

## Submission of results and executables

The objective of this document is to describe the structure and folder naming conventions for uploading segmentation-and-tracking and/or segmentation-only results for the test datasets and command-line versions of the algorithms used to produce them.

### Segmentation-and-tracking and segmentation-only results

At the FTP server (ftps://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 it is in the released training and test datasets. Participants are requested to upload their results only into these subfolders. For example, 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 format the results as described in [Naming and file content conventions.pdf](#).

### 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 to produce the submitted results must be uploaded into the SW subfolder. Furthermore, it is necessary to provide an individual entry-point file in the SW subfolder for each analyzed sequence. Entry-point files must be named as **DatasetName-SequenceID.extension**. For example, the Fluo-N2DL-HeLa-01.bat file shall produce results for the 01 sequence of the Fluo-N2DL-HeLa dataset in the predefined format. The entry-point files must be either batch files (.bat) for Windows users or shell scripts (.sh) for Linux users. They 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., myAlg.exe), or programming language interpreters (e.g., python myAlg.py). All necessary parameters to the participant's command-line executables, which may vary between datasets or sequences, must be specified inside the entry-point files. Furthermore, the entry-point files must assume that input images are located in **"../DatasetName/SequenceID"** and results will be saved into **"../DatasetName/SequenceID\_RES"**. Finally, all intermediate results must be handled in the current working directory, the folder where the entry-point files are located. Participants are welcome to add supplementary comments to the entry-point files (e.g., on a particular version of MATLAB or Python required).

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

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

REM Prerequisites: MATLAB R2023a (x64), Python 3.10

my_tracker.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 segmentation-and-tracking routine my_tracker.exe with five input parameters:
```

```
# input_sequence output_sequence param1 param2 param3
```

```
# Prerequisites: MATLAB R2023a (x64), Python 3.10
```

```
./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 segmentation-and-tracking results limited to the cells provided in the very first frames of the gold tracking truth, but also complete segmentation-only results that will automatically be filtered out by the evaluation software and used for the Cell Segmentation Benchmark. The complete segmentation-only results and command-line executables used to produce them must be uploaded into the prepared folders under the CSB subfolder.

## Specific instructions for generalizable submissions

Except for the output subfolder and entry-point file names, the same instructions, as specified above for regular submissions, apply to the generalizable submissions too. The only differences are that instead of uploading results into the SequenceID\_RES subfolders and providing DatasetName-SequenceID.extension entry-point files, upload the results into the **SequenceID\_RES-TrainingDataConfiguration** subfolders and provide **DatasetName-SequenceID-TrainingDataConfiguration.extension** entry-point files, with TrainingDataConfiguration being GT, ST, GT+ST, allGT, allST, or allGT+allST, depending on the training data configuration used.