PHOT 533: Biomedical image analysis and image processing

Project topics: project 1

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Introduction

There are two projects to be completed for the PHOT 533 course during this semester. This file contains all the project topics. You can work together on projects and you can ask help from me (asking help will not influence your project grade). However, your project report and corresponding script should be made individually and not copied from others or online resources.

The project problems and their descriptions are not strictly to be followed, they are more like guidelines, you can adapt them according to your own ideas. You can also propose your own completely different topic.

Type of report for project 1

You send in the script(s) used, data/images used (if not too large), and a report. In the report you describe in a concise manner what you did, any results, and how you obtained them. Describe the crucial steps that you undertook to tackle the problem at hand. Support your outcome with segmentation example results, comparisons with the ground truth images or features, etc. Guideline for the report length is between 2 and 4 pages including figures.

Grading of the project

This project will count for 20% of your grade. Points are given on the combined effort of the project and the oral explanation of it during the exam.

Project topics

Next is a list of 5 topics you can choose out for your project together with their task description.

(1) Counting stars

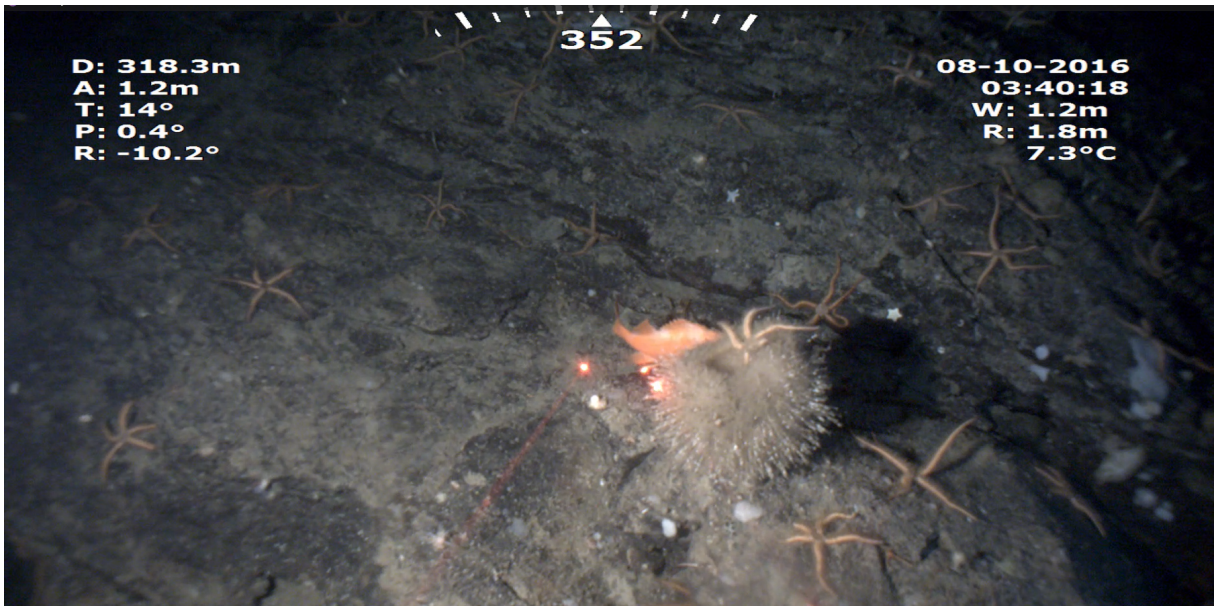

Figure 1: Snapshot of movie data

This project concerns the optimization of detection and tracking of starfish from the video data of an underwater movie featuring starfish (Bisque). The movie is an example of difficult tracking conditions: the field of view is a 3D projection (size of the tracked objects changes when coming closer), the starfish can move and change shape, meanwhile small objects (bubbles, other water creatures) can fly in front of the camera. The task can be divided into following sub-tasks:

- Download the data, verify whether you can download/extract any metadata.
- Use feature detection in scale space to detect the starfish.
- Perform the tracking, i.e. the linking of detected starfish of multiple frames by a Hungarian-based method (or nearest neighbors).
- Add additional features for the detection step: color, morphology, etc. to increase the detection and thereby tracking accuracy.

(2) Protein translocation and cell classification

Main topics: **2D cell segmentation**, **classification**, **CellProfiler**, and **CellAnalyzer**

Start from the BBBC image data set: this image data set is about translocation of a protein (transcription factor NFκB) from the cytoplasm to the nucleus against the background of breast (MCF-7 cells) and lung cancer (A549 cells) under various TNFα concentrations. This data belong to an example CellProfiler pipeline to which studies the protein translocation.

1. First download CellProfiler, download then the example pipeline and try to run it within CellProfiler.
2. Verify what the output means for nuclear translocation.
3. Extract more data, e.g., cell intensity and texture features.
4. Download the whole data set from the link above, and execute your extended pipeline on the whole data set.
5. Download CellAnalyzer and feed the extended data into CellAnalyzer. Thereby try to understand whether there is any correlation between cell morphology/texture/intensity and translocation.

(3) 3D cell segmentation and analysis

Main topics: **3D segmentation**, **Ground truth comparison**

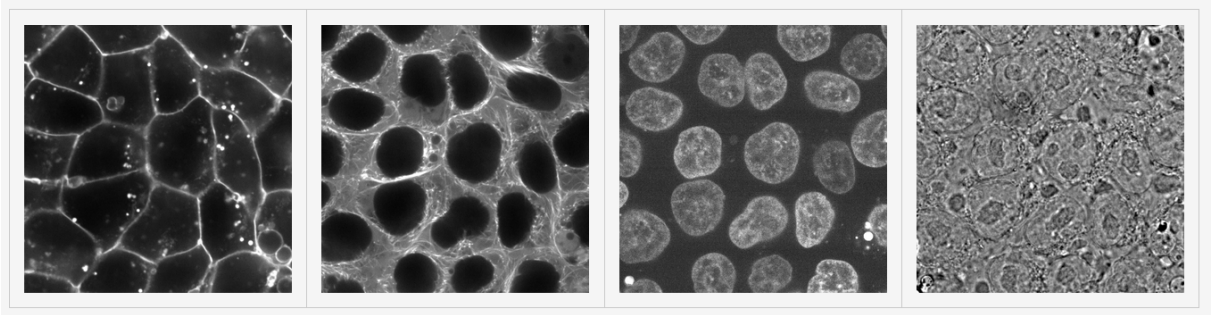

Figure 2: BBBC034 data set image channels: cell border, cytoskeleton, nuclei, bright-field.

Segmentation of 3D images is often harder as for most microscopy modalities the axial resolution is less good than the planar resolution. In this project the idea is to perform 3D cell segmentation of an annotated data set: 3D pluripotent stem cells. This data set contains 3 image stacks showing stained nuclei (DAPI), cytoskeleton (actin), membrane (CellMask), and bright-field images. Only one of them has ground truth and can be used for segmentation benchmarking.

- Download the data set
- First perform 3D cell segmentation using manual designed preprocessing (e.g. smoothening filters) and thresholding (with optional postprocessing steps).
- Compare your obtained segmentation results with the provided ground truth segmentation.
- Adapt your algorithm/pipeline to perform the main segmentation step by a nucleus/cytoplasm/cell border pixel classification.
- Compute some 3D morphological feature(s) such as surface to volume ratio, and see whether the different segmentations have influence on the feature(s).

(4) Ant movement analysis and tracking

Main topics: **2D instance detection**, **Object tracking**

Figure 3: Ant colony data set example

Social animals such as ants exhibit complex behavior within their motion and trajectories. Not only have ants be found to solve path-searching problems, their general behavior depends on their environment.

Tracking ants is a complex task due to multiple factors: their morphology is complex, their motion can be fast or slow (therefore camera frame rate needs to be high), they can crawl close to each other, they can carry various objects. Within this project the idea is to do the following:

- start from a well-known and researched image data set for ant tracking such as the Ant tracking indoor and outdoor data sets.
- Develop your detection algorithm first on the indoor (ants in a bucket) image data, then try the outdoor image data.
- Reproduce some of the tracking results by your own tracking algorithm.
- Afterwards try to improve the tracking results for a specific subset.
- Compare your results with the state-of-the-art ant-tracking algorithms, such as in AntTracker.

(5) Multi-modal cell segmentation

Deep learning and (convolutional) neural networks allow to extract image features based on image data. Therefore it became possible to generalize the target domain of image data types that such algorithms can handle. One very general goal required in many biomedical image analysis pipelines is cell segmentation. Algorithms which can perform cell segmentation of varied cell types and imaging modalities would be beneficial. In

this project the idea is to make a generalized cell segmentation pipeline based on neural networks based on the Grand Challenge: Cell Segmentation in Multi-Modality Microscopy Images and related publication in Nature Methods. This is one image-analysis problem from many other challenges available on the Grand-Challenge website.

Within this project (as a guideline) we will limit the used data mostly to the data of the test set. Further, we will step-wise increase the general applicability of the algorithm:

1. Create a neural network to segment the cells/nuclei. Use at first only one image resolution, modality, and cell type of choice.
2. Implement/use a metric to evaluate the accuracy of the segmentation by comparing them with the ground truth data.
3. Increase the data over different image resolutions and normalize the image data before providing it to your network. Compare the accuracy with the accuracy of more limited data.
4. Provide more cell types or different modalities. How is the network performing when offering more general images?