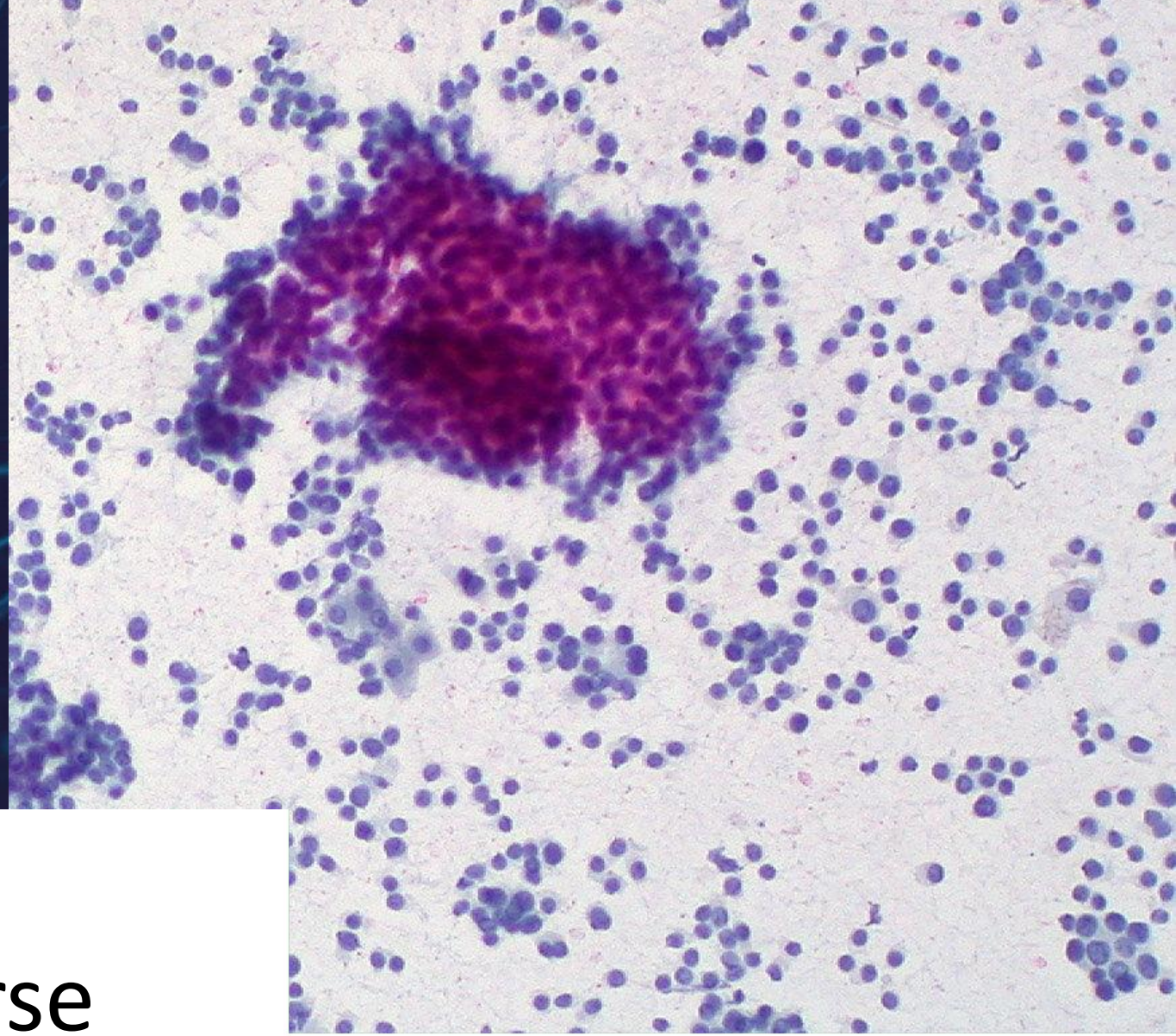


15-16 February 2021

COMETH Training course

From omics data

to tumor heterogeneity quantification

EIT Health is supported by the EIT, a body of the European Union

15 February 2021

Cometh web-app tutorial

EIT Health is supported by the EIT,
a body of the European Union

Choose a dataset to analyze

Datasets provided on our website

https://cancer-heterogeneity.github.io/

TCGA public cancer databas

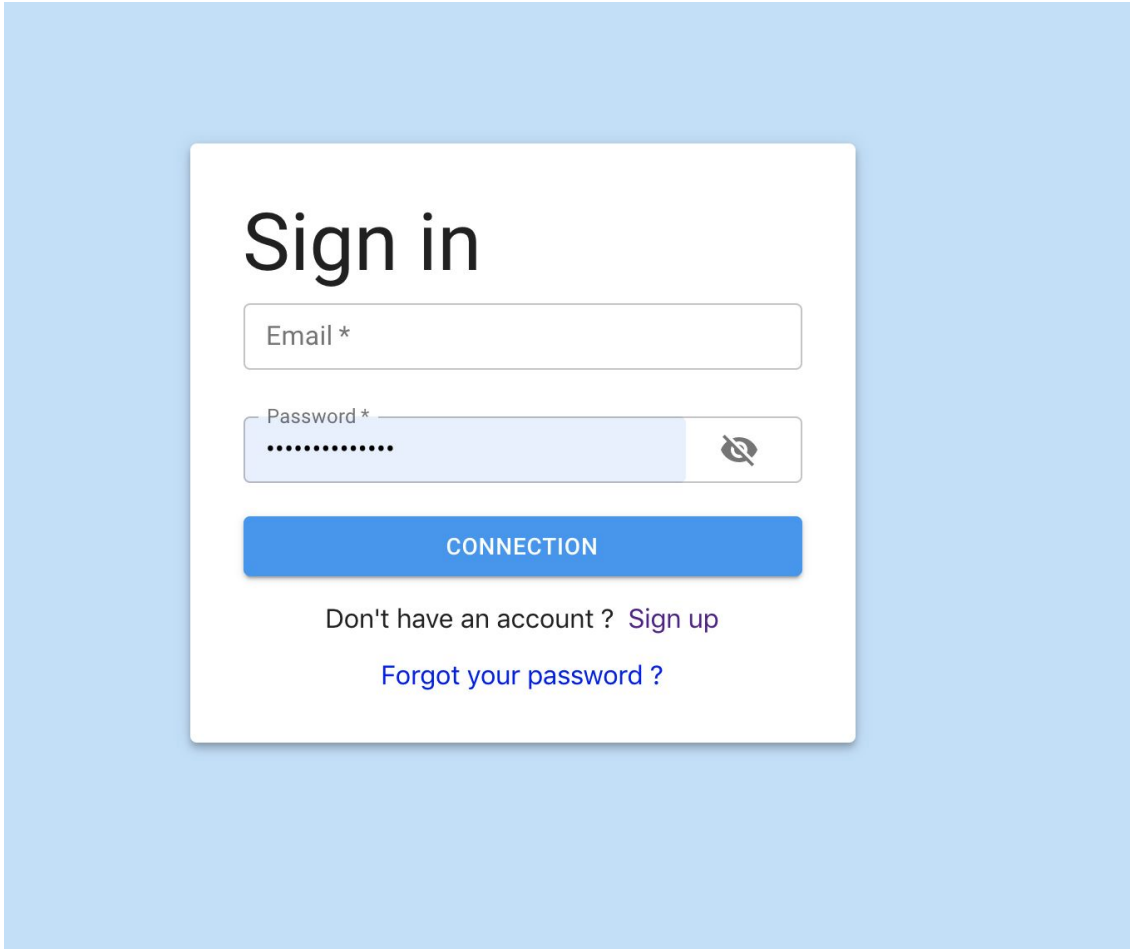
Omic type : transcriptome (fpkm from RNA-seq, linear scale)

- Breast cancer - brca
- Glioblastome - gbm
- Lund adenocarcinoma - luad
- Pancreatic adenocarcinoma - paad
- Skin cutaneous melanoma - skcm

Your own dataset

Be careful with the format:
.cvs with separator = “;” and decimal = “.”
Samples in column
Genes in row (use Gene Symbol as gene ID).

Cometh web-app



Cometh

https://staging-cometh.meteorlab.st/

General view

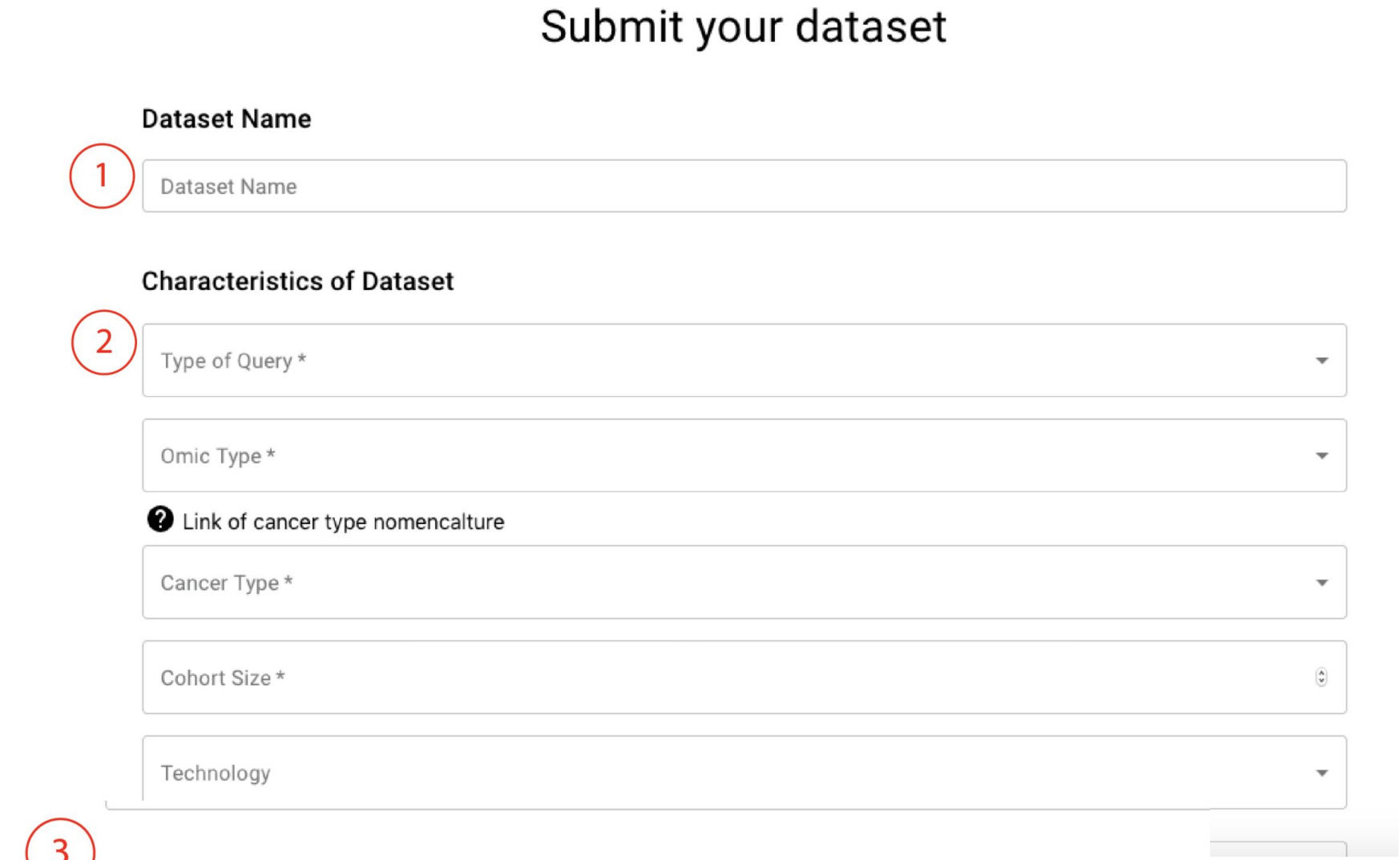
1

ADD NEW DATASET

	Dataset name	Caracterictics of the dataset	Number of methods	Additional informations	Creation date	Actions
2	brca	Cancer Type: brca Omic Type: Transcriptome Type of Query: All cell types	1		2021-02-08	VIEW BENCHMARK (3) VIEW RESULTS (4) DELETE (5)
	gbm	Cancer Type: gbm Omic Type: Transcriptome Type of Query: All cell types	1		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE
	paad	Cancer Type: paad Omic Type: Transcriptome Type of Query: All cell types	2		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE
	luad	Cancer Type: luad Omic Type: Transcriptome Type of Query: All cell types	1		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE
	skcm	Cancer Type: skcm Omic Type: Transcriptome Type of Query: Immune cell types	1		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE

- 1: Add a new dataset
- 2: For a given dataset: details on method run on the dataset (run status, run id…)
- 3: For a given dataset: View leaderboard of computational methods apply on similar datasets
- 4: For a given dataset: View the results of the methods applied on the dataset
- 5: For a given dataset: Delete the dataset

Submit a dataset



- 1: Name your dataset
- 2: Specify your type of query: do you want to quantify all cell type or only immune cell types?
- 3: Give information of your dataset and upload it

General view

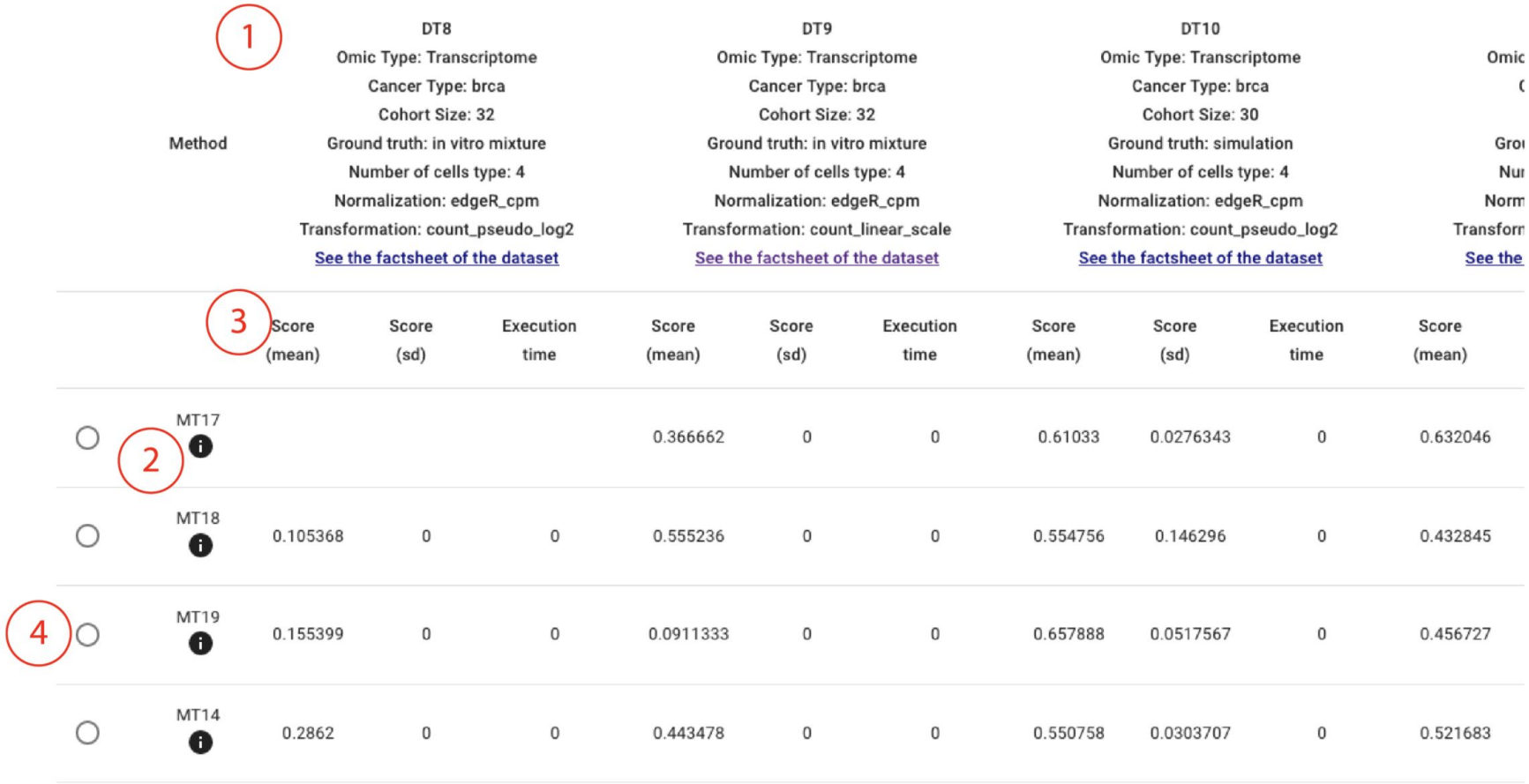
1

ADD NEW DATASET

	Dataset name	Caracterictics of the dataset	Number of methods	Additional informations	Creation date	Actions
2	brca	Cancer Type: brca Omic Type: Transcriptome Type of Query: All cell types	1		2021-02-08	VIEW BENCHMARK (3) VIEW RESULTS (4) DELETE (5)
	gbm	Cancer Type: gbm Omic Type: Transcriptome Type of Query: All cell types	1		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE
	paad	Cancer Type: paad Omic Type: Transcriptome Type of Query: All cell types	2		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE
	luad	Cancer Type: luad Omic Type: Transcriptome Type of Query: All cell types	1		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE
	skcm	Cancer Type: skcm Omic Type: Transcriptome Type of Query: Immune cell types	1		2021-02-08	VIEW BENCHMARK VIEW RESULTS DELETE

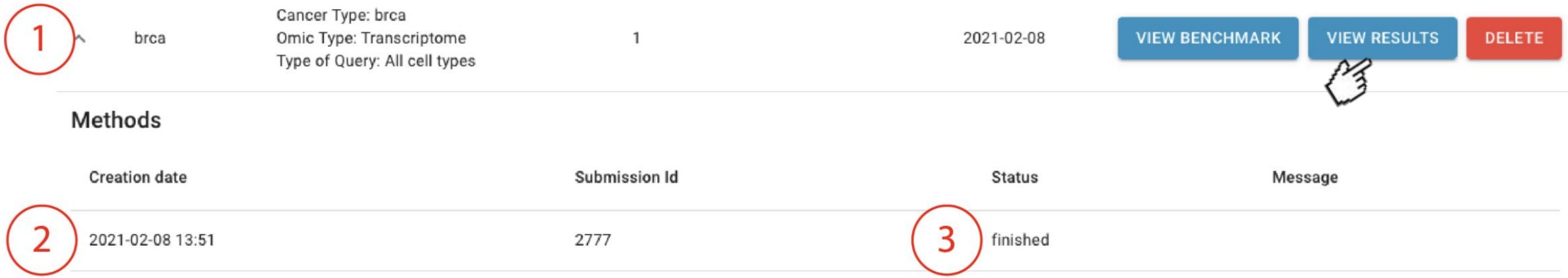
- 1: Add a new dataset
- 2: For a given dataset: details on method run on the dataset (run status, run id…)
- 3: For a given dataset: View leaderboard of computational methods apply on similar datasets
- 4: For a given dataset: View the results of the methods applied on the dataset
- 5: For a given dataset: Delete the dataset

View the leaderboard and run method on your dataset



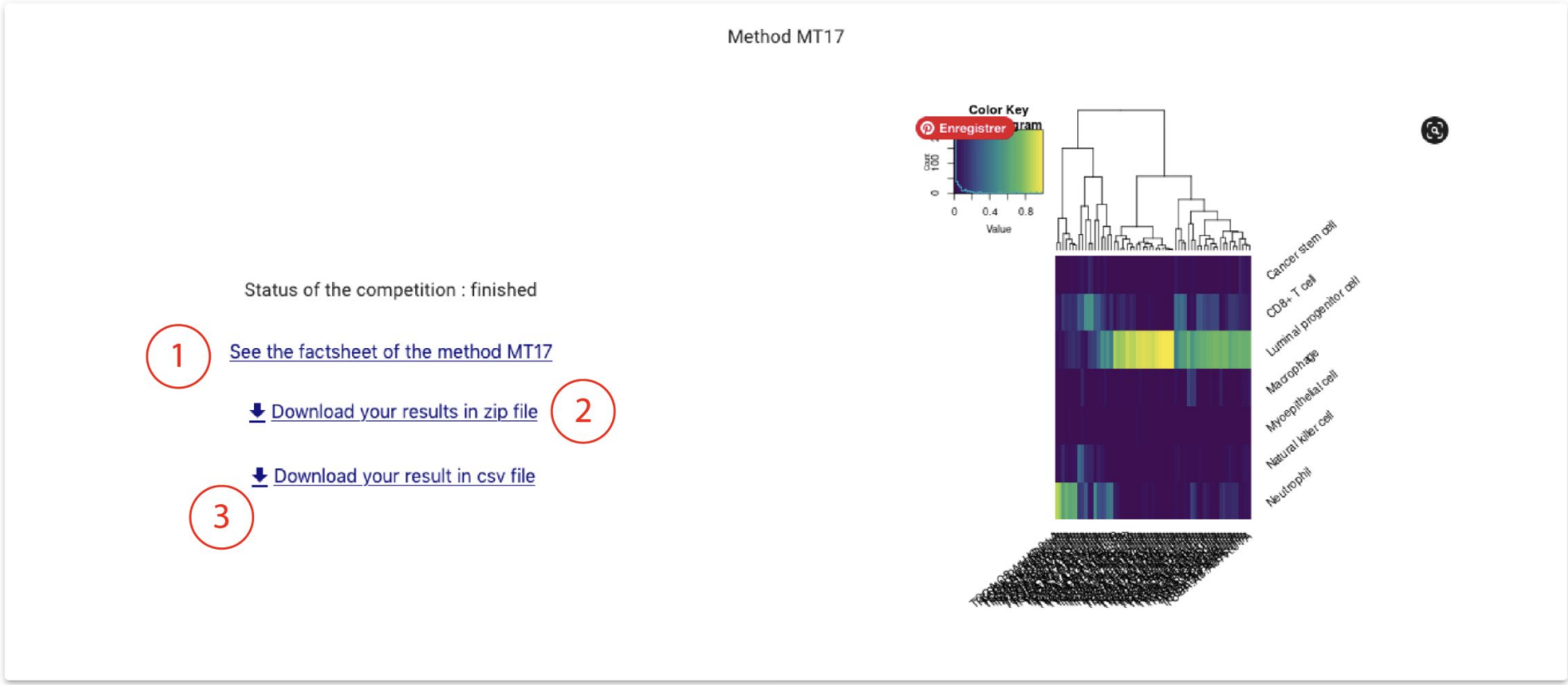
- 1: In columns: benchmark dataset similar to your clinical dataset according to the descriptors you entered while submitting your dataset. You can retreive more detailed information on each datase by clicking on the html link
- 2: Computational methods (MT) that have been applied to quantify heterogeneity of these benchmark dataset on codabench. You can retreive more detailed information on each datase by clicking on the “i” button (including the R code of the algorithm)
- 3: Accurary score (mean, standart deviation and computation time) given by the codabench platform. You can sort the scores by clicking on the column names
- 4: You can choose which method you want to run on your dataset by clicking on this button

Check status of methods run



- 1: Click on the arrow to view the Methoods run agains the dataset
- 2: Date of the run
- 3: Status of the run

View results



- 1: Get more information on the method
- 2: Download all results, including algorithm code, estimated proportion matrix and estimated cell-type specific profiles. In this folder, you have the following files:
  - the estimated proportion matrix in .csv and .rds format : `results_1.rds` and `results_A_1.csv`
  - the estimated reference profiles matrix in .csv and .rds format : `ref_1.rds` and `results_T_1.csv`
  - the input dataset in .rds format and associated metadata : `test_data.rds` (the clinician dataset), `cancer_type.rds` (the cancer type according to the TCGA nomenclature), `input_k_value.rds` (the number of cell type to consider when running unsupervised methods, this file in empty when running semi-supervised or supervised methods)
  - some log and metadata files generated by the codabench platform (not of use for results interpretation): `metadata` , `output_program.txt` , `Rprof.out` , `Rprof.rds`
- 3: Dowload only the estimated proportions in a .csv format (only the `results_A_1.csv` file)

COMETH Training course

- COMETH training course : objectives
- Digital platforms
  - Zoom plenary sessions
  - Discord discussion platform
  - Codabench
  - COMETH web application
  - COMETH Docker image deconExplorer
  - COMETH shiny application
- Material to download
  - For medical group
  - For bioinformatic group
- Presentation supports
  - DAY1
  - DAY2
- Course format and program
- Target Group
- Registration
- Trainers

GET THE ONLINE TUTORIAL

Yuna Blum, Ligue contre le Cancer

Jérôme Cros, APHP

Clémentine Decamps, Uni Grenoble Alpes

Carl Herrmann, Medical Faculty Heidelberg

Slim Karkar, Uni Grenoble Alpes

Yasmina Kermezli, Uni Grenoble Alpes

Magali Richard, Uni Grenoble Alpes

Ashwini Sharma, Uni Grenoble Alpes

https://cancer-heterogeneity.github.io/cometh_training.html

www.eithealth.eu | info@eithealth.eu

EIT Health is supported by the EIT, a body of the European Union