

15-16 February 2021

COMETH Training course

to tumor heterogeneity quantification

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





15 February 2021

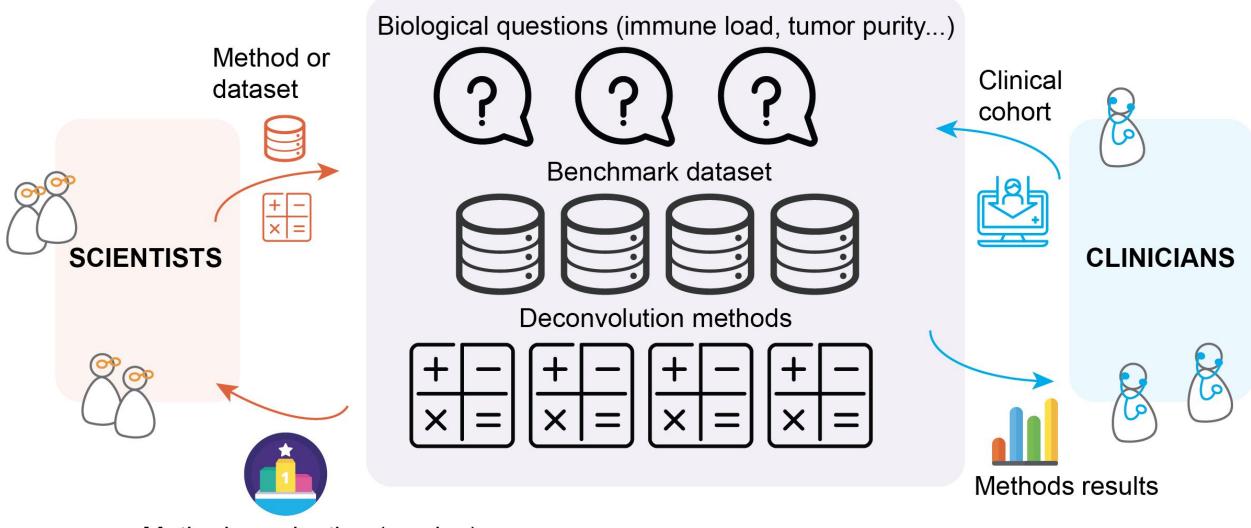
Digital tools Magali Richard





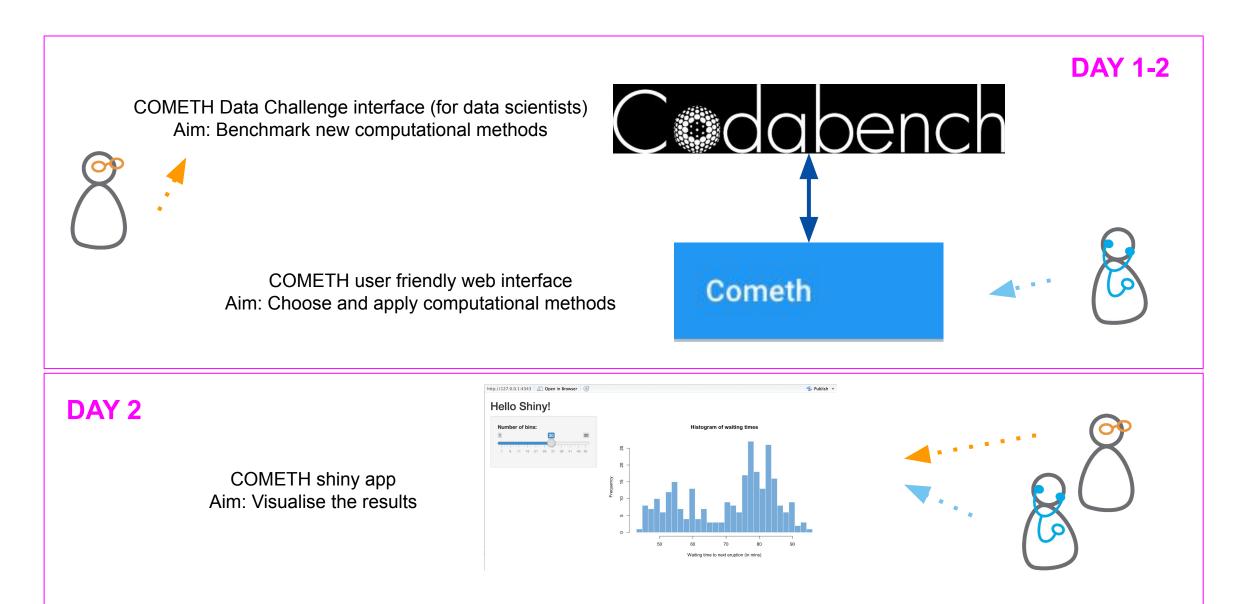


The COMETH program



Methods evaluation (scoring)

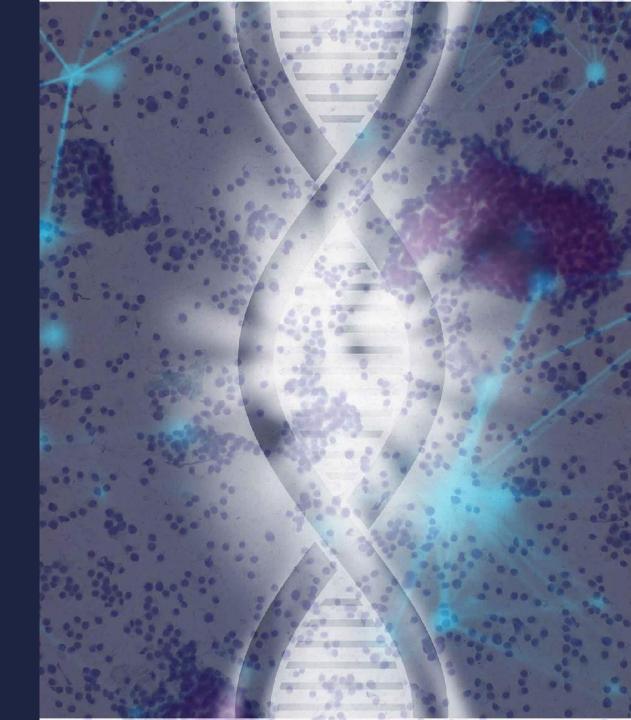
The COMETH interfaces



How to evaluate a computational method?

Compare your estimate with a ground truth Evaluate the accuracy of the estimation





The Ground Truth datasets used in COMETH project



Complex omic data on bulk samples







TRANSCRIPTOME

(RNA-seq)

Lung adenocarcinoma (luad) Colorectal adenocarcinoma (coad)

Pancreatic adenocarcinoma (paad)

TRANSCRIPTOME

·

Breast invasive carcinoma (brca)

TRANSCRIPTOME (RNA-seq)

METHYLOME (450K)

METHYLOME (27K)

METHYLOME (Meth-EPIC)

(RNA-seq)

The Ground Truth datasets used in COMETH project

In silico

In vitro

mixtures

simulations



Ground Truth (real tumor composition in cell types proportions)



Lung adenocarcinoma (luad)

Colorectal adenocarcinoma (coad)

Pancreatic adenocarcinoma (paad)

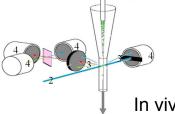
Breast invasive carcinoma (brca)

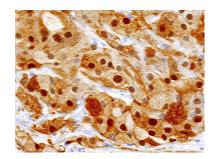






More to come...







In vivo FACS countings

In vivo immuno

The computational methods used in the COMETH project (transcriptome)



To quantify all cell types

To quantify immune cell types

Unsupervised

NMF-based (MT2 & MT19) ICA-based (MT1 & MT14) NMF-based (MT19) ICA-based (MT14)

Semi supervised

NMF-based (MT16, MT17 & MT18)

Cibersort (MT8) EPIC (MT9) Quantiseq (MT11)

Supervised

The computational methods used in the COMETH project (methylome)



To quantify all cell types

To quantify immune cell types

Unsupervised

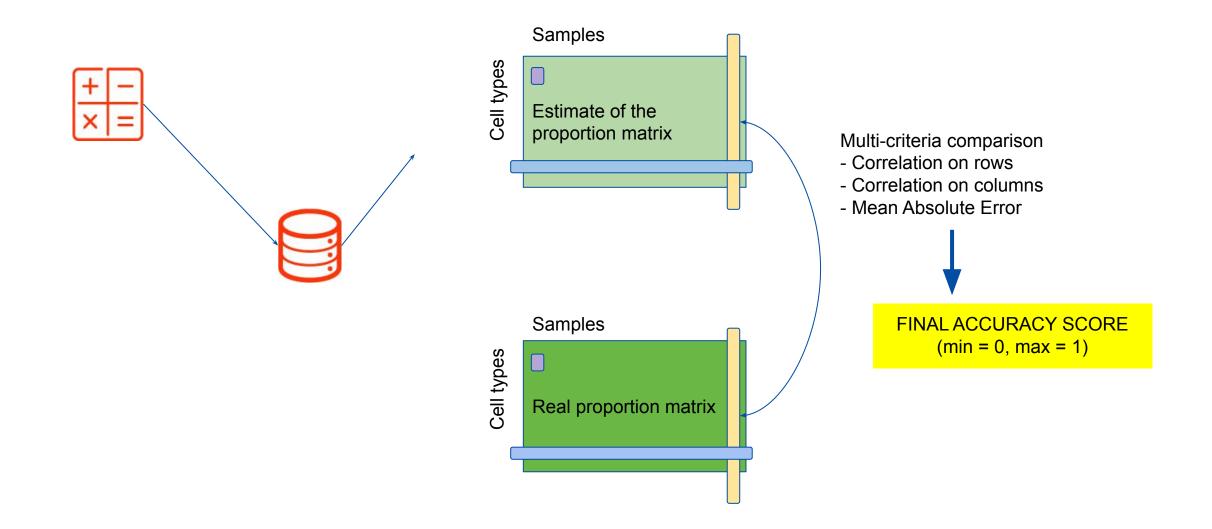
Edec (MT3) NMF-based (MT19) ICA-based (MT14)

Semi supervised

Supervised

EdiDISH (MT6)

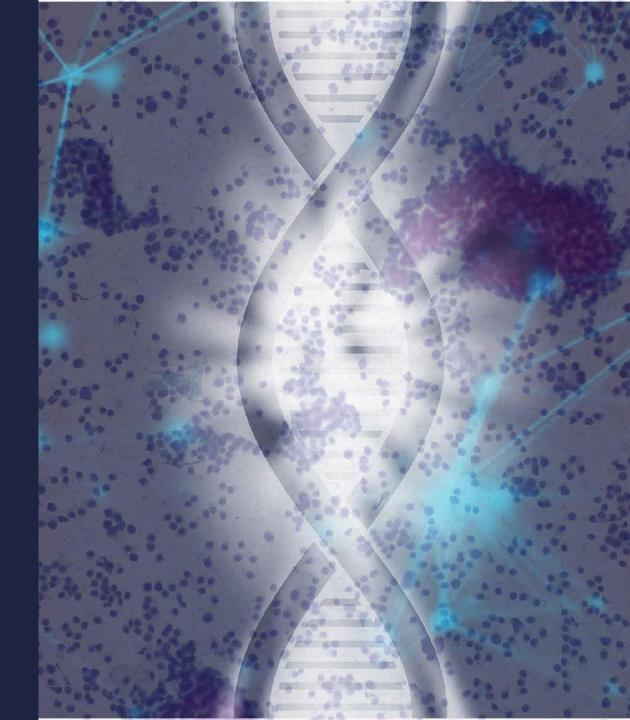
Evaluation of method performances (scoring)



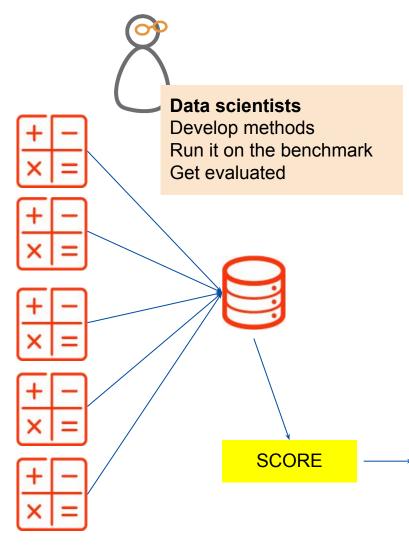
Which digital interfaces?

The COMETH data challenge interface The COMETH user-friendly web application The COMETH shiny app for visualisationn





Systematic method evaluation





Edit Participants Submissions Dumps Migrate

ORGANIZED BY: Magrichardtest CURRENT PHASE ENDS: Never CURRENT SERVER TIME: 9 Février 2021 À 10:10 UTC+1 Secret url: https://www.codabench.org/competitions/218/?secret_key=751dc324-449f-4c69-9db5-4847baf02549



Codabench Leaderboard

Results								
Task:		Fact Sheet Answers	MT1_v4			MT2_v4		
#	Participant	Submission ID?	Accuracy_mean	Accuracy_sd	Time	Accuracy_mean	Accuracy_sd	Time
ō	magrichardtest	DT1 pancreas	n/a	n/a	n/a	0.9721809186	0.0057113517	0.00000000
2	magrichardtest	DT pancreas linear	0.7299364238	0.0309803372	0.000000000	n/a	n/a	n/a
3	magrichardtest	DT8 brca log 32	0.2888423247	0.000000000	0.0000000000	n/a	n/a	n/a
4	magrichardtest	DT9 brca lin 32	0.4431279213	0.0000000000	0.0000000000	n/a	n/a	n/a
6	magrichardtest	DT11 breast linear	n/a	n/a	n/a	0.4200006067	0.2359621818	0.00000000
6	magrichardtest	DT10 breast log	n/a	n/a	n/a	n/a	n/a	n/a
7	magrichardtest	DT4	n/a	n/a	n/a	0.5660189192	0.000000000	0.00000000
8	magrichardtest	DT5	0.8315607989	0.000000000	0.000000000	n/a	n/a	n/a
0		DT1 pancreas	- 1-	- 2	- 1-	-	- 1-	-

Access current leaderboard Apply methods on clinical dataset



2) Run methods

3) Send results

0

0

0

0

0

MT16

0

0.432079

0

0

		DT8		DT9 Omic Type: Transcriptome				
	Om	ic Type: Trans	criptome					
		brca	Cancer Type: brca					
		Cohort Size	: 32	Cohort Size: 32				
Method	Ground truth: in vitro mixture			Ground truth: in vitro mixture				
	N	umber of cells	type: 4	Number of cells type: 4 Normalization: edgeR_cpm Transformation: count_linear_scale				
	Nor	malization: ed	lgeR_cpm					
	Transfor	mation: count	_pseudo_log2					
	See the factsheet of the dataset			See the factsheet of the dataset				
	Score	Score	Execution	Score	Score	Execution		
	(mean)	(sd)	time	(mean)	(sd)	time		
MT17				0.366662	0	0		
MT18	0.105368	0	0	0.555236	0	0		
MT19	0.155399	0	0	0.0911333	0	0		
MT14	0.2862	0	0	0.443478	0	0		

Cometh





0

0.223464

0

Clinicians Upload a dataset Check leaderboard Choose a method to run Get the results

In practical during the COMETH training

Migrate



Edit	Participants	Submissions	Dumps	

ORGANIZED BY: Magrichardtest CURRENT PHASE ENDS: 15 Mars 2021 À 01:00 UTC+1

CURRENT SERVER TIME: 9 Février 2021 À 10:26 UTC+1 Secret un: https://www.codabench.org/competitions/237/?secret_key=b164d1c1-07ca-4d0c-b55f-99e68af3a343

Computational group DAY 1-2

Learn how to contribute to the codabench benchmark using a toy data challenge



Learn how to use the user-friendly COMETH web application to run methods on toy TCGA clinical datasets



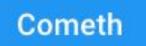


Learn how to biologically interpret the results of the methods

Important Note



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All digital platform develop within COMETH program are now at staging state of development The URLs provided during the training course are TEMPORARY Please fill up the final questionnaire and indicate your interest in the program to be informed when all the tools will be at production state (final public URLs) LET'S START THE PRACTICAL WORK ON...



discord







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

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Practical session medical group

