

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



Choose a dataset to analyze

Datasets provided on our website

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



Your own dataset

Be careful with the format:

.csv with separator = “;” and decimal = “.”

Samples in column

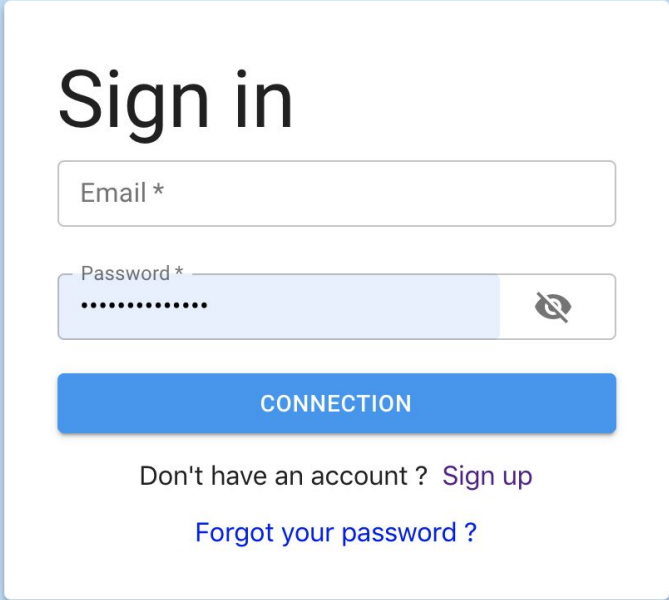
Genes in row (use Gene Symbol as gene ID).

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](#)

Cometh web-app



Sign in

Email *

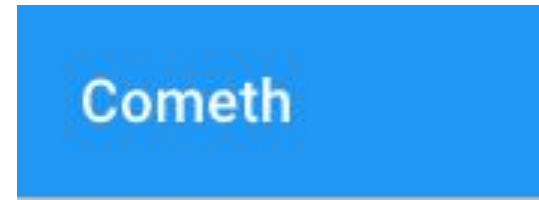
Password *

.....

CONNECTION

Don't have an account ? [Sign up](#)

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

General view

1

ADD NEW DATASET

	Dataset name	Characteristics 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	3 VIEW BENCHMARK	4 VIEW RESULTS	5 DELETE
	▼ 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


Submit your dataset

Dataset Name

1

Characteristics of Dataset

2

 Link of cancer type nomenclature

3

- 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	Characteristics 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	3 VIEW BENCHMARK	4 VIEW RESULTS	5 DELETE
	▼ 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

	DT8			DT9			DT10			Omic
	Omic Type: Transcriptome			Omic Type: Transcriptome			Omic Type: Transcriptome			Omic
	Cancer Type: brca			Cancer Type: brca			Cancer Type: brca			(
	Cohort Size: 32			Cohort Size: 32			Cohort Size: 30			
Method	Ground truth: in vitro mixture			Ground truth: in vitro mixture			Ground truth: simulation			Gro
	Number of cells type: 4			Number of cells type: 4			Number of cells type: 4			Nur
	Normalization: edgeR_cpm			Normalization: edgeR_cpm			Normalization: edgeR_cpm			Norm
	Transformation: count_pseudo_log2			Transformation: count_linear_scale			Transformation: count_pseudo_log2			Transfor
	See the factsheet of the dataset			See the factsheet of the dataset			See the factsheet of the dataset			See the
	Score (mean)	Score (sd)	Execution time	Score (mean)	Score (sd)	Execution time	Score (mean)	Score (sd)	Execution time	Score (mean)
<input type="radio"/> 2 MT17 i				0.366662	0	0	0.61033	0.0276343	0	0.632046
<input type="radio"/> MT18 i	0.105368	0	0	0.555236	0	0	0.554756	0.146296	0	0.432845
4 <input type="radio"/> MT19 i	0.155399	0	0	0.0911333	0	0	0.657888	0.0517567	0	0.456727
<input type="radio"/> MT14 i	0.2862	0	0	0.443478	0	0	0.550758	0.0303707	0	0.521683

- 1: In columns: benchmark dataset similar to your clinical dataset according to the descriptors you entered while submitting your dataset. You can retrieve more detailed information on each dataset 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 retrieve more detailed information on each dataset by clicking on the “i” button (including the R code of the algorithm)
- 3: Accuracy score (mean, standard 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	brca	Cancer Type: brca Omic Type: Transcriptome Type of Query: All cell types	1	2021-02-08	VIEW BENCHMARK	VIEW RESULTS	DELETE
Methods							
	Creation date		Submission Id		Status	Message	
2	2021-02-08 13:51		2777		3 finished		

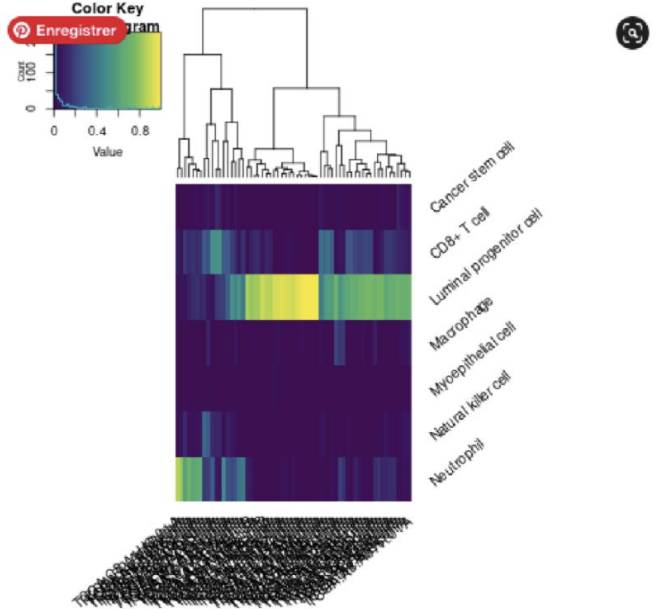
- 1: Click on the arrow to view the Methods run against the dataset
- 2: Date of the run
- 3: Status of the run

View results

Method MT17

Status of the competition : finished

- 1 [See the factsheet of the method MT17](#)
- 2 [Download your results in zip file](#)
- 3 [Download your result in csv file](#)



- 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 is 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: Download only the estimated proportions in a .csv format (only the `results_A_1.csv` file)

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Yuna Blum, Ligue contre le Cancer

Jérôme Cros, APHP

Clémentine Decamps, Uni Grenoble Alpes

Carl Herrmann, Medical Faculty Heidelberg

Slim Karkar, Uni Grenoble Alpes

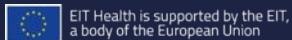
Yasmina Kermezli, Uni Grenoble Alpes

Magali Richard, Uni Grenoble Alpes

Ashwini Sharma, Uni Grenoble Alpes

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

www.eithealth.eu | info@eithealth.eu



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