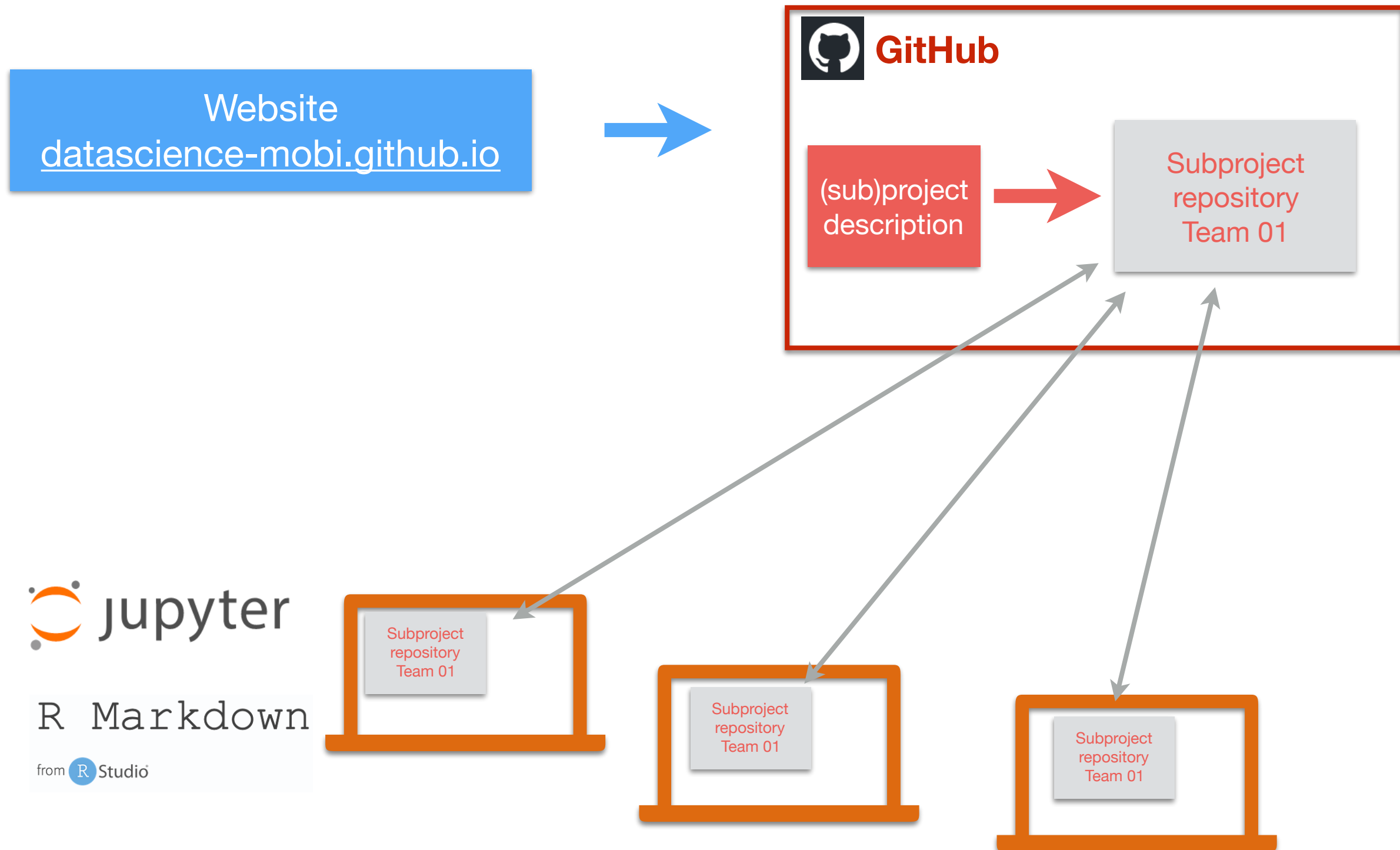
- Listen to the description of the projects / sub-projects
- Check this webpage  
<https://datascience-mobi.github.io/>
- Once you have selected your team and project, **register your team** in the Google sheet  
<https://docs.google.com/spreadsheets/d/1LEQLH2LaDuIMq3Qepx-7-5KWjgZjK4dfWDDIbm1vu0Q/edit?usp=sharing>
- ***Selection of the projects should be done by 24/04 10am !***



# Organizing your work



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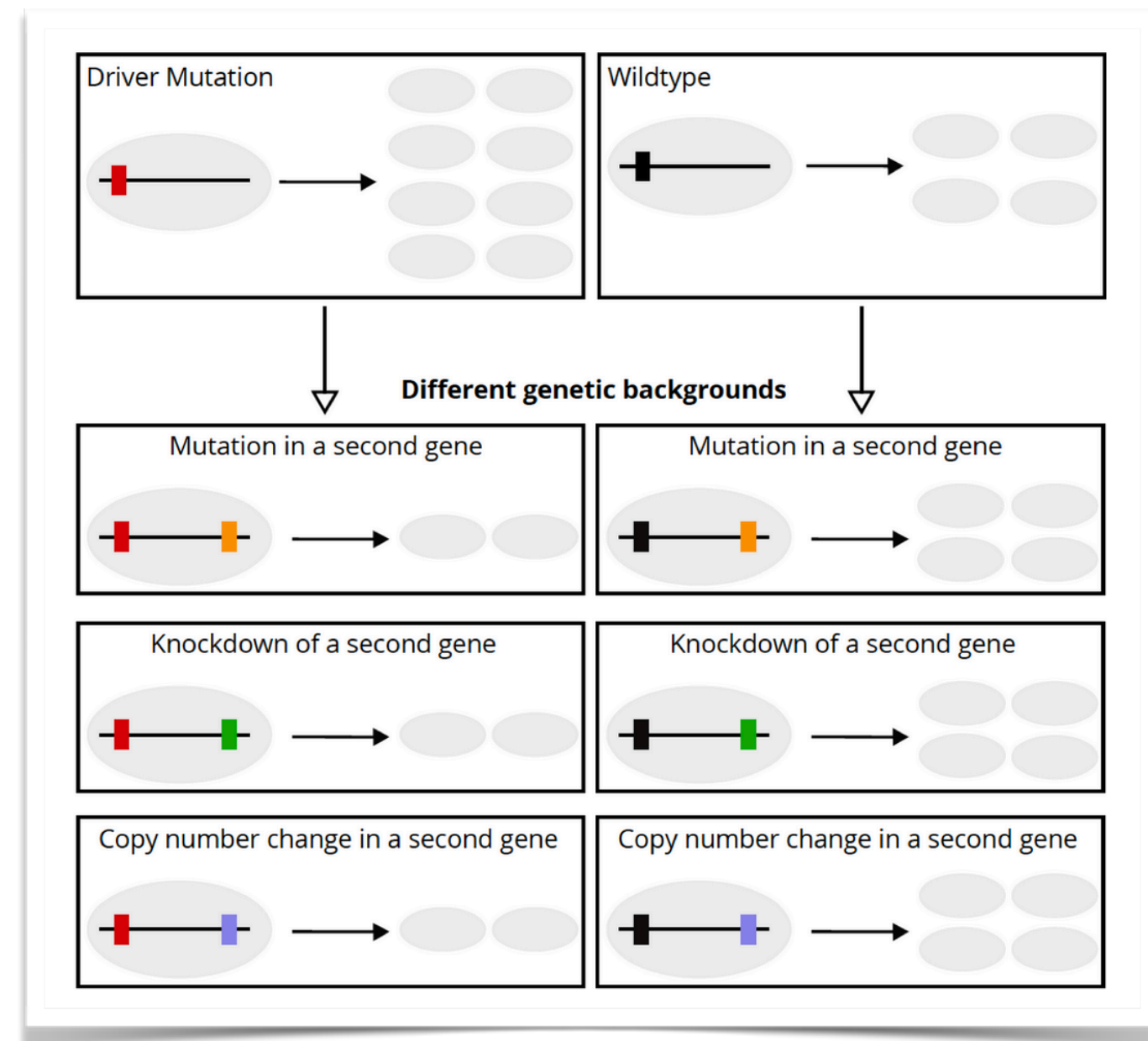


# Project 01: genetic interactions in Cancer cells



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- Find **synthetic lethal interactions** in cancer cell lines for driver mutations
- Which mutation / copy-number alteration does lead together with a driver mutation to a significant phenotype in cancer cells?  
→ identify potential therapeutic targets

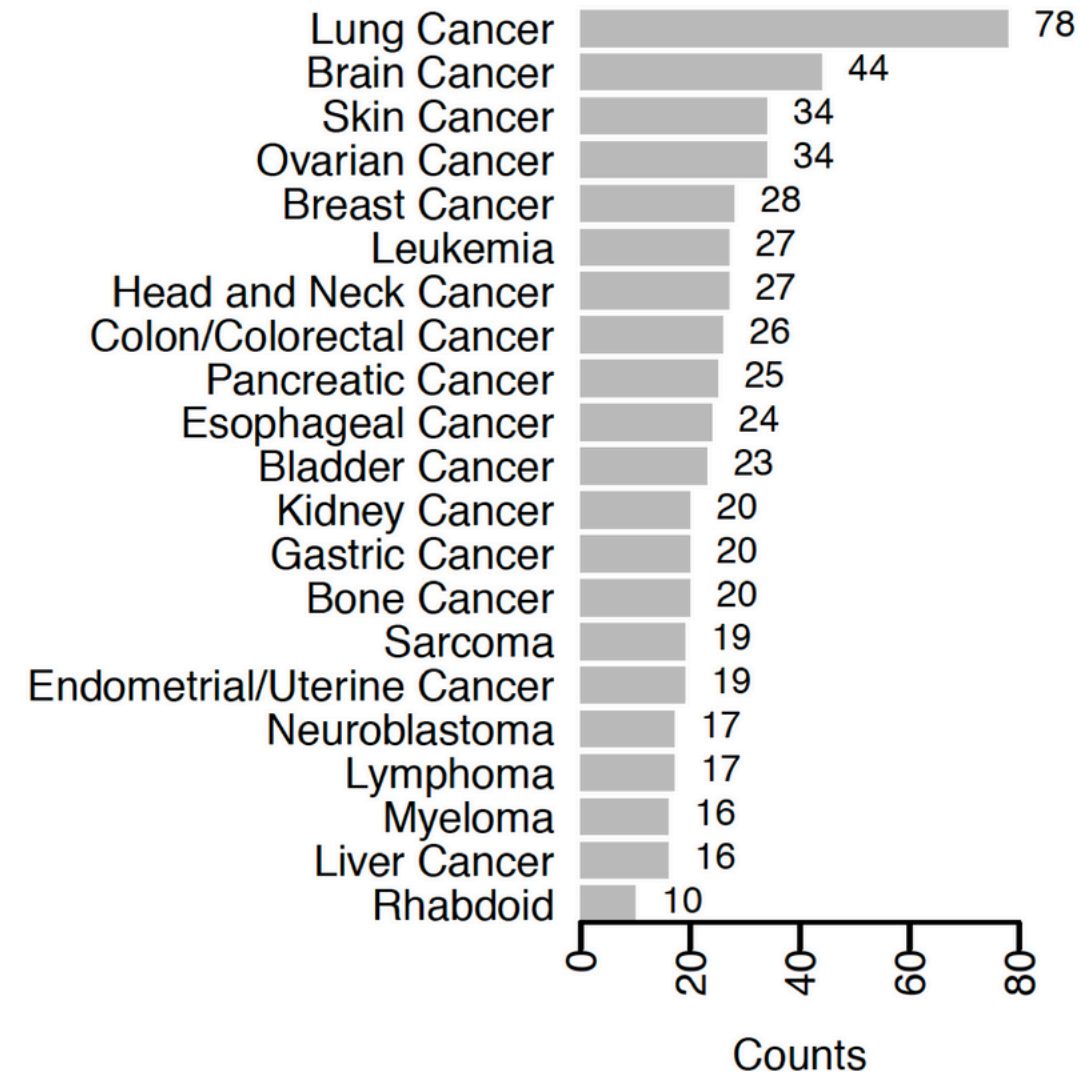
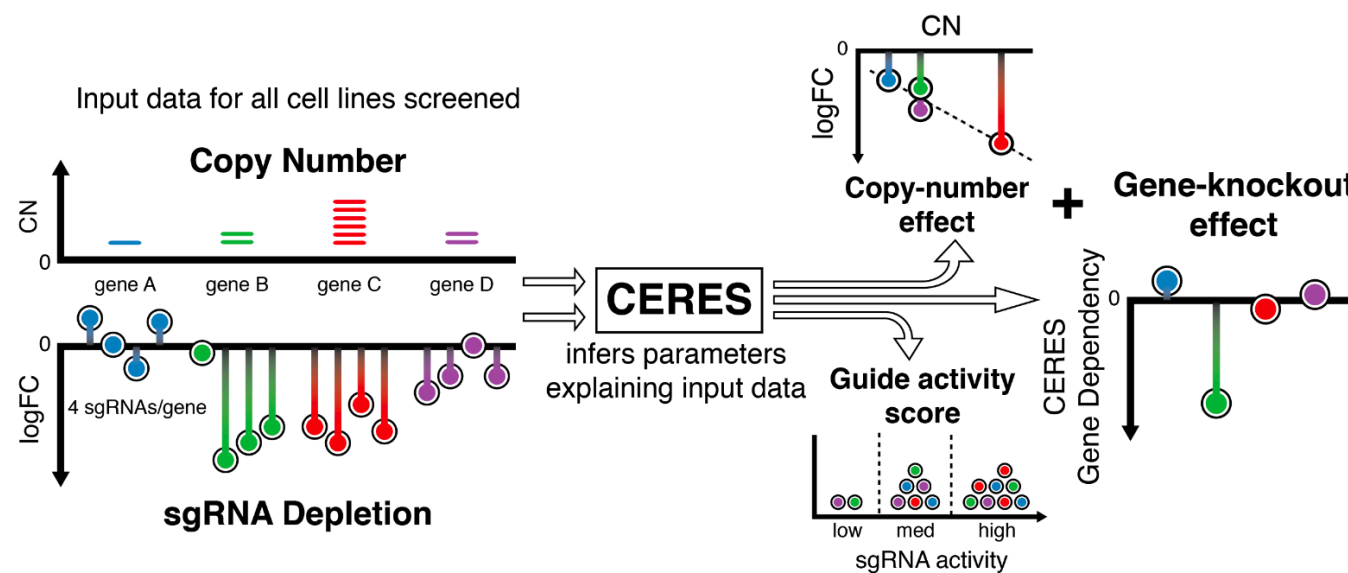


# Project 01: genetic interactions in Cancer cells



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- Knockdown assays (Project DepMap/CERES):  
CRISPR-Cas9 for ~17.000 genes  
across 544 cell lines



[Meyer et al., 2017]



# Datasets

- **Gene expression** in various cancer cell lines
- **Mutations** in genes in each cell line & copy-number alterations in each cell line
- **Knock-down sensitivity** in all cell lines for 17.000 genes
- **Annotations** for cell lines (tissue, ...)

	ACH-000004	ACH-000005	ACH-000007	ACH-000009	ACH-000011	ACH-000012	ACH-000013
<b>TSPAN6</b>	2.61588707	3.06695024	4.06608919	6.50795317	4.57773093	5.82094479	5.53387478
<b>TNMD</b>	0.00000000	0.00000000	0.00000000	0.09761080	0.00000000	0.00000000	0.05658353
<b>DPM1</b>	5.32337007	5.76261458	5.88996020	7.98162436	5.53574194	6.00652245	7.53216108
<b>SCYL3</b>	2.40599236	2.99276843	3.04963077	2.24792751	2.08746284	1.91456452	1.91073266
<b>C1orf112</b>	3.90207358	5.35966172	3.76022095	4.49121176	2.64616266	3.75167795	3.54720302
<b>FGR</b>	0.92599942	0.23878686	0.02856915	0.00000000	0.00000000	0.02856915	0.02856915
<b>CFH</b>	4.88898672	5.70016225	0.01435529	0.02856915	0.35614381	2.68929916	1.98550043

Hugo_Symbol	Entrez_Gene_Id	NCBI_Build	Chromosome	Start_position	End_position	Strand	Variant_Classification
RNF207	388591	37	1	6279339	6279339	+	Missense_Mutation
RNF207	388591	37	1	6279339	6279339	+	Missense_Mutation
PLEKHG5	57449	37	1	6533165	6533165	+	Missense_Mutation
PDPN	10630	37	1	13940848	13940848	+	Missense_Mutation
CASP9	842	37	1	15819484	15819484	+	Missense_Mutation
RAP1GAP	5909	37	1	21924552	21924552	+	Missense_Mutation
C1QC	714	37	1	22974054	22974054	+	Silent
CNKSR1	10256	37	1	26514778	26514778	+	Frame_Shift_Del
AHDC1	27245	37	1	27875454	27875454	+	Missense_Mutation
COL16A1	1307	37	1	32133218	32133218	+	Silent
CSMD2	114784	37	1	32133218	34383844	+	Silent
LRRC8C	84230	37	1	90179033	90179033	+	Missense_Mutation
SPAG17	200162	37	1	118567972	118567973	+	Frame_Shift_Del
TBX15	6913	37	1	119427935	119427935	+	Missense_Mutation

	ACH-000004	ACH-000005	ACH-000007	ACH-000009
<b>A1BG</b>	0.1346453616	-0.212445060	0.043317923	0.0705119999
<b>A1CF</b>	0.0755362715	0.233123579	0.066837574	0.0084297636
<b>A2M</b>	-0.1402086015	0.044364933	-0.036196515	0.0271141959
<b>A2ML1</b>	0.0139284337	0.173837240	0.134781001	0.0559267727
<b>A3GALT2</b>	0.0291310328	-0.124389318	0.082995584	0.0463253889
<b>A4GALT</b>	-0.1472838445	-0.298849014	0.119084008	0.0159682666
<b>A4GNT</b>	0.2758291936	0.120259815	0.057116006	0.0535023006
<b>AAAS</b>	-0.3636329615	-0.339925280	-0.352541473	-0.4988600588

# Project 01: genetic interactions in Cancer cells



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- Select cancer type and corresponding cell lines
- Determine driver mutations from the literature (e.g. EGFR mutations in lung cancer)
- Determine potential synthetic lethal mutations/ copy- number alterations from knock-down screens by splitting **mutated/non-mutated** cell lines

non-  
mutated  
cell lines

mutated  
cell lines