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Learning to Automatically Detect and Track Cells in Microscopic Imaging

by

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Contents

Appendices

A. Installation instructions for the image annotations tools

Both the Image Annotation Tool and the Trajectory Annotation Viewer are provided as Windows executables that need to be installed. The installation only requires an active internet connection to automatically download the MATLAB Compiler Runtime[1].

[1] http://www.mathworks.co.uk/products/compiler/mcr/

B. Installation instructions and usage example for the cell detector and tracker

B.1. Installation instructions

The source code of the cell detector and tracker requires the manual installation of several dependencies which have to be manually downloaded and added to the MATLAB search path[1]. The dependencies, including the tested version numbers, are:

1. VLFeat[2] (version 9.18), an open source library of popular computer vision algorithms.
2. svm-struct-matlab[3] (version 1.2), a MATLAB wrapper for SVM$^{\text{struct}}$.
3. The MATLAB code for the inference in the pylon model[4]
4. QPBO[5] (version v1.31) from Vladimir Kolmogorov.

A Bash script is available in the source code in *cell_tracker/+detector/setup/setup.sh* to automate the installation of the required dependencies. Before running the script it is advisable to review it and configure the installation path in the first few lines of the script.

The code has been tested in MATLAB R2014a under Ubuntu 14.04.1 LTS. However, the code should work also in version R2013b. Additionally the following MATLAB toolboxes are needed:

1. Statistics Toolbox
2. Image Processing Toolbox
3. Computer Vision System Toolbox
4. Neural Network Toolbox
5. Optimization Toolbox

[1] `http://www.mathworks.co.uk/help/matlab/matlab_env/what-is-the-matlab-search-path.html`
[2] `http://www.vlfeat.org/`
[3] `http://www.robots.ox.ac.uk/~vedaldi/code/svm-struct-matlab.html`
[4] `http://www.robots.ox.ac.uk/~vilem/`
[5] `http://pub.ist.ac.at/~vnk/software.html`

6. Parallel Computing Toolbox

7. System Identification Toolbox

B.2. Usage example

In this section we describe how to configure the system to train and test the cell detector and tracker on your own image sequences.

First, configure the data directories in *dataFolders.m*. This will include appending a block of code similar to this:

```
% dataFolders.m
% ...
case 7 % dataset ID: use the next number of the sequence
    dotFolder = '<folderNamesWithDotAnnotations>';
    linkFolder = '<folderNamesWithLinkAnnotations>';
    outFolder = '<outputFolderName>';
    numAnnotatedFrames = 30;      % the number of dot-annotated frames
    numAnnotatedTrajectories = 4; % the total number of annotated trajectories
% ...
```

The *dotFolder* should contain images in the *pgm* format named sequentially as *im001.pgm* and correspondingly named *mat* files with dot-annotations for the first frames of the sequence, as indicated by *numAnnotatedFrames*. The *mat* files can be generated by the Image Annotation Tool.

The *linkFolder* should contain images and annotations files in the same format as the *dotFolder*. The *mat* files should not only contain annotated dots but also at least a few fully annotated cell trajectories (as indicated by *numAnnotatedTrajectories*) required to train the tracker. Note that in general *dotFolder* and *linkFolder* can be the same.

The *outFolder* is the folder where the detector and tracker will output temporary and final results.

Second, in the file named *runner.m* it is required to insert the dataset ID as above, and select which of the actions should be executed:

```
% runner.m
% ...
datasetIDs   = [7];    % Look into dataFolders.m

trainDetector = true; % Use annotations in dotFolder to train a new detector
trainTracker = true;  % Use annotations in linkFolder to train a new tracker

testDetector = true;  % Evaluate the trained detector on the full image sequence
testTracker  = true;  % Evaluate the trained tracker on the full image sequence
```

```
showTracks   = true;   % Display a figure containing the generated trajectories
% ...
```

Note that it is possible to insert several dataset IDs and the code will be executed on each of them sequentially. The file *runner.m* can then be executed using MATLAB.

C. Cell detection results

This chapter includes three-dimensional figures of the results of the cell detection module on each of the studied datasets.

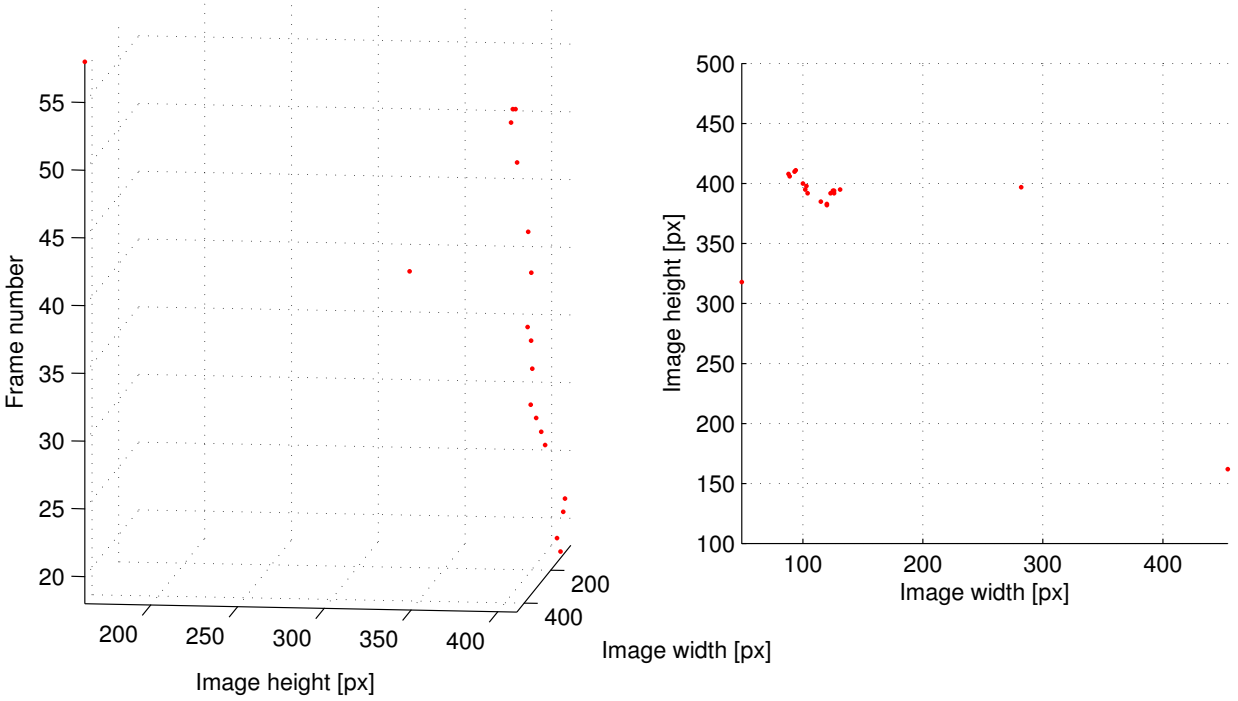

Figure C.1.: Three-dimensional view and orthographic projection from the top of the detection results for dataset A.

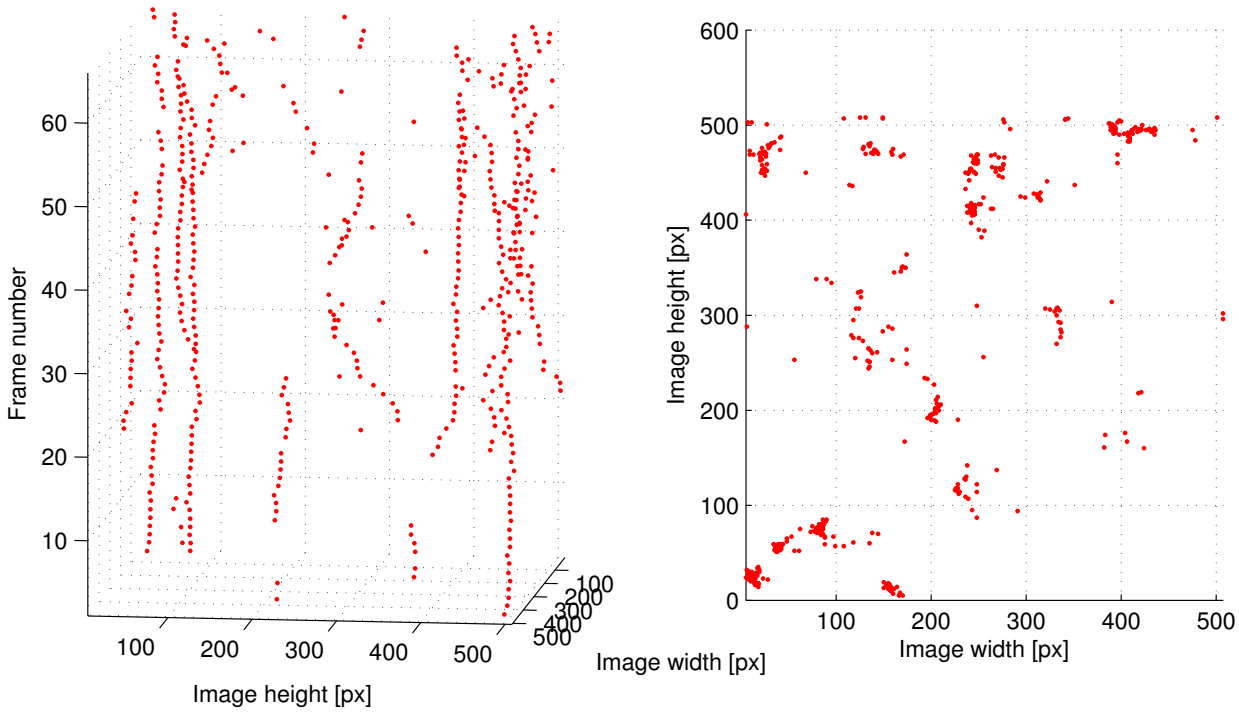

Figure C.2.: Three-dimensional view and orthographic projection from the top of the detection results for dataset B.

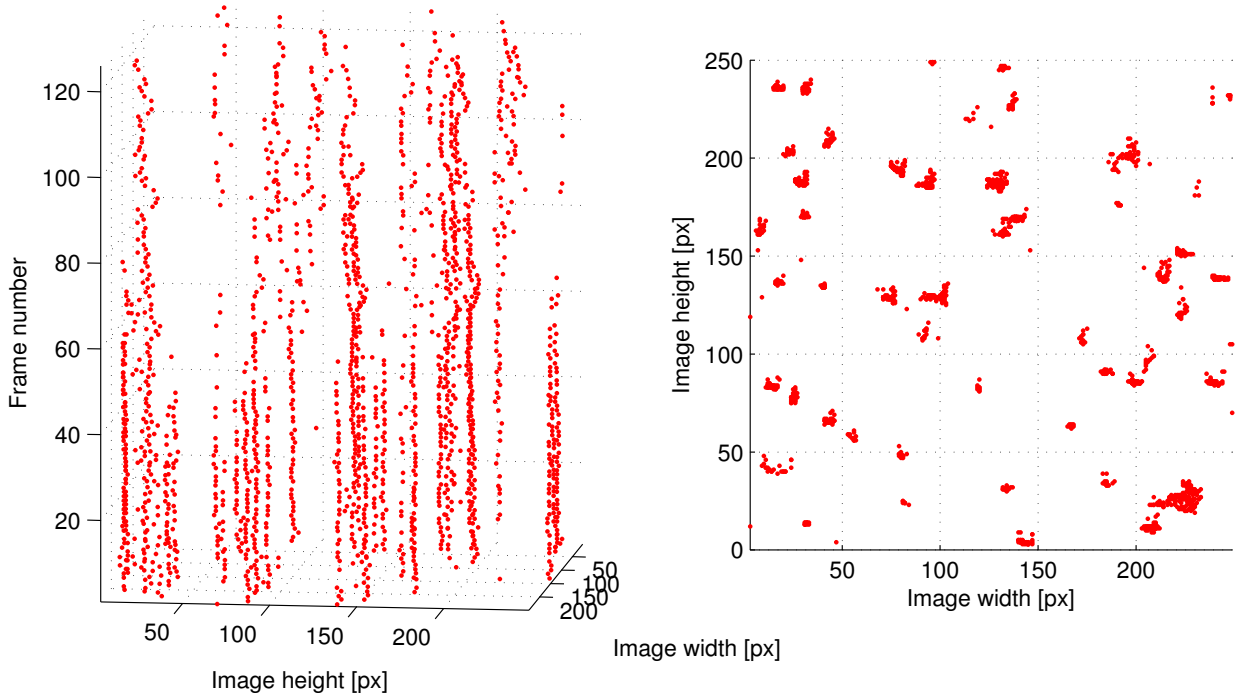

Figure C.3.: Three-dimensional view and orthographic projection from the top of the detection results for dataset C.

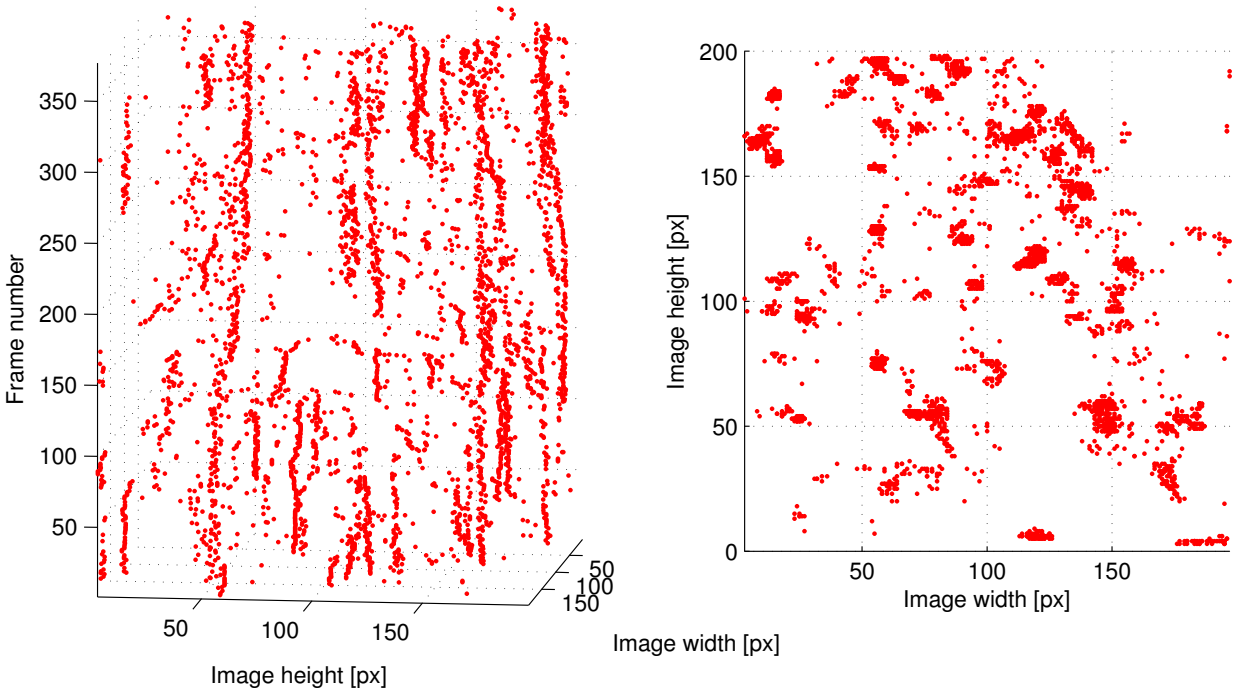

Figure C.4.: Three-dimensional view and orthographic projection from the top of the detection results for dataset D.

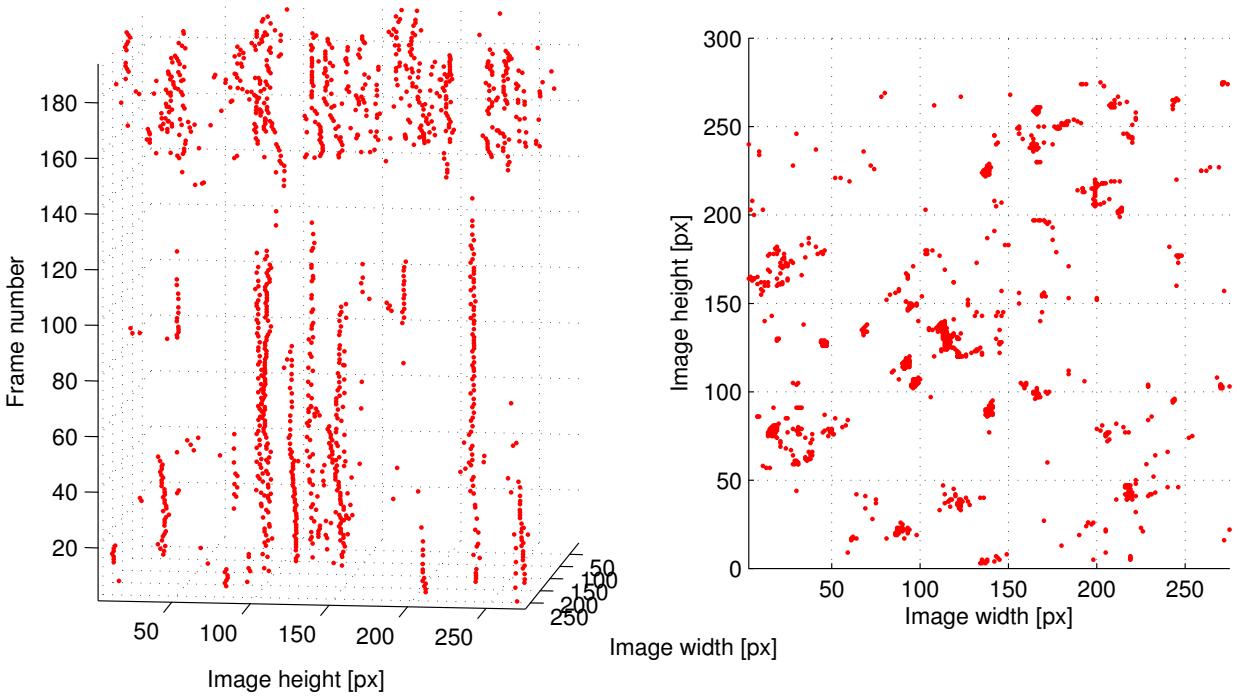

Figure C.5.: Three-dimensional view and orthographic projection from the top of the detection results for dataset E.

D. Cell tracking results

This chapter includes three-dimensional figures of the trajectories generated by the cell tracking module on four of the studied datasets.

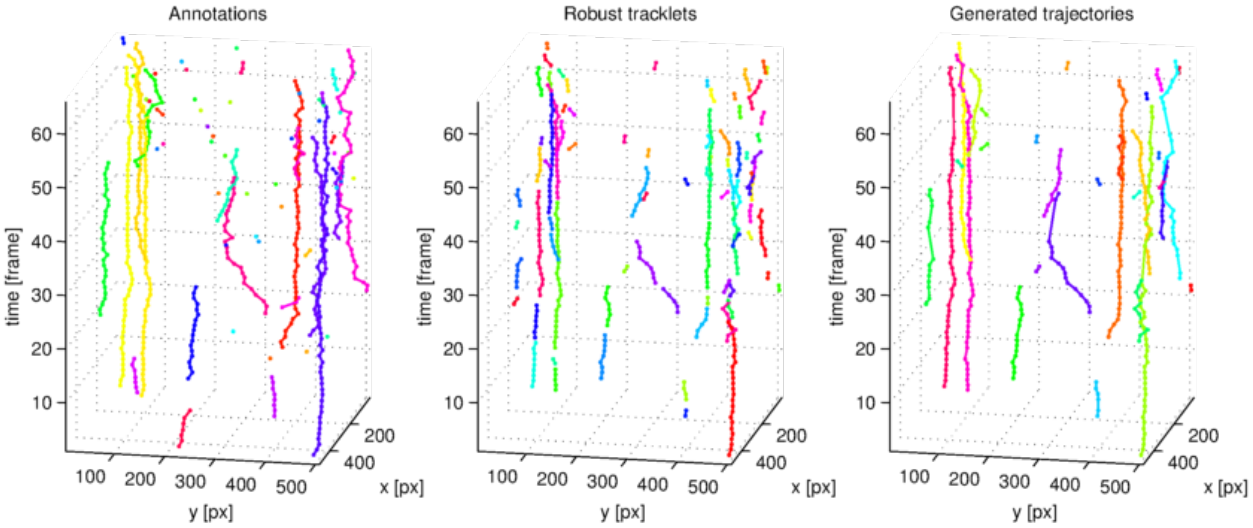

Figure D.1.: Generated trajectories for dataset B. The parameters of the tracker were set to $\pi_{init} = 1$, $\pi_{term} = 1$, $\pi_{link} = 1$ and $\pi_{FP} = 1$ and configured to close gaps up to size 9.

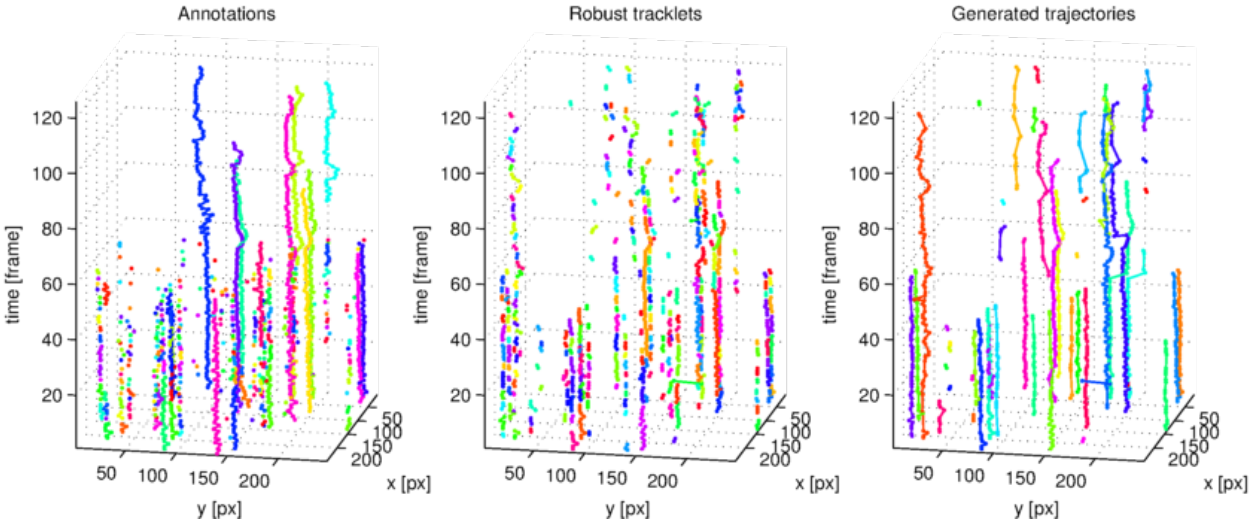

Figure D.2.: Generated trajectories for dataset C. The parameters of the tracker were set to $\pi_{init} = 1$, $\pi_{term} = 1$, $\pi_{link} = 1$ and $\pi_{FP} = 1$ and configured to close gaps up to size 9.

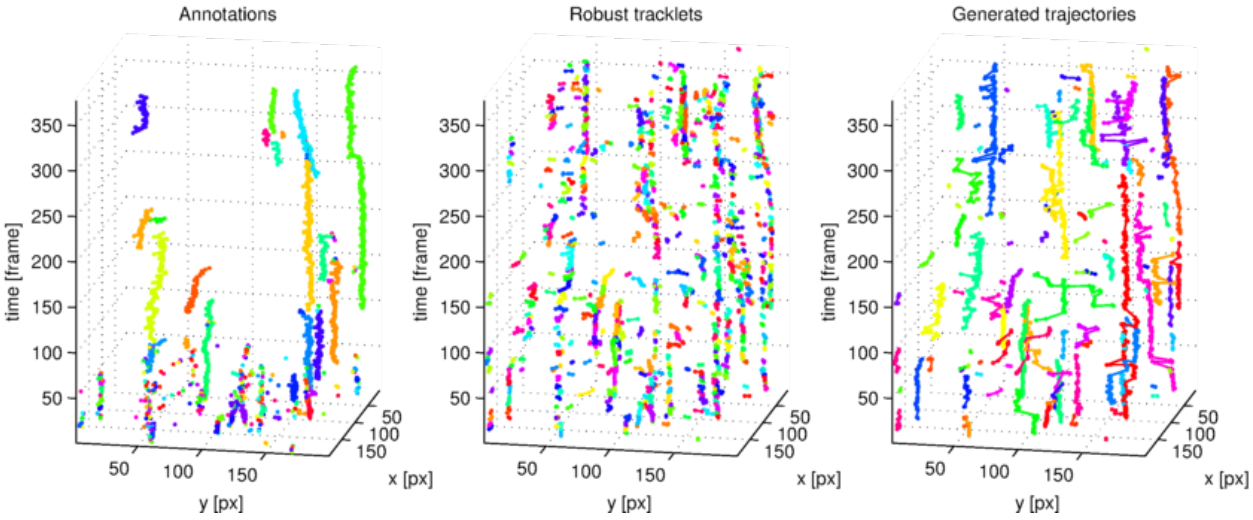

Figure D.3.: Generated trajectories for dataset D. The parameters of the tracker were set to $\pi_{init} = 1$, $\pi_{term} = 1$, $\pi_{link} = 1$ and $\pi_{FP} = 1$ and configured to close gaps up to size 9.

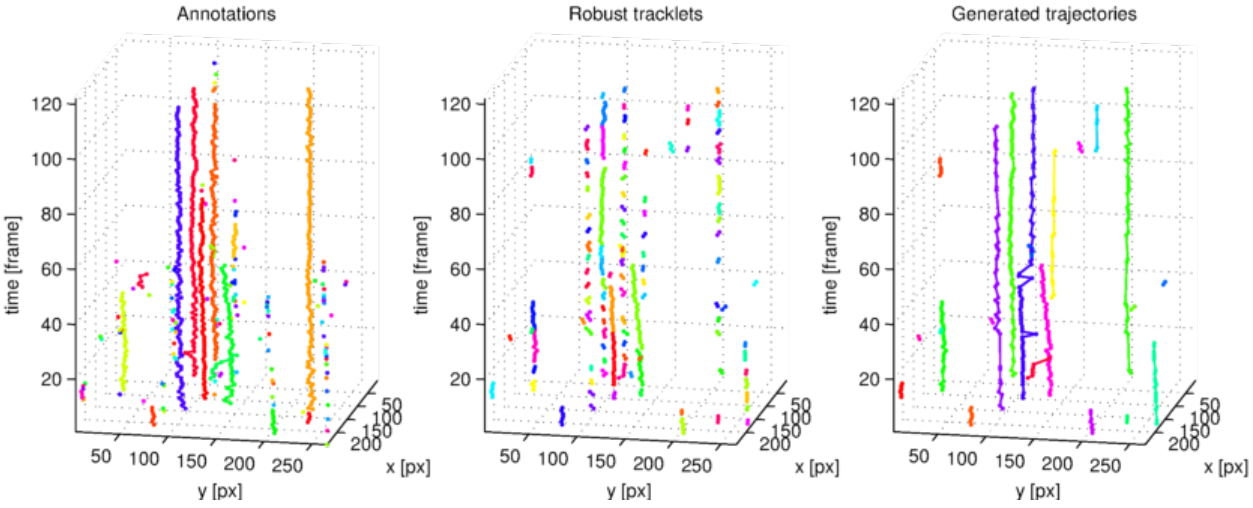

Figure D.4.: Generated trajectories for dataset E. The parameters of the tracker were set to $\pi_{init} = 3$, $\pi_{term} = 3$, $\pi_{link} = 1$ and $\pi_{FP} = 1$ and configured to close gaps iteratively up to size 9 and then up to size 20.

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