

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 individual benchmarks included in the challenge 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 root folders with subfolders specifically prepared for individual benchmarks. The benchmark subfolders contain dataset subfolders of the same structure as 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 within the Cell Tracking Benchmark must be uploaded into the CTB/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 versions of algorithms

The command-line versions of algorithms, 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 interprets (e.g., python myAlg.py). All necessary parameters to the 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 raw 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_tracker "../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 versions of algorithms used to produce them must be uploaded into the prepared folders under the CSB benchmark subfolder.

Specific instructions for submissions to the Cell Linking Benchmark

The same instructions, as specified above for regular submissions to the Cell Tracking Benchmark and the Cell Segmentation Benchmark, apply to submissions to the Cell Linking Benchmark too. The only difference is that the entry-point files must further assume that perfect/imperfect segmentation masks are located in `"../DatasetName/SequenceID_ERR_SEG"`. An example call of a command-line executable can look like as follows:

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

Specific instructions for generalizable submissions to the Cell Tracking Benchmark and the Cell Segmentation Benchmark

Except for the output subfolder and entry-point file names, the same instructions, as specified above for regular submissions to the Cell Tracking Benchmark and the Cell Segmentation Benchmark, apply to generalizable submissions to these benchmarks 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.