

Submission of results and executables

The objective of this document is to describe the structure and folder naming conventions for uploading segmentation and/or tracking results for the challenge datasets and for uploading command-line executables used for producing the submitted results.

Segmentation and/or tracking results

At the FTP server (<https://ftp.celltrackingchallenge.net> on the port number 21 with explicit TLS/SSL encryption enabled), all registered participants have their own private folders. The private folders contain subfolders prepared with the same structure as is in the released training and challenge datasets. Participants are kindly requested to upload their results only into these subfolders. For example, segmentation and/or tracking results for the 01 sequence of the Fluo-N2DL-HeLa dataset must be uploaded into the Fluo-N2DL-HeLa/01_RES subfolder. If a participant does not want to submit results for some sequence, the corresponding subfolder remains empty. Note that it is the responsibility of each participant to provide complete segmentation and/or tracking results for a particular sequence and to format the results as described in [Naming and file content conventions.pdf](#). Any results uploaded into other than the prepared subfolders or not being complete (i.e., there are some files missing or of incorrect names or file format), will not be evaluated.

Command-line executables

The command-line executables, including all dependencies (e.g., dynamically linked libraries in case of precompiled C++ codes, or independent text files with all necessary packages including their versions in case of Python scripts) used for producing the submitted segmentation and/or tracking results must be uploaded into the SW subfolder located in the participant's private folder. Furthermore, it is necessary to provide an individual entry point file in the SW subfolder for each submitted segmentation and/or tracking results. Entry files must be named as **DatasetName-SequenceID.extension**. For instance, the Fluo-N2DL-HeLa-01.bat file shall produce segmentation and/or tracking results for the 01 sequence of the Fluo-N2DL-HeLa dataset in the predefined format. The entry files must be either batch files (extension is then .bat) for Windows users or shell scripts (extension is then .sh) for Linux users. They are, basically, front-ends to the participant's command-line executables. The entry file itself must not require any parameters, but may execute other commands. It is allowed to execute only standard system commands (e.g., cd or echo), user-supplied, command-line executables (e.g., myAlg1.exe), or programming language interprets (e.g., python myAlg1.py). All necessary parameters to the participant's command-line executable, which may possibly vary between datasets or sequences, must be specified inside the entry file. As the organizers will verify that the submitted entry files produce the submitted segmentation and/or tracking results, the participant's SW folder will be moved to the ChallengeDatasets folder and the entry files will be executed from there. Therefore, an entry file, for instance, Fluo-N2DL-HeLa-01.bat must assume that input images are located in `"../Fluo-N2DL-HeLa/01"` and segmentation and/or tracking results will be saved into `"../Fluo-N2DL-HeLa/01_RES"`. Furthermore, all intermediate results must be handled in the current working directory, the folder where the entry file is located. Participants are welcome to add supplementary comments in the entry files (e.g., on a particular version of MATLAB or Python).

Example entry point file for Windows – Fluo-N2DL-HeLa-01.bat

```
@echo off
REM Run the tracking routine my_track.exe with five input parameters:
REM input_sequence output_sequence param1 param2 param3

REM Prerequisites: MATLAB 2020b (x64), Python 3.8

my_track.exe "..\Fluo-N2DL-HeLa\01" "..\Fluo-N2DL-HeLa\01_RES" param1 param2 param3
```

Example entry point file for Linux – Fluo-N2DL-HeLa-01.sh

```
#!/bin/bash

# Run the tracking routine my_track with five input parameters:
# input_sequence output_sequence param1 param2 param3

# Prerequisites: MATLAB 2020b (x64), Python 3.8

./my_track "../Fluo-N2DL-HeLa/01" "../Fluo-N2DL-HeLa/01_RES" param1 param2 param3
```

Specific instructions for Fluo-N3DL-DRO, Fluo-N3DL-TRIC, and Fluo-N3DL-TRIF

Due to different treatment of extra detected and segmented cells in the Cell Tracking Benchmark and the Cell Segmentation Benchmark for these datasets, the Cell Tracking Benchmark participants are encouraged to submit not only tracking results limited to the cells provided in the first frames of the gold reference tracking annotations, but also complete segmentation results that will automatically be purified from all extra detected and segmented cells by the evaluation software and used for the Cell Segmentation Benchmark. The complete segmentation results and command-line executables used to produce them shall be uploaded into the prepared particular folders under the CSB subfolders.