

A complex fluorescence microscopy image showing a dense network of cells or fibers. The image is characterized by numerous bright, elongated, and branching structures in shades of cyan, magenta, and orange, set against a dark background. These structures appear to be interconnected, forming a web-like pattern. The overall effect is one of intense biological activity and structural complexity.

Bioimage Analysis for Quantitative Microscopy course

Sep 30 - Oct 04, 2024

BioCity Turku

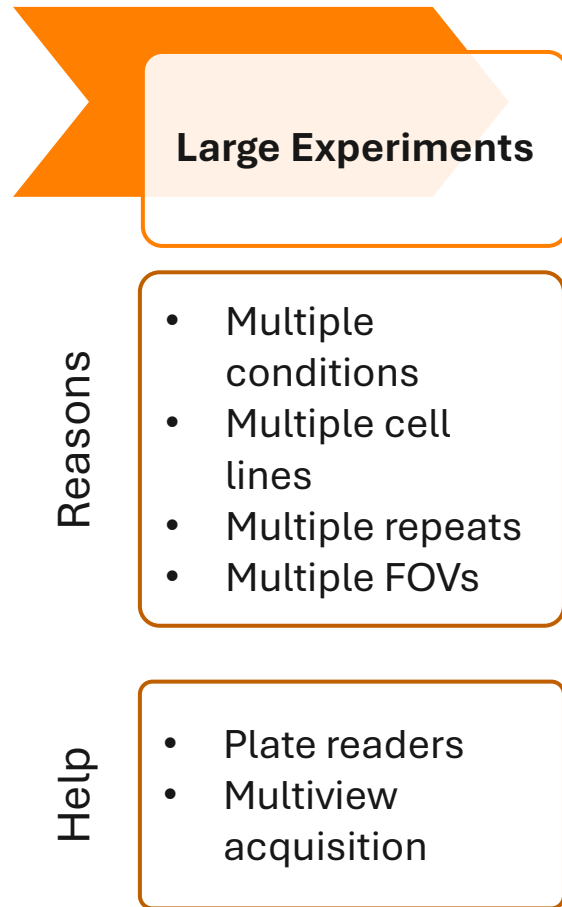
(Again) Before we start

We would love some feedback 😊



[Link to the form](#)

Why CellTracksCollab



The platform

PLOS BIOLOGY

BROWSE

PUBLISH

ABOUT

SEARCH






advanced search

OPEN ACCESS

PEER-REVIEWED

METHODS AND RESOURCES

CellTracksColab is a platform that enables compilation, analysis, and exploration of cell tracking data

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Subject Areas 

Abstract

Introduction

Results

Discussion

Abstract

In life sciences, tracking objects from movies enables researchers to quantify the behavior of single particles, organelles, bacteria, cells, and even whole animals. While numerous tools now allow automated tracking from video, a significant challenge persists in compiling, analyzing, and exploring the large datasets generated by these approaches. Here, we introduce

[GitHub page for CellTracksColab](#)

CellTracksCollab

How it works



ICY



Fiji



Icy



CellProfiler



TrackMate

Track ID	X	Y	Z	t
0	6.8	15	1.0	1
1	7.9	0.0	2.6	2

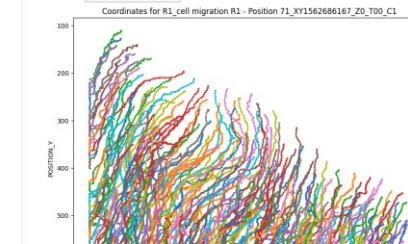
[!] CellTracksColab does not (yet) support track splitting

5	67	2.4	5.1	6
6	91	5.3	1.3	7
...

Run the cell and choose the file you want to inspect

Show code

File Name: R1_cell_migration-R1 - Position w



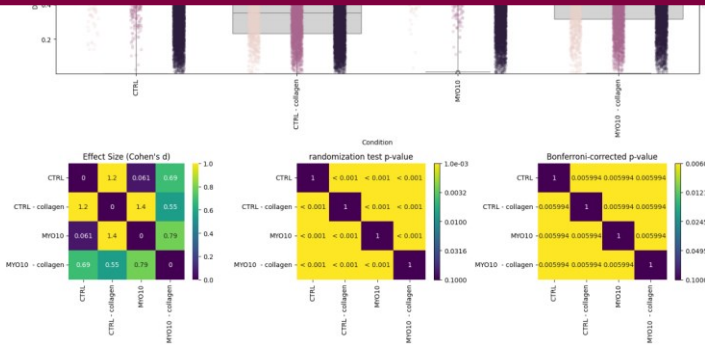
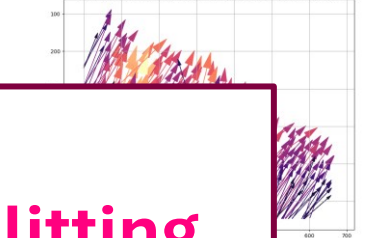
2.5 Plot the migration vectors for each field of view

Plot the migration vectors

Show code

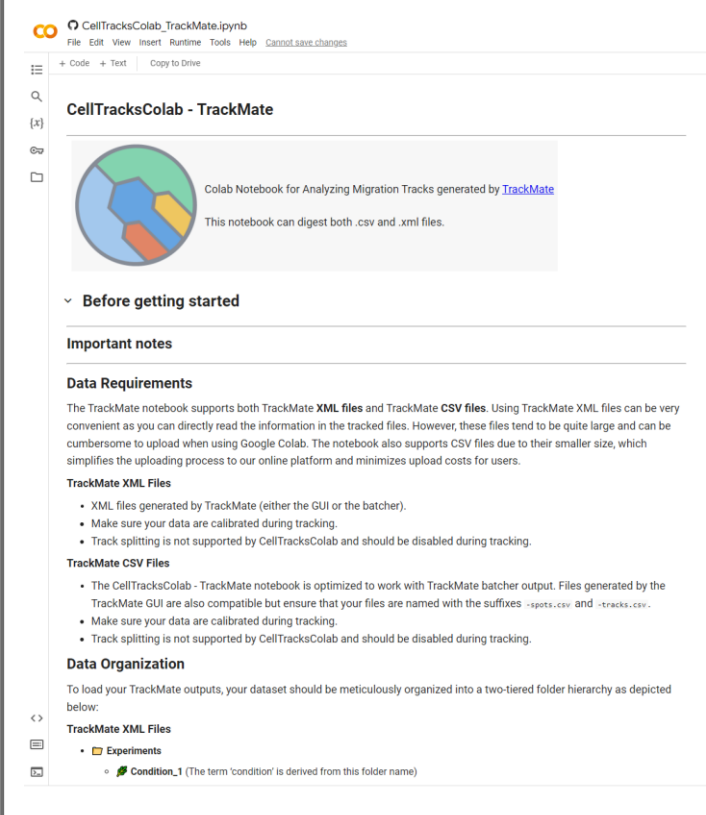

Selected: R1_cell_migration-R1 - Position w

Vector plot



CellTracksColab

Where it works



CellTracksColab - TrackMate

Colab Notebook for Analyzing Migration Tracks generated by [TrackMate](#)

This notebook can digest both .csv and .xml files.

Before getting started

Important notes

Data Requirements

The TrackMate notebook supports both TrackMate **XML files** and TrackMate **CSV files**. Using TrackMate XML files can be very convenient as you can directly read the information in the tracked files. However, these files tend to be quite large and can be cumbersome to upload when using Google Colab. The notebook also supports CSV files due to their smaller size, which simplifies the uploading process to our online platform and minimizes upload costs for users.

TrackMate XML Files

- XML files generated by TrackMate (either the GUI or the batcher).
- Make sure your data are calibrated during tracking.
- Track splitting is not supported by CellTracksColab and should be disabled during tracking.

TrackMate CSV Files

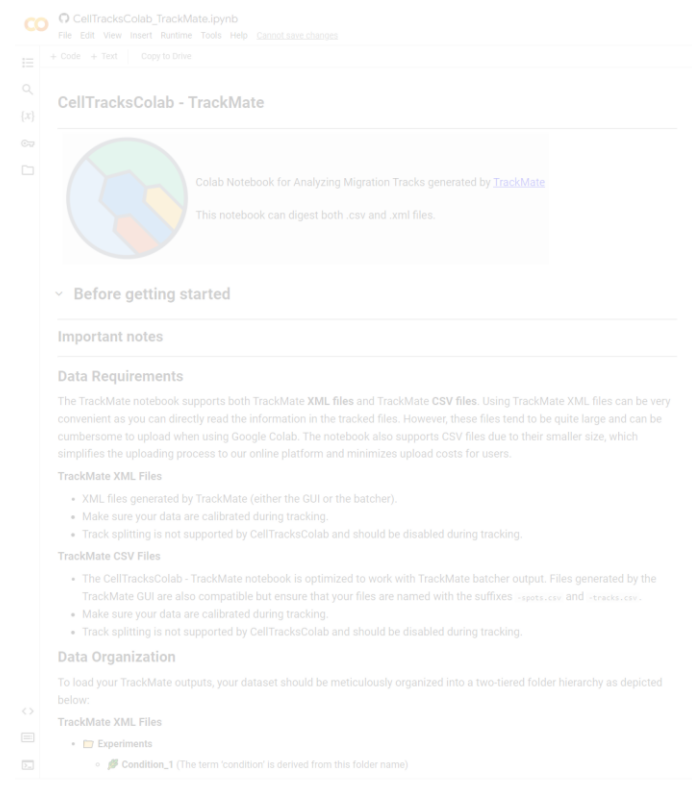

- The CellTracksColab - TrackMate notebook is optimized to work with TrackMate batcher output. Files generated by the TrackMate GUI are also compatible but ensure that your files are named with the suffixes `-spots.csv` and `-tracks.csv`.
- Make sure your data are calibrated during tracking.
- Track splitting is not supported by CellTracksColab and should be disabled during tracking.

Data Organization

To load your TrackMate outputs, your dataset should be meticulously organized into a two-tiered folder hierarchy as depicted below:

TrackMate XML Files

- Experiments
 - Condition_1 (The term 'condition' is derived from this folder name)



CellTracksColab - TrackMate

Colab Notebook for Analyzing Migration Tracks generated by [TrackMate](#)

This notebook can digest both .csv and .xml files.

Before getting started

Important notes

Data Requirements

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TrackMate CSV Files

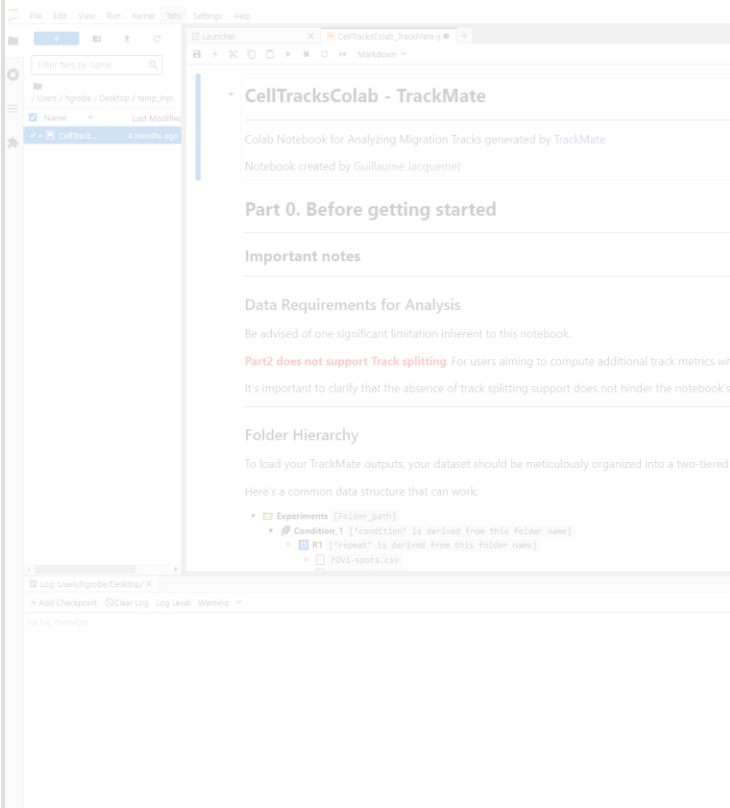

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CellTracksColab - TrackMate

Colab Notebook for Analyzing Migration Tracks generated by TrackMate

Notebook created by Guillaume Jacquemet

Part 0. Before getting started

Important notes

Data Requirements for Analysis

Be advised of one significant limitation inherent to this notebook.

Part2 does not support Track splitting. For users aiming to compute additional track metrics with Part2, this limitation is a concern. It's important to clarify that the absence of track splitting support does not hinder the notebook's functionality.

Folder Hierarchy

To load your TrackMate outputs, your dataset should be meticulously organized into a two-tiered folder hierarchy as depicted below:

Here's a common data structure that can work:

- Experiments [Folder_path]
 - Condition_1 ['condition' is derived from this folder name]
 - R1 ['repeat' is derived from this folder name]
 - F0V1-spots.csv

Now WE go!



Tracking results from the TrackMate sessions
Datasets provided

[TrackingData](#)



Plot the data and find something

[CellTracksColab](#)



30 min (15:00)
15 min

work time
check in

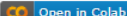


Where we go

Quick Start

The easiest way to start using **CellTracksColab** is in the cloud using Google Collaboratory, but it can also be used on your own computer using Jupyter Notebooks. See our [wiki](#) for installation instructions.

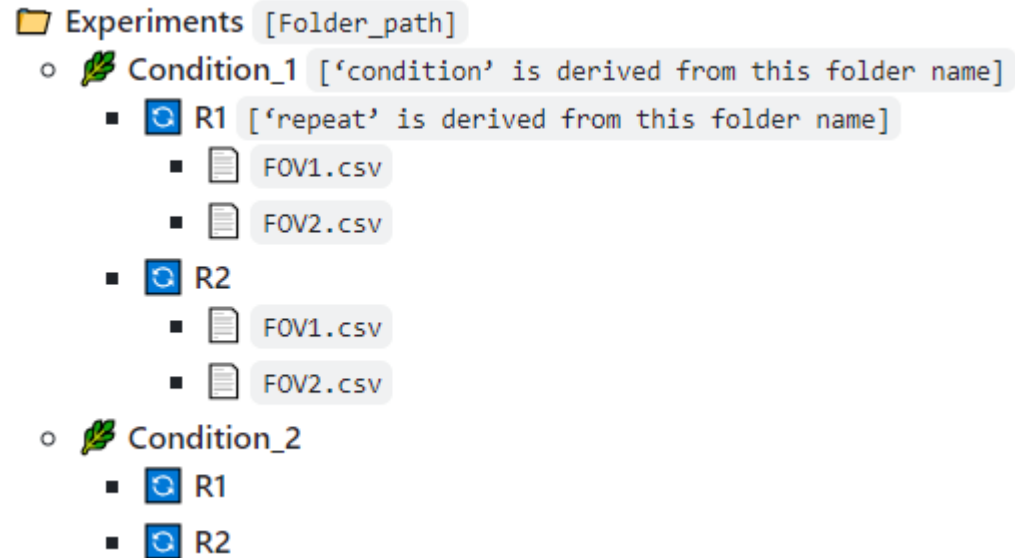
1. Load and Plot Your Data

We provide three notebooks for loading and analyzing your data depending on its format:

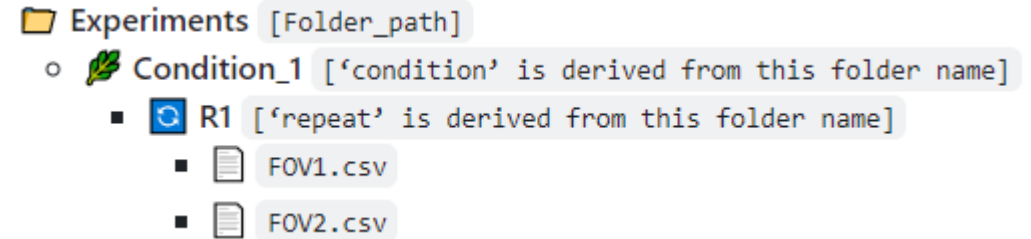
Notebook	Purpose	Required File Format	Link
CellTracksColab - TrackMate	Load and analyze TrackMate data. More info here .	CSV or XML files	 Open in Colab
CellTracksColab - Custom	Analyze data from CellProfiler, ICY, ilastik, or Fiji Manual Tracker. More info here .	CSV files	 Open in Colab
CellTracksColab - Viewer	Load and share data in the CellTracksColab format.	CellTracksColab format	 Open in Colab

The folder structure

> Multiple conditions and repeats

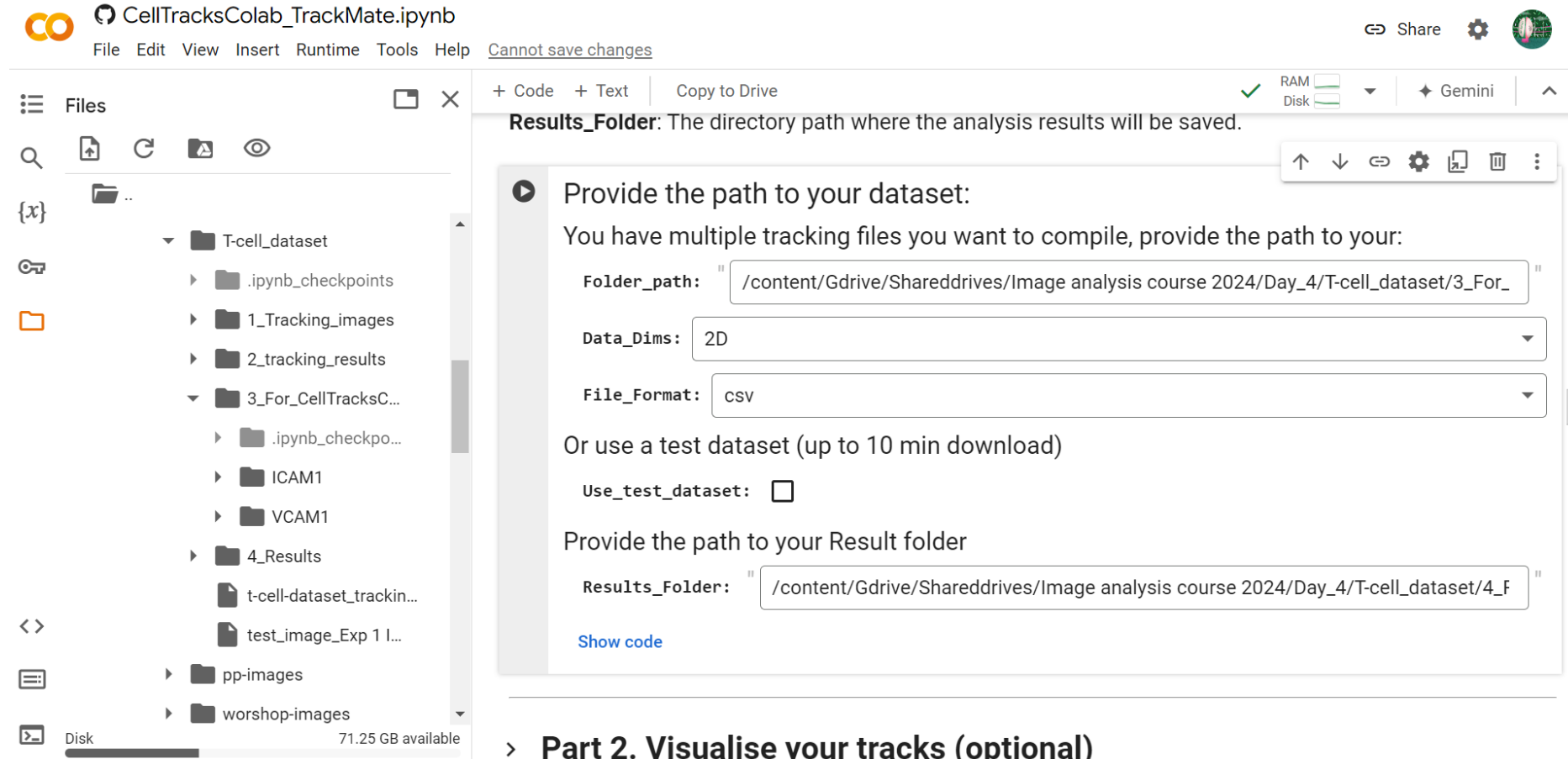


> Single condition and repeat



see also the extensive wiki on [GitHub](#)

Load the data (Part 0 and 1)



The screenshot displays the CellTracksColab TrackMate.ipynb interface. On the left, a file explorer shows a directory structure with folders like 'T-cell_dataset', '1_Tracking_images', '2_tracking_results', '3_For_CellTracksC...', '4_Results', 'pp-images', and 'worshop-images'. The main area contains a configuration panel for loading data. It includes a 'Results_Folder' label, a text input for 'Folder_path' (set to '/content/Gdrive/Shareddrives/Image analysis course 2024/Day_4/T-cell_dataset/3_For_'), a dropdown for 'Data_Dims' (set to '2D'), and another dropdown for 'File_Format' (set to 'CSV'). There is also a checkbox for 'Use_test_dataset' and a text input for 'Results_Folder' (set to '/content/Gdrive/Shareddrives/Image analysis course 2024/Day_4/T-cell_dataset/4_F'). A 'Show code' link is present at the bottom of the configuration panel.

CellTracksColab_TrackMate.ipynb

File Edit View Insert Runtime Tools Help [Cannot save changes](#)

+ Code + Text Copy to Drive

Results_Folder: The directory path where the analysis results will be saved.

Provide the path to your dataset:

You have multiple tracking files you want to compile, provide the path to your:

Folder_path: "/content/Gdrive/Shareddrives/Image analysis course 2024/Day_4/T-cell_dataset/3_For_"

Data_Dims: 2D

File_Format: CSV

Or use a test dataset (up to 10 min download)

Use_test_dataset: ☐

Provide the path to your Result folder

Results_Folder: "/content/Gdrive/Shareddrives/Image analysis course 2024/Day_4/T-cell_dataset/4_F"

[Show code](#)

> Part 2. Visualise your tracks (optional)

Visualize the data (Part 2)

CellTracksCollab_TrackMate.ipynb

File Edit View Insert Runtime Tools Help [Cannot save changes](#)

Files

- ..
- .config
- CellTracksCollab
- Gdrive
- Encrypted
- Trash-0
- file-revisions-by-id
- shortout-targets-by-id
- MyDrive
- Shared drives
- CellTracksCollab
- Filopodia at junctions
- Image analysis course 20...
- Day_1
- Day_2
- Day_3
- Day_4
- Breast_cancer_dat...
- Fiji_macros
- T-cell_dataset
- ipynb_checkpoi...
- 1_Tracking_ima...
- 2_tracking_resu...
- 3_For_CellTracks...
- ipynb_check...
- ICAM1
- VCAM1
- 4_Results
- t-cell-dataset_trac...
- test_image_Exp 1...
- pp-images
- worshop-images
- 1_Trackmate_lecture...
- 1_Trackmate_lecture...

Part 2. Visualise your tracks (optional)

2.1 Visualise your tracks in each field of view

Visualizing raw tracks is the first critical step, ensuring that your data is loaded correctly:

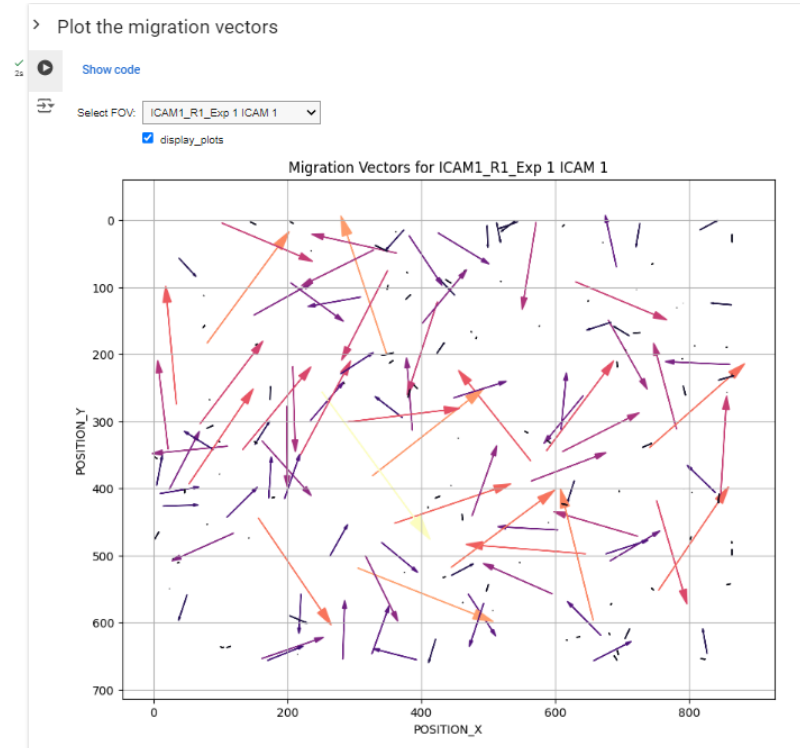
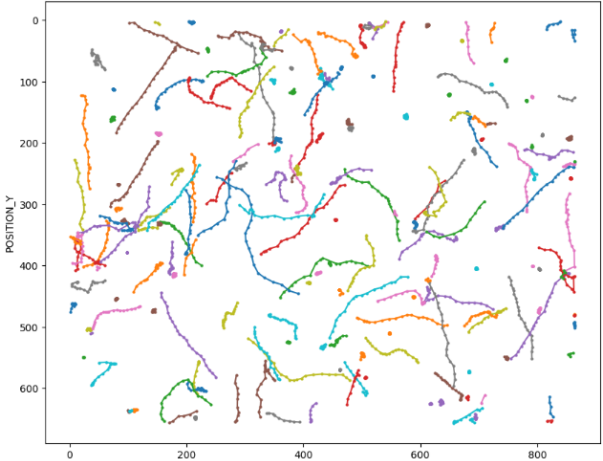
- The platform visualizes tracks for each loaded field of view.
- Use the dropdown menu to select and inspect individual files dynamically.
- One current limitation is that the tracks are only displayed in 2D space.

Run the cell and choose the file you want to inspect

Show code

File Name: ICAM1_R1_Exp 1 ICAM 1

Coordinates for ICAM1_R1_Exp 1 ICAM 1



Filter the data (Part 3)



› Run to compute basic track metrics for filtering purpose

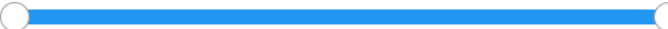
✓ [8] [Show code](#)

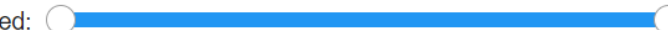
Calculating track metrics for filtering purpose: 100%  2158/2158 [00:03<00:00, 670.75it/s]

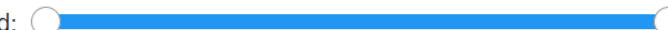
› Run to filter and smooth your tracks (slow when the dataset is large)


✓ 0s  [Show code](#)


 Smoothing Neighbors:  3

Duration:  1.00 – 20.00

Mean Speed:  0.22 – 16.50

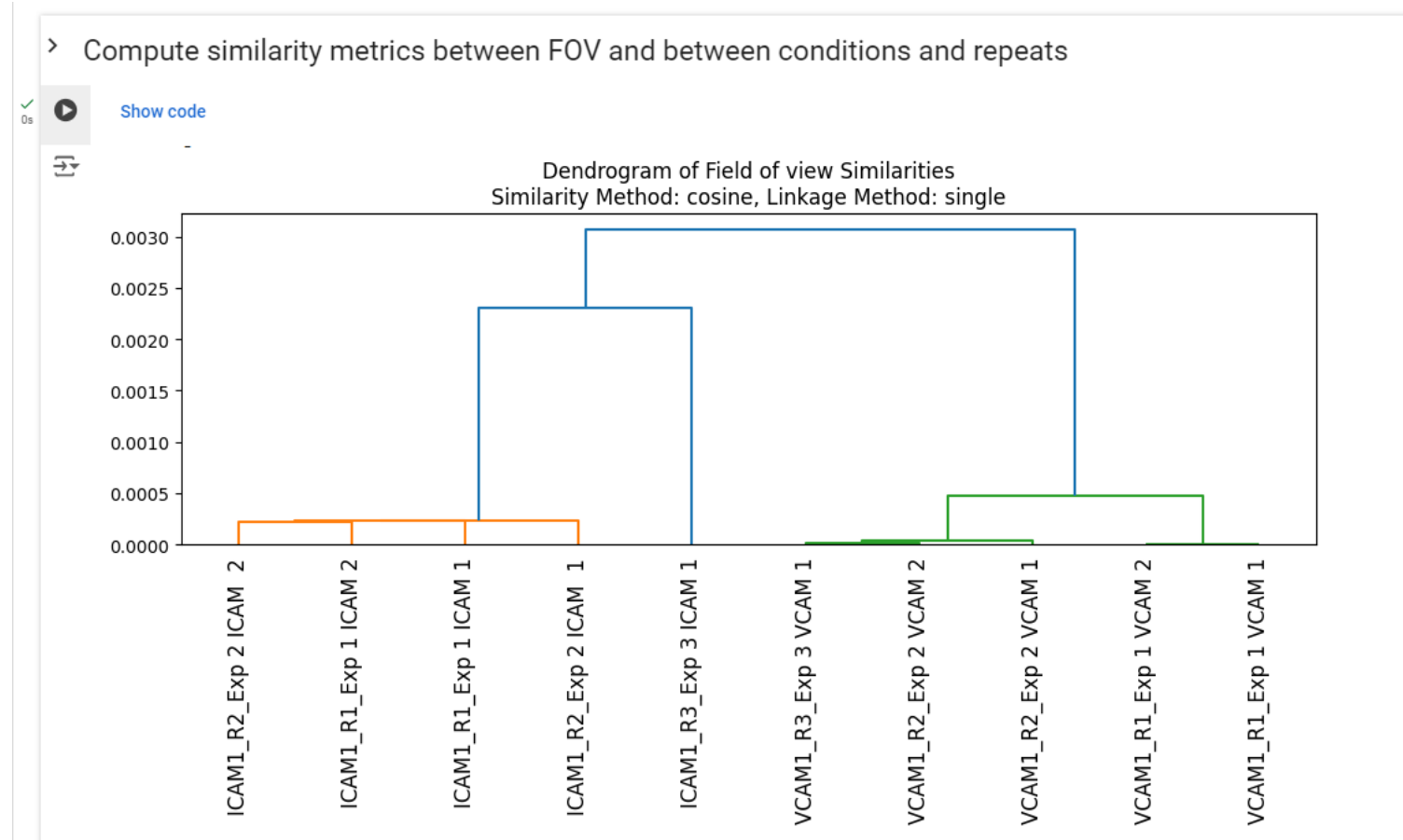
Max Speed:  0.22 – 28.98

Min Speed:  0.00 – 15.58

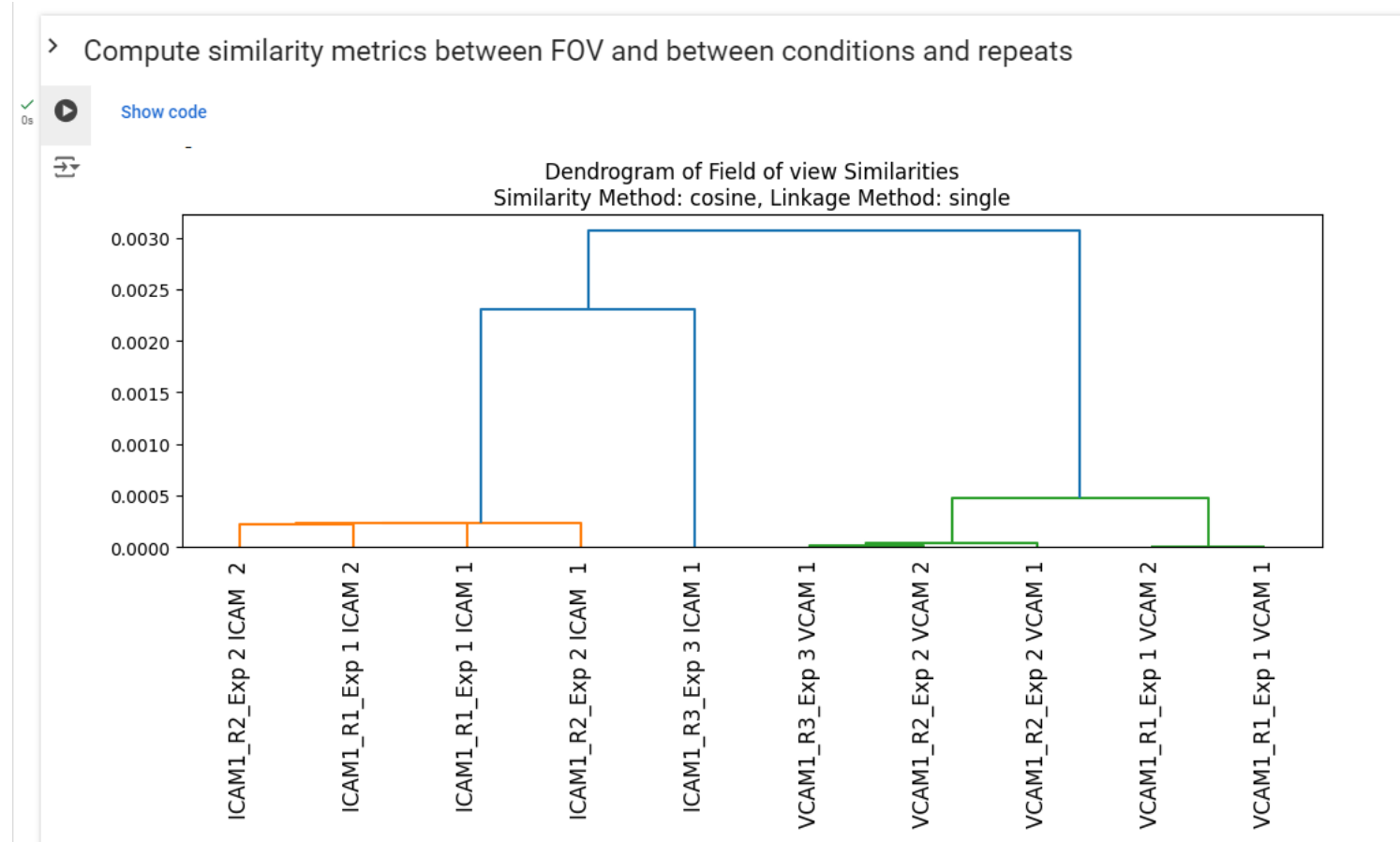
Total Distance:  0.22 – 296.70

[Apply Filters](#)

Quality control (Part 5)



Quality control (Part 5)



Plot your data (Part 6)

> Plot track parameters (entire dataset)



[Show code](#)



Select Conditions

Conditions:

ICAM1
VCAM1

Metrics Computed in CellTracksColab

Metrics Imported from your Tracking Software

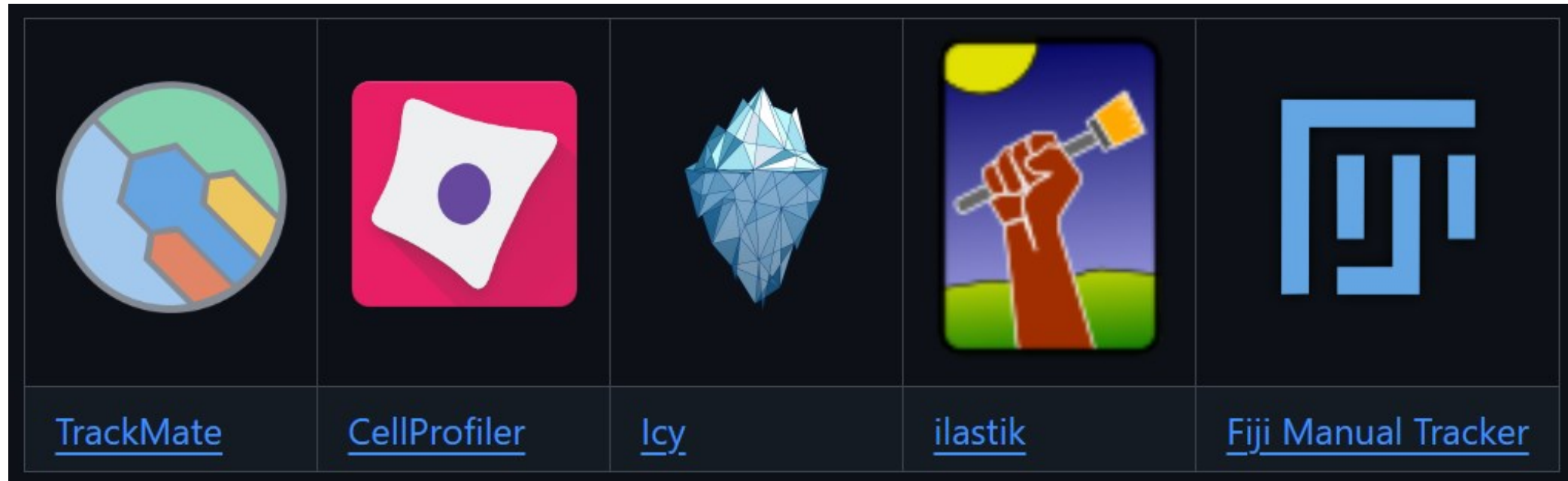
- | | | | |
|--|---|--|---|
| <input type="checkbox"/> Select All Metrics Imported from... | <input type="checkbox"/> DIVISION_TIME_MEAN | <input type="checkbox"/> DIVISION_TIME_STD | <input type="checkbox"/> NUMBER_SPOTS |
| <input type="checkbox"/> NUMBER_GAPS | <input type="checkbox"/> NUMBER_COMPLEX | <input type="checkbox"/> NUMBER_SPLITS | <input type="checkbox"/> NUMBER_MERGES |
| <input type="checkbox"/> TRACK_DISPLACEMENT | <input type="checkbox"/> LONGEST_GAP | <input checked="" type="checkbox"/> TRACK_MEAN_SPEED | <input type="checkbox"/> TRACK_DURATION |
| <input type="checkbox"/> TRACK_MIN_SPEED | <input type="checkbox"/> TRACK_MEDIAN_SPEED | <input type="checkbox"/> TRACK_MAX_SPEED | <input type="checkbox"/> TRACK_STD_SPEED |
| <input type="checkbox"/> TRACK_MEAN_QUALITY | <input type="checkbox"/> TOTAL_DISTANCE_TRAVELED | <input type="checkbox"/> MAX_DISTANCE_TRAVELED | <input type="checkbox"/> LINEARITY_OF_FORWARD_... |
| <input type="checkbox"/> CONFINEMENT_RATIO | <input type="checkbox"/> MEAN_STRAIGHT_LINE_SP... | | |
| <input type="checkbox"/> File_name_raw | | | |

Stat Method: randomization test ▼

Plot Selected Variables

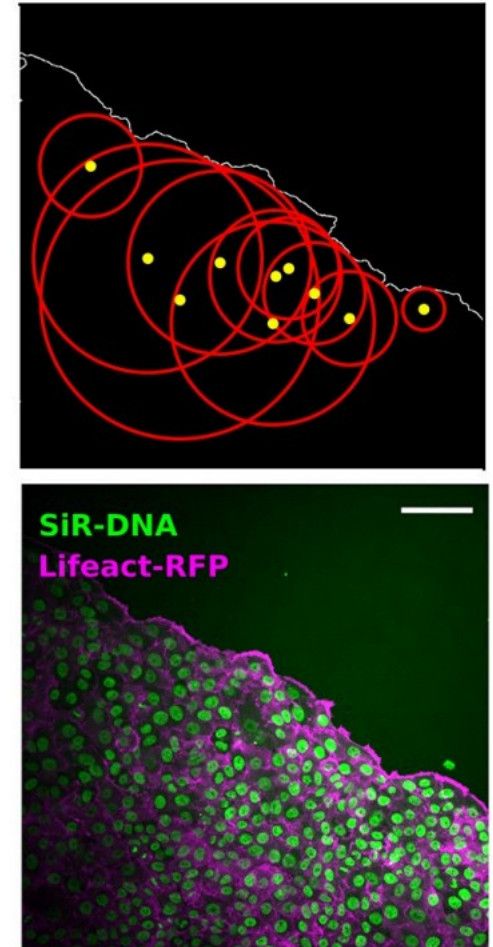
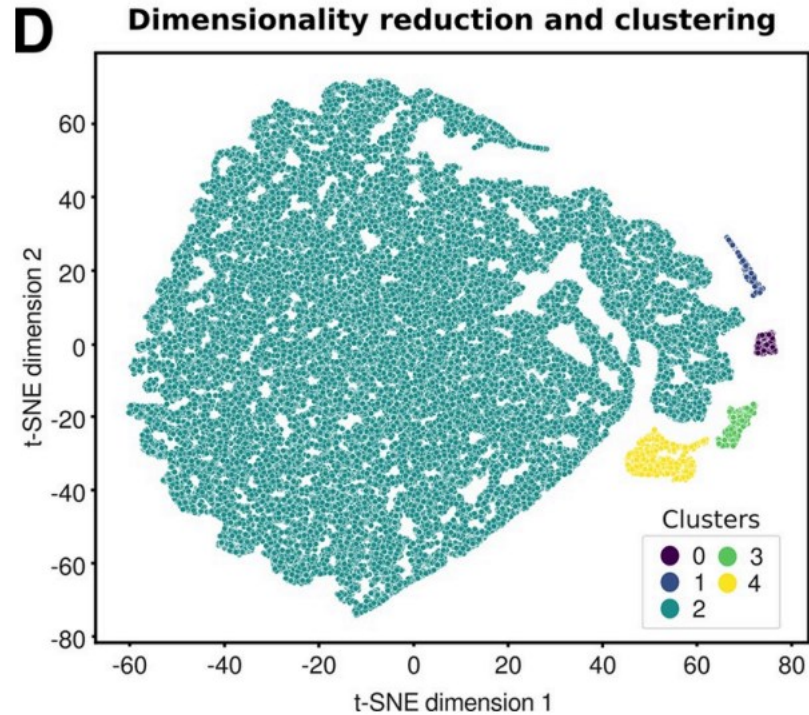
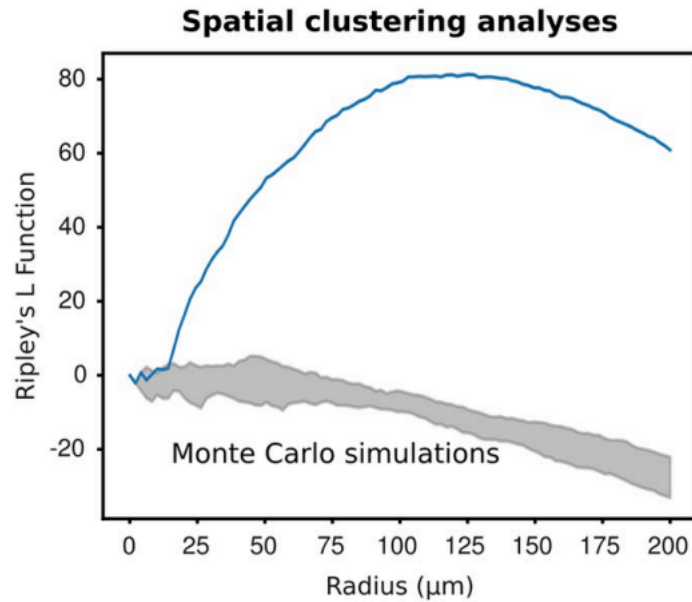
Additional features

Different data sources:



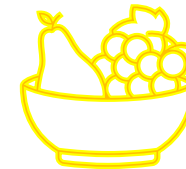
For more information: [CellTracksColab Wiki](#)

Additional features



For more information: [CellTracksColab Wiki](#)

Break time



BREAK