

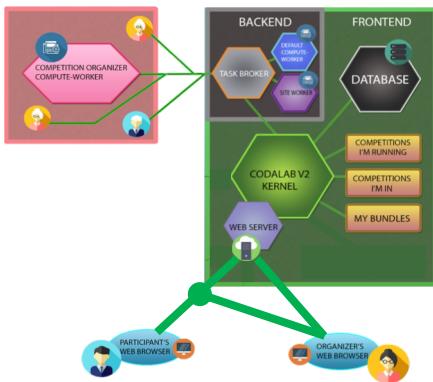
HADACA – Health Data Challenge

Deconvolution methods to quantify tumor heterogeneity

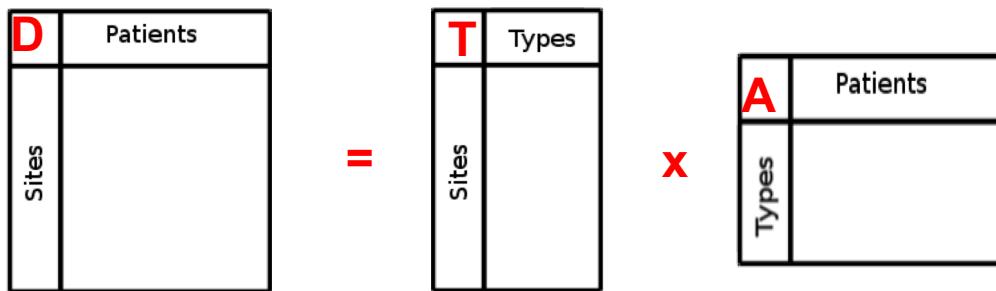


Restitution on challenge #1

Introduction to the challenge #2



1) How to use the challenge platform codalab?



2) Challenge #2 Starting kit

CHALLENGE #2 - Files

[Learn the Details](#)[Phases](#)[Participate](#)[Results](#)[Public Submissions](#)[Forums](#) ➔[Data](#)[Files](#)[Submit / View](#)[Results](#)

	Download	Size (mb)	Phase
	Starting Kit	0.270	#1 CHALLENGE #1
	Public Data	173.181	#1 CHALLENGE #1
	Starting Kit	0.270	#2 CHALLENGE #2 // Phase 1 // Exploration
	Public Data	173.198	#2 CHALLENGE #2 // Phase 1 // Exploration

CHALLENGE #2 - Starting Kit & Public Data

■ What files are in the starting kit :

- ▶ *starting_kit_p2.html* :
- ▶ a summary of the challenge with all the required informations

- ▶ *submission_script_p2.Rmd* :
- ▶ a Rmd file to modify with your code
- ▶ this file generates the zip files to upload on Codalab

■ What files are in public data :

- ▶ DC2_D_met.rds : methylome data
- ▶ DC2_D_rna.rds : transcriptome data

CHALLENGE #2 – Submit Results

[Learn the Details](#)[Phases](#)[Participate](#)[Results](#)[Public Submissions](#)[Forums !\[\]\(5a132f13505a6571904d622757b7a8f0_img.jpg\)](#)[Data](#)[CHALLENGE #1](#)[CHALLENGE #2 // Phase 1 // Exploration](#)[Files](#)[CHALLENGE #2 // Phase 2 // Validation](#)[Submit / View
Results](#)

Phase description

Estimate the proportion matrix A from a mixture matrix D (either DNAm or RNA-seq). Submit your script (program) on the platform.
(Data type correspondence : 1.0 = met, 2.0 = rna)

Max submissions per day: 20

Max submissions total: 20

Click the Submit button to upload a new submission.

*Team name (20 characters max):

*Method name (20 characters max):

*Method description:

[Submit](#)

CHALLENGE #2 – Submitted Results

■ What files are in the submitted zip file (phase 1) :

- ▶ *results.rds* → your estimation of A
- ▶ *dataType.rds* → the variable ‘*dataType*’ = both

■ What files are in the submitted zip file (phase 2) :

- ▶ *program.R* → a R file with :
 - your code inside the function ‘*program*’
 - the variable ‘*dataType*’ = met or rna (based on your team name)
- ▶ *metadata* → a file required by Codalab
 - use the one generated by the starting kit and don’t modify it !

CHALLENGE #2 – Leaderboard

Learn the Details Phases Participate Results

Public Submissions Forums ➔

CHALLENGE #1

CHALLENGE #2 // Phase 1 // Exploration

CHALLENGE #2 // Phase 2 // Validation

Phase description

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Max submissions per day: 20

Max submissions total: 20

[Download CSV](#)

[Download all submissions on leaderboard](#)

Results

#	User	Entries	Date of Last Entry	Team Name	MAE ▲	MAE 1 ▲	MAE 2 ▲	Data Type ▲	Detailed Results
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CHALLENGE – Public Submissions & Forum

Public Submissions

[Go Back to Competition Homepage](#)

[CHALLENGE #1](#) [CHALLENGE #2 // Phase 1 // Exploration](#)

[CHALLENGE #2 // Phase 2 // Validation](#)

No submissions have been made public!

Forums

Health Data Challenge 2019 Forum

[Go back to competition](#) [Start a new topic](#)

Title	Started by	Date created	Latest post	Posts	
↗ FAQ	Alexis_Arnaud	Nov 21, 2019	3 days, 5 hours	1	

CHALLENGE #2: STARTING KIT

■ Your goal: estimate the matrix A

► The matrix A represents the proportion of each cell type in each patient.

You have this

↓

D	Patients
Sites	

=

T	Types
Sites	

x

You search this

↓

A	Patients
Types	

CHALLENGE #2: STARTING KIT

■ Data format

- ▶ RNAseq and DNA methylation
- ▶ 21,566 genes / 772,316 probes
- ▶ 30 patients
- ▶ ? cell types

D	Patients
Sites	

=

T	Types
Sites	

x

A	Patients
Types	

CHALLENGE #2

Last name	First name	Institution	TEAM
Nazarov	Petr	Luxembourg Institute of Health	A
Avila Lobos	Francisco	Center for Medical Genetics, UGent	A
Chuffart	Florent	INSERM	A
BAHENA HERNANDEZ	Silvia Yahel	Uppsala University	A
		University of Heidelberg	B
		CEA	B
		University of Grenoble Alpes	B
Doncevic	Daria	Uppsala University	B
Jardillier	Rémy	Verteego	C
Newar	Kapil	Verteego	C
Nyrén	Karl	Institut Curie	C
Dirian	Lara	Institut Curie	C
		Verteego	C
		Verteego	C
		Institut Curie	C
Marécaille	Jules	Institut Curie	C
Merlevède	Jane	Institut Curie	C
Sompairac	Nicolas	Institut Curie	C
Kondili	Maria	INSERM , UMRS 938 - Hôpital Saint-Antoine, SIRIC-CURAMUS	D
Novella Rausell	Claudio	Uppsala University	D
		Uppsala University	D
Zacharouli	Markella-Achilleia	Uppsala University	D
Jumentier	Basile	Université Grenoble Alpes	E
Batista	Luciana	Innate Pharma	E
Jeanmougin	Marine	Norwegian Radium Hospital	E
Xie	Ting	INSERM-CRCT	E
Maïé	Tiago	Institute for Computational Genomics, RWTH University Hospital Aachen, Germany	F
		INSERM	F
		Uppsala University	F
BATTO	Anne-Françoise	UMRS 1138 - Centre de Recherche des Cordeliers	G
Waury	Katharina	Vitebsk State Medical University	G
		Max-planck-Institut für Informatik, Saarbrucken	G
		Institut Curie	G
		International Agency for Research on Cancer	G
MEYLAN	Maxime	CNRS - IMAG	H
Kakoichankava	Aliaksandra	INSERM	H
		UGA	H
		DC2_Team_A	DC2_Team_H
Scherer	Michael	DC2_Team_B	
LIU	JING	DC2_Team_C	
Alcala	Nicolas	DC2_Team_D	
DURIF	Ghislain	DC2_Team_E	
Jakobi	Milan	DC2_Team_F	
Jedynak	Pau	DC2_Team_G	