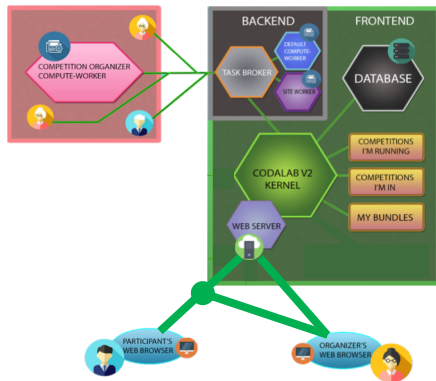


# HADACA – Health Data Challenge

Deconvolution methods to quantify tumor heterogeneity

Restitution on challenge #1

# Introduction to the challenge #2



1) How to use the challenge platform codalab?

<b>D</b>	Patients
Sites	

=

<b>T</b>	Types
Sites	

x

<b>A</b>	Patients
Types	

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

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Forums ↻

[Data](#)  
[Files](#)  
[Submit / View Results](#)

CHALLENGE #1

CHALLENGE #2 // Phase 1 // Exploration

CHALLENGE #2 // Phase 2 // Validation

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

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

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

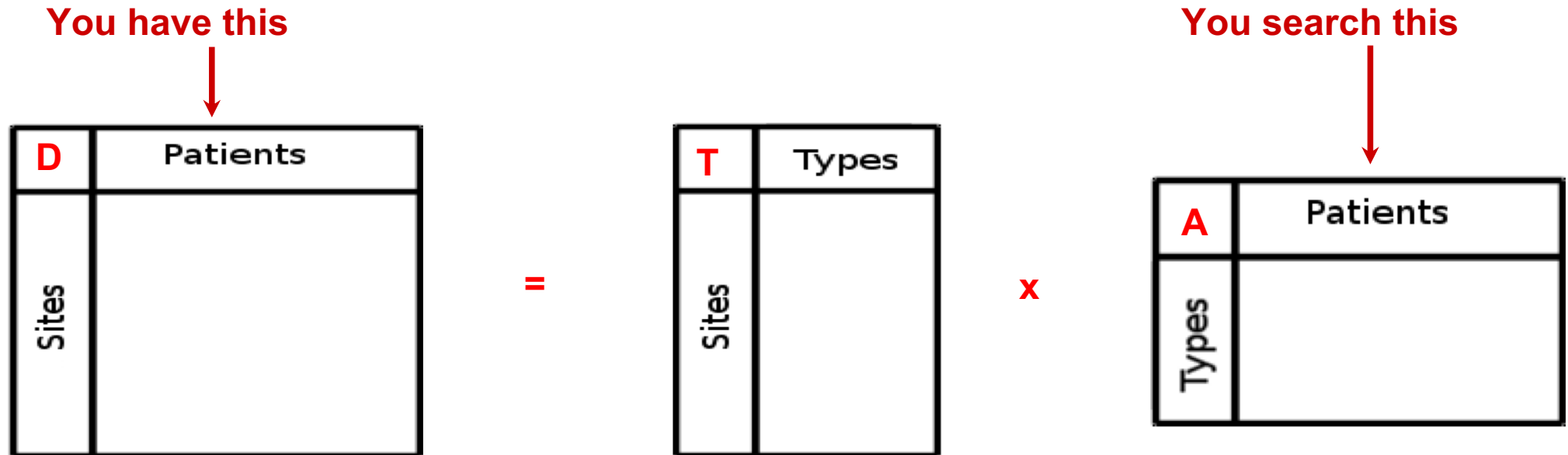
[Go back to competition](#)[Start a new topic](#)

Title	Started by	Date created	Latest post	Posts	
 <a href="#">FAQ</a>	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.



# CHALLENGE #2: STARTING KIT

## ■ Data format

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

<b>D</b>	Patients
Sites	

=

<b>T</b>	Types
Sites	

x

<b>A</b>	Patients
Types	

## CHALLENGE #2

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