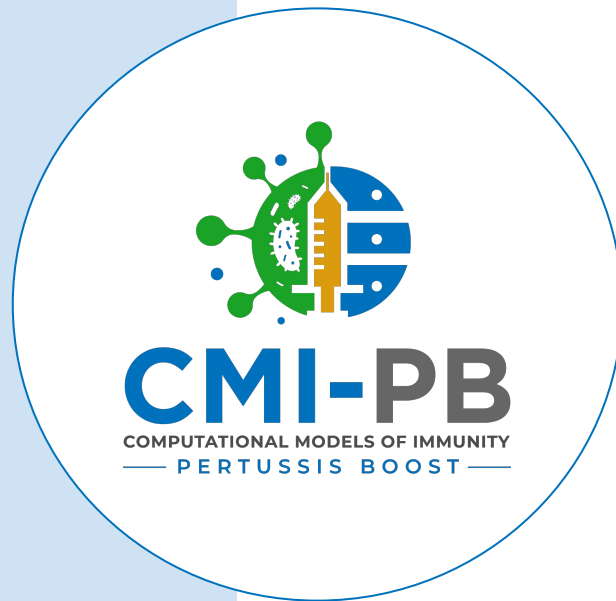


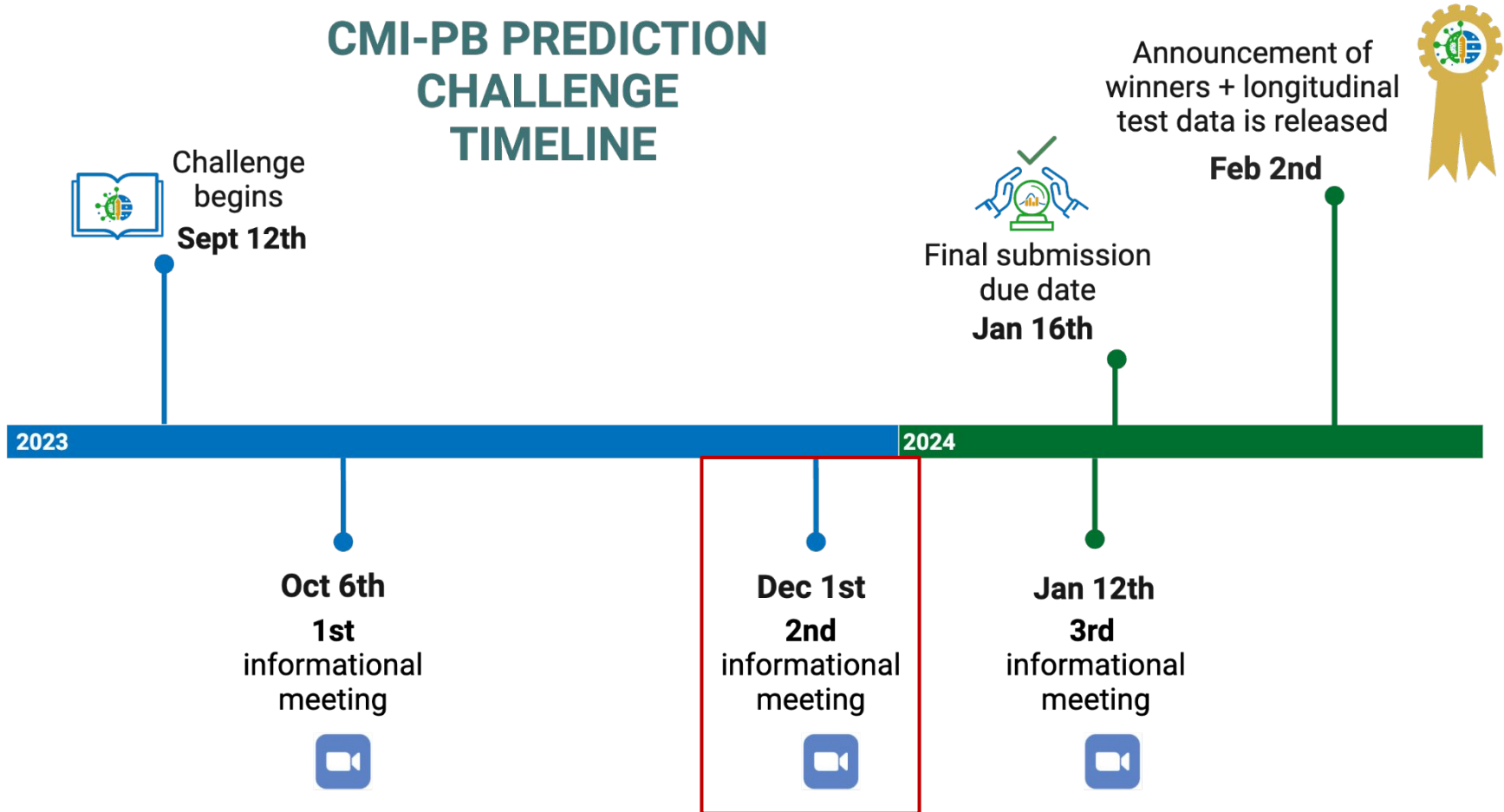
CMI-PB Prediction Challenge

2nd Informational Session
December 1st, 2023

La Jolla Institute for Immunology



CMI-PB PREDICTION CHALLENGE TIMELINE



Agenda for Today's Session

1.
Frequently
Asked
Questions

2.
Submission
Process

3.
Reminders


4.
Q & A

Agenda for Today's Session





1. Codebase.R Availability

- We added all the codebase related data processing pipeline as GitHub [repo](#) as well.
- To find a more comprehensive discussion, access the Solutions Center [here](#).

Is codebase.R (used in data processing tutorial to visualize the processed R object data) available anywhere? 

■ Invited Participants Challenge ■ data-organization

 This is the first time clee has posted — let's welcome them to our community!



clee





Oct 23

Hello,
 At [RPubs - Preparation of training dataset for 2nd CMI-PB challenge](#) ⁴, there's example code that uses "Codebase.R". I couldn't find this file at the github [GitHub - CMI-PB/second-challenge-training-dataset-preparation: Assessing data noise, feature filtering, batch effects between 2020 and 2021 CMI-PB datasets.](#) ³ .
 Is this file available somewhere else?


Thanks!

✔ Solved by [Pramod](#) in [post #2](#) ▼


Thanks for your comment. I am uploading it here for your reference and I will update the Git repo later today. [codebase.R](#) (26.8 KB) Edit 1 (Oct 23, 2023): Git repo has been updated! Best, Pramod

    Reply

created

 Oct 23

last reply

 Oct 23


2 replies

41 views


2 users


2 likes


2 links



▼



Pramod 

 Oct 23

Thanks for your comment. I am uploading it here for your reference and I will update the Git repo later today.
[codebase.R](#) (26.8 KB)

Edit 1 (Oct 23, 2023): Git repo has been updated!

Best,
 Pramod

2. 2020 Gene expression data (actual day relative to boost)

- When `actual_day_relative_to_boost` is 0, the sample was collected from the donor on the same day, but after, the tdap booster was administered.
- To find a more comprehensive discussion, access the Solutions Center [here](#).

Gene expression data, sample check
Invited Participants Challenge

J Joe 1 Oct 13

Could you please check the 2020 gene expression data, pid 24 and 25? Could you please clarify the actual Day0 was happened prior to or post vaccine? I see that -13 and -6 are "Day0", but the actual day "0" is still prior to vaccination or "day1"?

specimen_id	subject_id	actual_day_relative_to_boost	planned_day_relative
114	181	24	-13
115	182	24	0
116	183	24	2
117	184	24	6
118	185	24	13
119	191	25	-6
120	192	25	0
121	193	25	2
122	194	25	6
123	195	25	13

♥ 🔗 ⋮ ↶ Reply

created last reply 1 39 2
Oct 13 Oct 13 reply views users


P Pramod 1 Oct 13

For subject IDs 24 and 25, the `actual_day_relative_to_boost = 0` occurred after the vaccination. The specimens from these two subjects were collected on the day of the tdap booster vaccination but after the vaccine was administered. That's why these two specimens fall under day 1 of `planned_day_relative_to_boost`.


♥ 🔗 ⋮ ↶ Reply

3. Master processed training data


- Ab titer, cytokine, and cell frequency assays are normalized on a yearwise basis and a batch effect correction pipeline is applied afterward.
- For the gene expression assay, only the standard batch effect correction pipeline is applied.
- To find a more comprehensive discussion, access the Solutions Center [here](#).

Questions about the master_processed_training_data RDS object 

■ Invited Participants Challenge



rtippalagama


1  25d


Hello

Ab titre, cytokine and cell frequency assays in the RDS object all have normalized and batch-corrected matrices but the gene expression assay only has a batch-corrected matrix. Why is that? Was there no normalization done on the batch-corrected matrix?

For the other assays, which matrix should we use, the batch-corrected or normalized matrix? What are the colnames in each matrix? do they correspond to specimen ID or subject ID?

Thank you








Pramod 

25d

Thanks, [@rtippalagama](#), for raising these queries.

1. That's correct. We initially normalized Ab titer, cytokine, and cell frequency assays on a yearwise basis using baseline median normalization. Afterward, we applied a batch effect correction pipeline. As for the gene expression assay, we followed the standard batch effect correction pipeline without any prior dataset normalization. That's why you see normalization and batch-corrected files for Ab titer, cytokine, and cell frequency assays and only batch-corrected files for the gene expression dataset.
2. We leave the choice of the most suitable computable matrices to the contestants. Some models/packages come with built-in functionality for batch effect correction (e.g., DESeq), which may be better suited for specific tasks.
3. Both batch-corrected or normalized matrices have feature names as row headers and specimen_id as column headers.

I hope this provides clarity. Please don't hesitate to reach out if you have any further questions.

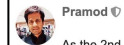
 1     Reply

4. CMI-PB Challenge Data Set tracking

- Participants have noticed inconsistencies and minor issues with the dataset which has prompted us to change some information.
- The current dataset can be found [here](#) or on the CMI-PB site in the Prediction Challenge section under Data and Resources.
- To follow updates and find a more detailed conversation about the legacy of datasets, please refer to [this discussion](#) on the Solutions Center.

2nd Challenge Dataset changes tracking

■ Invited Participants Challenge ■ website ■ api-access



Pramod

4 Oct 13

As the 2nd challenge progresses, contestants might notice inconsistencies or issues in the dataset. This might result in challenge datasets to undergo modifications over time. This page is dedicated to organizing and tracking all changes related to the datasets. Older (legacy) versions of the dataset are stored in the [legacy repository](#), and the updated (current) datasets are available [here](#).

2023 Sept 12

- Datasets are made available to 2nd challenge contestants via [API](#) and [direct download](#).
- This version of the dataset can be found in the [legacy repository](#).

2023 Oct 10 (current dataset version)

- Few contestants reported issues when accessing the data files. The identified issues include:
 1. Inconsistencies in the actual dates relative to the boost.** A more detailed discussion on this can be found [here](#).
 2. The names of cell populations in the prediction dataset differed from those in the training dataset.** A more detailed discussion on this can be found [here](#).
- This is the current version of the challenge dataset and is accessible [here](#).



Joe

Oct 13

could you please check file "2020LD_pbmc_cell_frequency.tsv" in this path (cmipb_challenge_datasets/current/2nd_challenge/raw_datasets/training_data/), file size indicates not all cell freq data included in the file. See this below:

```
unique(cellfreq_2020$cell_type_name)
[1] "Monocytes" "CD33HLADR" "Classical_Monocytes" "Non-Classical_Monocytes"
"Intermediate_Monocytes" "Bcells"
[7] "CD3CD19" "CD3CD19neg" "CD3 Tcells" "CD4Tcells" "CD8Tcells" "Tregs"
[13] "TemraCD4" "NaiveCD4" "TemCD4" "TemCD4" "TemraCD8" "NaiveCD8"
[19] "TemCD8" "TcmCD8" "NK" "Basophils" "mDC" "pDC"
[25] "ASCs (Plasmablasts)"
```



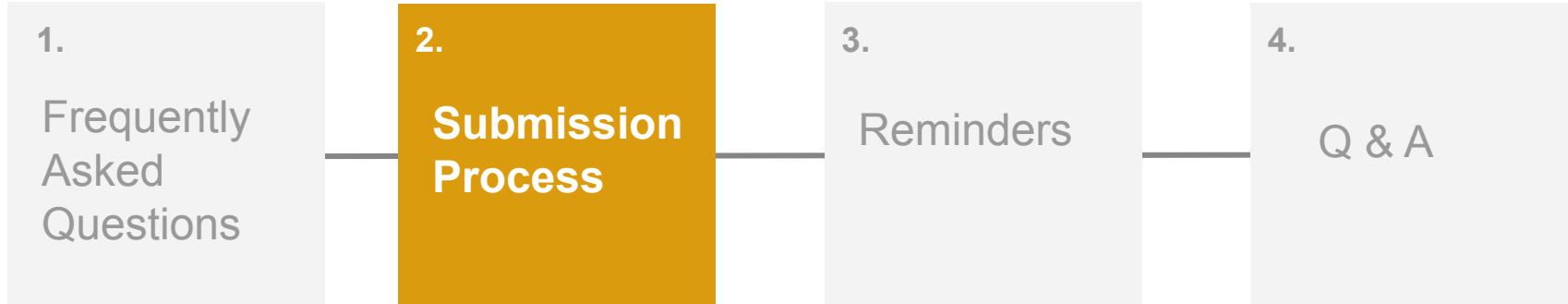
Pramod

Oct 13

Hi @Joe 2020 cohort has different feature counts when compared to 2020 and 2021 datasets. The 2020 cohort's cell frequency dataset comprises 25 cell types, as you pointed out., while the 2021 and 2022 datasets each have 50 cell types.

Similarly, the 2020 plasma_cytokine_concentration (Olink) data has 263 cytokines, while the 2021 and 2022 plasma_cytokine_concentration datasets each have 45 cytokines. Genes in all three datasets are identical. I hope this information is helpful.

Agenda for Today's Session



Final submissions

December 1, 2023 - January 16, 2024

- **Note:** Submissions during the preliminary submissions phase (September 12 - November 30) will not be considered a final submission. You must re-submit your entry at any point from December 1, 2023 to January 16, 2024 to be entered into the challenge.

Submission Process Demonstration

<https://www.cmi-pb.org/>

- 1) Manual data entry using Google sheets
- 2) Using coding pipeline



2nd CMI-PB Prediction Challenge

Revolutionizing computational modelling approach for immune response prediction

Learn more: [Training data](#), [Prediction tasks](#), [1st challenge](#) | [Participate](#)

The mission of CMI-PB is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of Pertussis booster vaccination.

LEARN ABOUT THE CMI-PB



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[A community prediction challenge](#)
[Pertussis vaccination](#)
[Tale of Two Pertussis Vaccines](#)
[Annual prediction challenges](#)

UNDERSTAND THE DATA



[Study outline](#)
[Sample and data collection](#)
[Data standardization](#)
[Database schema](#)
[Terminology](#)

ACCESS THE DATA



[Data composition](#)
[Use the API in your programs](#)
[Download all data \(SFTP\)](#)

PREDICTION CHALLENGE



[List of tasks](#)
[Examples of models](#)
[Data and resources](#)
[Submit preliminary predictions \(open\)](#)

TEACHING MATERIALS



[Pertussis vaccines](#)
[The resurgence of pertussis cases](#)

SOLUTIONS CENTER



[Access tasks for 2nd challenge.](#)
[Data preprocessing questions.](#)
[FAQ: 2nd challenge](#)

Antibody levels

Search

Home > 2nd CMI-PB Prediction challenge: Overview > Prediction challenge Submission

2nd CMI-PB Prediction challenge Submission

Table of contents

- [Prepare submission file](#)
- [Make preliminary submission](#)
- [Access past submissions](#)

Welcome to the 2nd CMI-PB Prediction challenge. Please follow the steps below to submit your prediction challenge. Currently, we have If you have any issues, use our [solutions center](#) to post your questions.

Step 1: Prepare Submission File

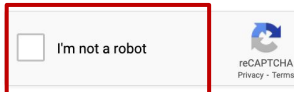
Create a model and complete your analysis. We only accept submissions in the given Tab-separated values (TSV) file format:

1. Download the [submission template](#)
2. Submit your prediction in the prescribed format.

Step 2: Make Preliminary Submission

- We've begun accepting preliminary submissions for testing. Kindly note that these submissions will not be assessed. The official window for final submissions will open on Dec 1, 2023.
- Your submission should be a TSV file with 22 rows including a header and 10 columns.
- Sample submission files are available [here](#).

Select a submission file: No file chosen



Submit

Submission File Errors

Subject ID	Age	Biological Sex at Birth	Vaccine Priming Status	1.1) IgG-PT-D14-titer-Rank	1.2) IgG-PT-D14-FC-Rank	2.1) Monocytes-D1-Rank	2.2) Monocytes-D1-FC-Rank	3.1) CCL3-D3-Rank	3.2) CCL3-D3-FC-Rank
97	35	Male	wP	14				LJI	
98	28	Female	wP	3				4	
99	22	Female	aP	7				15	
100	20	Female	aP	20				9	
101	18	Male	aP	19				1	
102	18	Male	aP	5				2	
103	27	Female	wP	21				10	
104	32	Female	wP	15				7	
105	27	Female	wP	9					
106	25	Female	aP	1					
107	23	Female	aP	2					
108	26	Female	wP	10					
109	32	Female	wP	8					
110	24	Female	aP	12					
111	25	Male	wP	11					
112	25	Male	aP	4					
114	31	Male	wP	13					
115	19	Female	aP	18					
116	21	Male	aP	8					
117	27	Female	aP	17					
118	23	Male	aP	16					

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Select a submission file: No file chosen

Column 3.1) CCL3-D3-Rank: All rank values in the column must be within the specified range (1-21). ✕

I'm not a robot



Submission file error: rank values outside the specified range

Subject ID	Age	Biological Sex at Birth	Vaccine Priming Status	1.1) IgG-PT-D14-titer-Rank	1.2) IgG-PT-D14-FC-Rank	2.1) Monocytes-D1-Rank	2.2) Monocytes-D1-FC-Rank	3.1) CCL3-D3-Rank	3.2) CCL3-D3-FC-Rank
97	35	Male	wP						
98	28	Female	wP						
99	22	Female	aP						
100	20	Female	aP						
101	18	Male	aP						
102	18	Male	aP						
103	27	Female	wP						
104	32	Female	wP						
105	27	Female	wP						
106	25	Female	aP						
107	23	Female	aP						
108	26	Female	wP						
109	32	Female	wP						
110	24	Female	aP						
111	25	Male	wP						
112	25	Male	aP						
114	31	Male	wP						
115	19	Female	aP						
116	21	Male	aP						
117	27	Female	aP						
118	23	Male	aP						

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Select a submission file: No file chosen

Your submission file appears to be empty. ✕



I'm not a robot



reCAPTCHA
Privacy · Terms

Submit

Submission file
error: empty file

Subject ID	Age	Biological Sex at Birth	Vaccine Priming Status	1.1) IgG-PT-D14-titer-Rank	2.1) Monocytes-D1-Rank	2.2) Monocytes-D1-FC-Rank	3.1) CCL3-D3-Rank	3.2) CCL3-D3-FC-Rank
97	35	Male	wP	1				
98	28	Female	wP	2				
99	22	Female	aP	3				
100	20	Female	aP	4				
101	18	Male	aP	5				
102	18	Male	aP	6				
103	27	Female	wP	7				
104	32	Female	wP	8				
105	27	Female	wP	9				
106	25	Female	aP	10				
107	23	Female	aP	11				
108	26	Female	wP	12				
109	32	Female	wP	13				
110	24	Female	aP	14				
111	25	Male	wP	15				
112	25	Male	aP	16				
114	31	Male	wP	17				
115	19	Female	aP	18				
116	21	Male	aP	19				
117	27	Female	aP	20				
118	23	Male	aP	21				

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- Sample submission files are available [here](#).

Select a submission file: No file chosen

The header does not align with the expected columns specified in the submission template ✕

I'm not a robot



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Privacy - Terms

Submit

Submission file error:
missing/incorrect header

Subject ID	Age	Biological Sex at Birth	Vaccine Priming Status	1.1) IgG-PT-D14-titer-Rank	1.2) IgG-PT-D14-FC-Rank	2.1) Monocytes-D1-Rank	2.2) Monocytes-D1-FC-Rank	3.1) CCL3-D3-Rank	3.2) CCL3-D3-FC-Rank
97	35	Male	wP	21.0	0.5184224663718740		1986-03-26	-6.0	
98	28	Female	wP	NaN	0.13537829856527300	7Mit	1983-12-19	3.0	
99	22	Female	aP	8.0			200		
100	20	Female	aP	10.0			2013		
101	18	Male	aP	16.0		1.0	1984		
102	18	Male	aP				1989		
103	27	Female	wP	7.0	0.41319137332251700	mt	1995		
104	32	Female	wP	15.0	0.625817503853245	kR6tp	2009		
105	27	Female	wP	-6.0		hh	199		
106	25	Female	aP	15.0		w	2012		
107	23	Female	aP	12.0		NRuc	198		
108	26	Female	wP	0.7179399154087560			2014		
109	32	Female	wP				199		
110	24	Female	aP	6.0			2000		
111	25	Male	wP						
112	25	Male	aP	2.0		798.0	201		
114	31	Male	wP	14.0		-6.0	2002		
115	19	Female	aP			0.08064911179233690			
116	21	Male	aP				2013		
117	27	Female	aP			0.9132040742497730	2004		
118	23	Male	aP						

provided at our Solutions center [here](#).

- Your submission should be a TSV file with 22 rows including a header and 10 columns. The maximum allowed file size is 100 KB.
- Sample submission files are available [here](#).

Select a submission file: No file chosen

Column 1.1) IgG-PT-D14-titer-Rank: All rank values in the column must be within the specified range (1-21).


Column 1.2) IgG-PT-D14-FC-Rank: All rank values in the column must be within the specified range (1-21).

Column 2.1) Monocytes-D1-Rank: All rank values in the column must be within the specified range (1-21).

Column 2.2) Monocytes-D1-FC-Rank: All rank values in the column must be within the specified range (1-21).

Column 3.1) CCL3-D3-Rank: All rank values in the column must be within the specified range (1-21).

Column 3.2) CCL3-D3-FC-Rank: All rank values in the column must be within the specified range (1-21).

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Submission file with multiple errors

Successful Submissions

Submission with all tasks

Subject ID	Age	Biological Sex at Birth	Vaccine Priming Status	1.1) IgG-PT-D14-titer-Rank	1.2) IgG-PT-D14-FC-Rank	2.1) Monocytes-D1-Rank	2.2) Monocytes-D1-FC-Rank	3.1) CCL3-D3-Rank	3.2) CCL3-D3-FC-Rank
97	35	Male	wP	14	6	15	21	11	17
98	28	Female	wP	3	7	13	15	4	1
99	22	Female	aP	7	2	18	12	15	13
100	20	Female	aP	20	20	10	11	9	6
101	18	Male	aP	19	5	1	8	1	19
102	18	Male	aP	5	21	11	17	2	9
103	27	Female	wP	21	4	4	7	10	12
104	32	Female	wP	15	12	14	16	7	14
105	27	Female	wP	9	15	17	13	20	11
106	25	Female	aP	1	11	3	18	19	3
107	23	Female	aP	2	16	19	10	5	4
108	26	Female	wP	10	17	7	1	21	5
109	32	Female	wP	8	18	12	20	8	15
110	24	Female	aP	12	13	16	19	12	2
111	25	Male	wP	11	8	20	5	14	16
112	25	Male	aP	4	10	5	9	3	20
114	31	Male	wP	13	1	21	14	13	8
115	19	Female	aP	18	3	8	2	18	21
116	21	Male	aP	8	19	8	4	8	7
117	27	Female	aP	17	9	9	8	17	18
118	23	Male	aP	16	14	2	3	16	10

*Populated with random numbers

Submission with two tasks

Subject ID	Age	Biological Sex at Birth	Vaccine Priming Status	1.1) IgG-PT-D14-titer-Rank	1.2) IgG-PT-D14-FC-Rank	2.1) Monocytes-D1-Rank	2.2) Monocytes-D1-FC-Rank	3.1) CCL3-D3-Rank	3.2) CCL3-D3-FC-Rank
97	35	Male	wP	14				11	
98	28	Female	wP	3				4	
99	22	Female	aP	7				15	
100	20	Female	aP	20				9	
101	18	Male	aP	19				1	
102	18	Male	aP	5				2	
103	27	Female	wP	21				10	
104	32	Female	wP	15				7	
105	27	Female	wP	9				20	
106	25	Female	aP	1				19	
107	23	Female	aP	2				5	
108	26	Female	wP	10				21	
109	32	Female	wP	8				8	
110	24	Female	aP	12				12	
111	25	Male	wP	11				14	
112	25	Male	aP	4				3	
114	31	Male	wP	13				13	
115	19	Female	aP	18				18	
116	21	Male	aP	8				8	
117	27	Female	aP	17				17	
118	23	Male	aP	16				16	

*Populated with random numbers

Antibody levels



Search

2nd CMI-PB Prediction challenge Submission

Your submission has been recorded successfully. A confirmation email has been sent to you. Thank you!

Useful links:

- [Past submissions](#)
- [CMI-PB home](#)

Please let us know if you have any questions at our [CMI-PB solutions center](#).

GET HELP

[Solutions Center](#)
[About Us](#)

DATASETS

Latest build: September 2023
[Version history](#)
[APIs](#)
[Downloads](#)

PUBLICATIONS

[BioRxiv 2023](#)
[JCI Insights 2021](#)

**La Jolla
Institute**
FOR IMMUNOLOGY

**Life
Without
Disease.**®



submission@cmi-pb.org via lji.org

to me, aazhan ▾

12:13 PM (27 minutes ago)



WELCOME TO THE 2ND CMI-PB PREDICTION CHALLENGE

Dear sorfield@lji.org,

Thank you for submitting your response to the 2nd CMI-PB Prediction challenge. Your response is now successfully recorded.

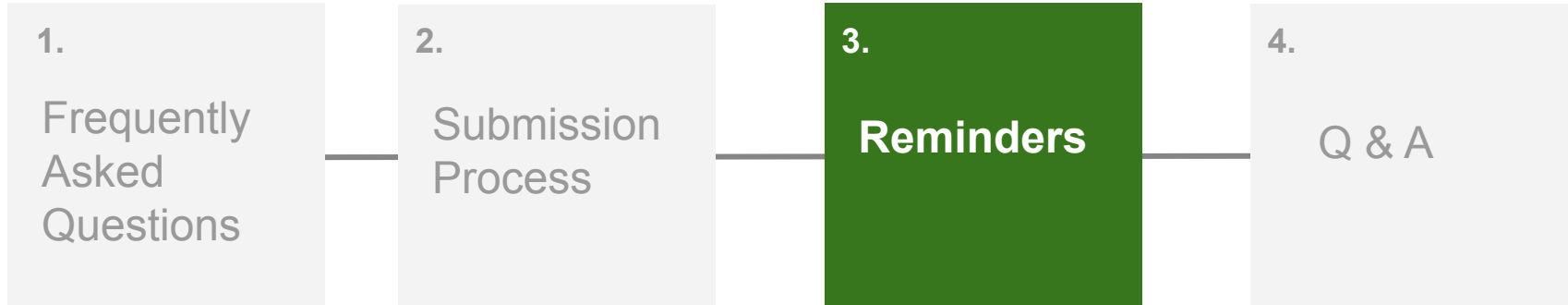
The submitted file is attached here for your reference. Feel free to access all your past submissions [here](#). If you ever change your mind and want to re-submit, please make sure to enter all your answers in the sheet again as your new submission overrides all previous submissions.

We look forward to reviewing your results! In the meantime, please let us know if you have any questions at our [CMI-PB solutions center](#).

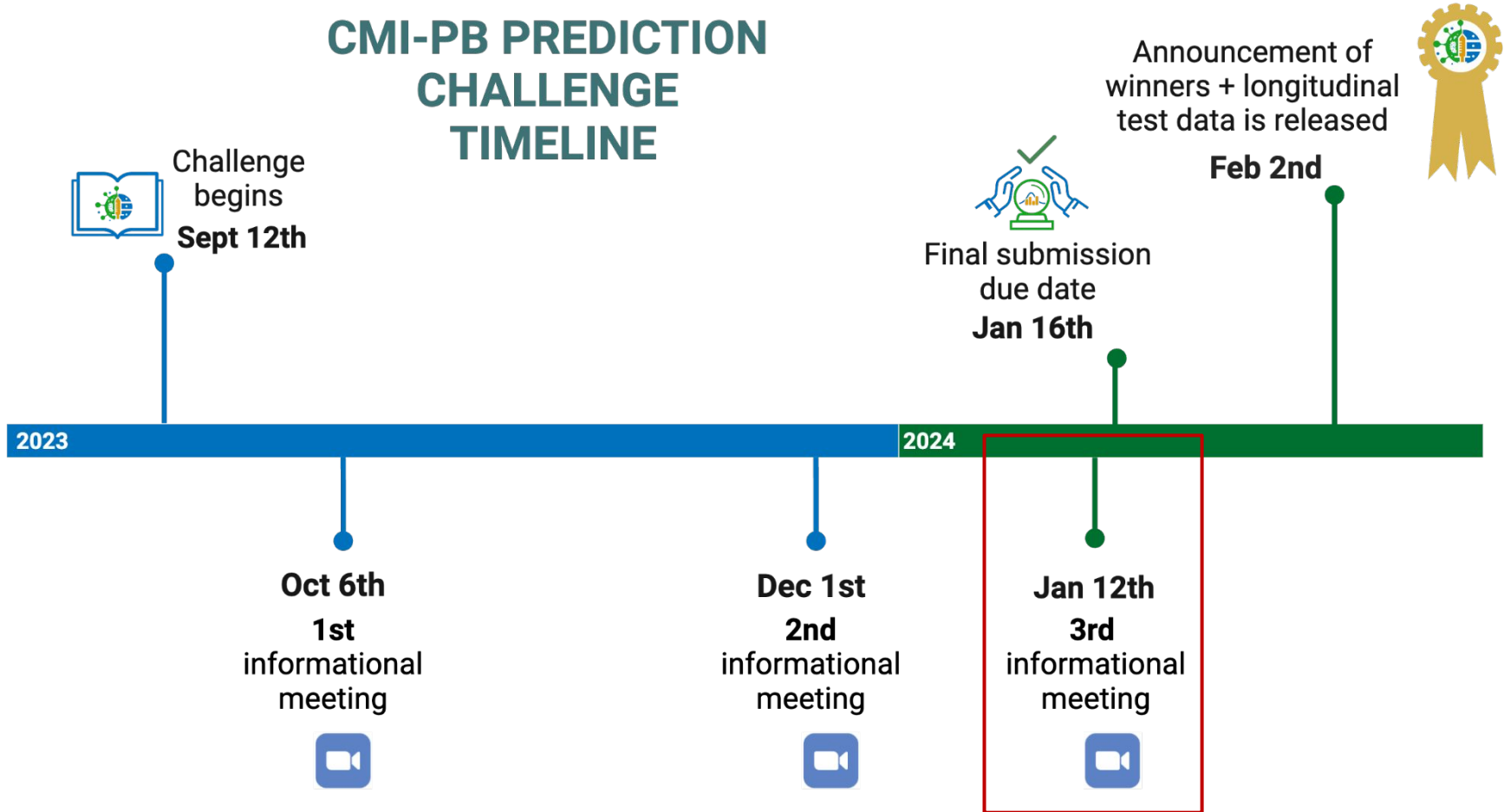
Best wishes,
CMI-PB Team

You will receive an email confirmation once your submission is received.

Agenda for Today's Session



CMI-PB PREDICTION CHALLENGE TIMELINE



Challenge begins
Sept 12th

2023

Oct 6th
1st
informational
meeting



Dec 1st
2nd
informational
meeting



Jan 12th
3rd
informational
meeting



2024

Final submission
due date
Jan 16th

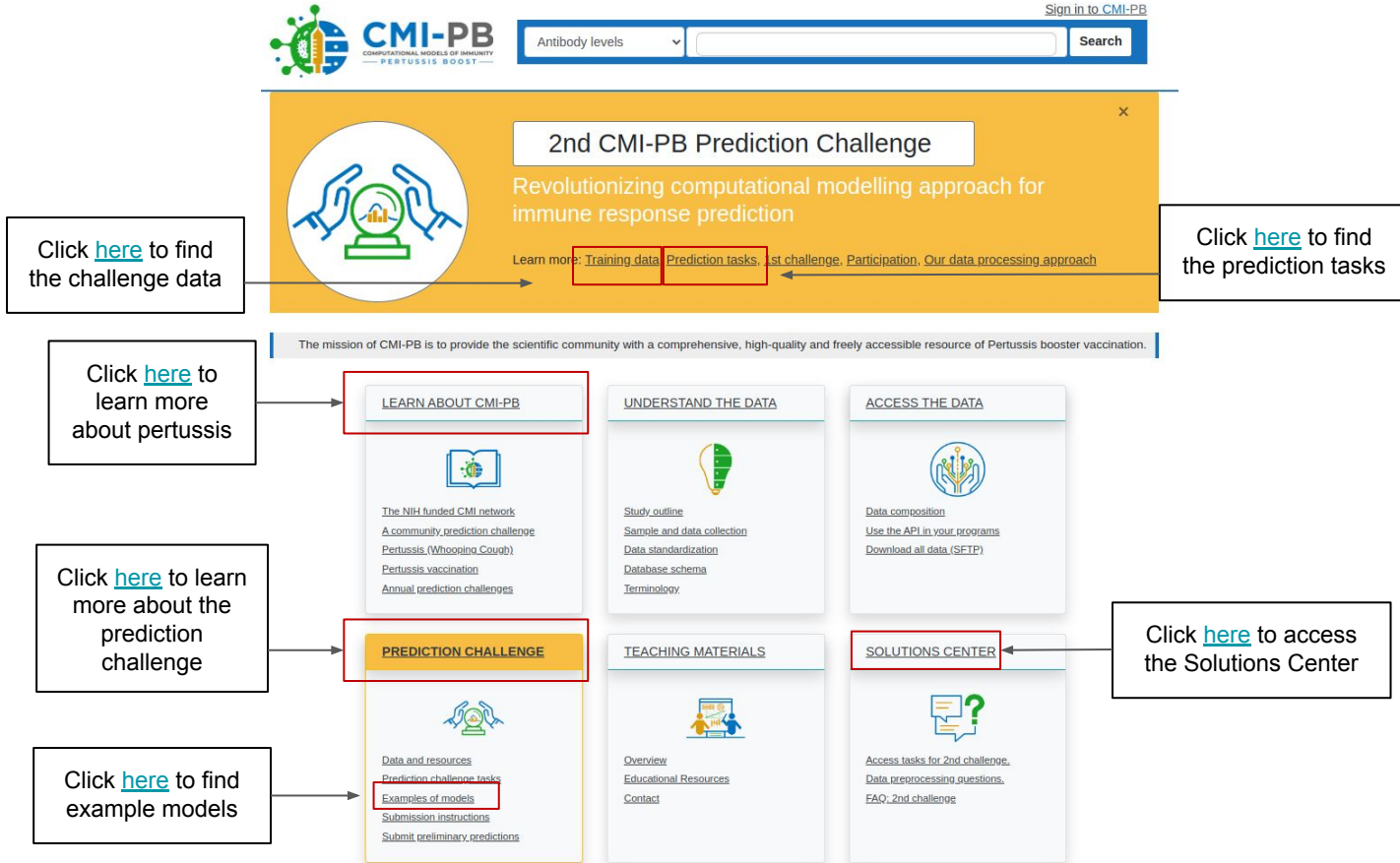


Announcement of
winners + longitudinal
test data is released

Feb 2nd









Other resources on the site



2nd CMI-PB Prediction Challenge
Revolutionizing computational modelling approach for immune response prediction

Learn more: [Training data](#), [Prediction tasks](#), [1st challenge](#), [Participation](#), [Our data processing approach](#)

The mission of CMI-PB is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of Pertussis booster vaccination.

LEARN ABOUT CMI-PB	UNDERSTAND THE DATA	ACCESS THE DATA
 <p>The NIH funded CMI network A community prediction challenge Pertussis (Whooping Cough) Pertussis vaccination Annual prediction challenges</p>	 <p>Study outline Sample and data collection Data standardization Database schema Terminology</p>	 <p>Data composition Use the API in your programs Download all data (SFTP)</p>
PREDICTION CHALLENGE	TEACHING MATERIALS	SOLUTIONS CENTER
 <p>Data and resources Prediction challenge tasks Examples of models Submission instructions Submit preliminary predictions</p>	 <p>Overview Educational Resources Contact</p>	 <p>Access tasks for 2nd challenge. Data preprocessing questions. FAQ, 2nd challenge</p>

Click [here](#) to find the challenge data

Click [here](#) to find the prediction tasks

Click [here](#) to learn more about pertussis

Click [here](#) to learn more about the prediction challenge

Click [here](#) to access the Solutions Center

Click [here](#) to find example models

The CMI-PB team

Kleinsteinstein Lab (Yale)



- Expertise: A combination of "big data" analysis and immunology domain.
- Collaborating on data and models being released to the community to support reproducibility and the prediction contest, and also participate in the prediction challenge.

Steven Kleinstein
Jeremy Gygi
Leying Guan
Anna Konstorum

Grant Lab (UCSD)



- Expertise: the use of computational approaches, based on both biophysics and bioinformatics, to study the structure, function and evolution of key biological macromolecules.
- Dr. Grant will engage and advise over 40 biology graduate students in the CMI-PB Prediction Challenge.

Barry Grant

Ay Lab (LJI)



- Expertise: Development of bioinformatics tools that utilize high-dimensional and high-throughput datasets to deduce insights into chromatin conformation, genetic variation, and the regulation of gene expression.
- The Ay lab is focused on developing predictive machine learning models, which will serve as examples and baselines for participants in the CMI-PB challenge.

Ferhat Ay
Joaquin Reyna

Peters Lab (LJI)



- Expertise: Both experimental and computational studies to better understand human immune responses in the context of infectious diseases, allergy, cancer and vaccines.
- The team is responsible for the generation of experimental data, making it accessible in a central and standardized fashion, and coordinating the creation and coordination of the prediction contest.

Bjoern Peters
Jason Greenbaum
James Overton
Brendan Ha

Pramod Shinde
Mari Kojima
Rasteh Haji Kazem Nili

Jiyeun Lee
Lisa Willemsen
Shelby Orfield

And thank you to the Sette Lab, Crotty lab, LJI Clinical Core, LJI Bioinformatics Core

The CMI-PB team members



Bjoern Peters



Steven Kleinstein



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Pramod Shinde



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Ferran Soldevila



Rasteh Nili



Jason Greenbaum



Brendan Ha



Jiyeun Lee



Ricardo De Silva Antunes



Jeremy Gygi



Anna Konstorum

Agenda for Today's Session

1.
Frequently
Asked
Questions

2.
Submission
Process

3.
Reminders

4.
Q & A



Questions?

Please email cmi-pb-challenge@lji.org at any time throughout the challenge with any questions.