steinbock

A dockerized multi-channel image segmentation framework

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Motivation

Challenges with existing implementation:

- **Installation**: documentation, environments & dependencies
- **Usage**: documentation, usability, efficiency, reproducibility
- **Maintenance & support**: compatibility, extensibility

The `steinbock` framework

Framework for pixel classification-based cell segmentation

- Python package with integrated command-line interface (CLI)
- Versioned Docker container exposing the `steinbock` CLI, with third-party software (e.g., Ilastik, CellProfiler) pre-installed
- Documentation: bodenmillergroup.github.io/steinbock
- Maintenance & support: Lars Malmström, Jonas Windhager

Implemented multi-channel image segmentation approaches:

- Zanotelli et al. (Zenodo, 2017). *ImcSegmentationPipeline: A pixel classification-based multiplexed image segmentation pipeline*.

Installation

1. Install Docker
2. Pull `steinbock` Docker image:
   ```
   docker pull jwindhager/steinbock:0.2.0
   ```
3. Configure system to enable the `steinbock` command

Usage

```
> steinbock --help

Usage: steinbock [OPTIONS] COMMAND [ARGS]...

Options:
--help  Show this message and exit.

Commands:
preprocess  Extract and preprocess images from raw data
classify    Perform pixel classification to create probability images
segment     Perform cell segmentation to create cell masks
measure     Extract single-cell data from segmented cells
```

Example

```
# See https://bodenmillergroup.github.io/steinbock/beta-testing

steinbock preprocess imc --hpf 50                # hifi, ...

steinbock classify ilastik prepare --seed 123
steinbock classify ilastik app                   # train pixel classifier
steinbock classify ilastik run

steinbock segment cellprofiler prepare
steinbock segment cellprofiler app               # modify pipeline
steinbock segment cellprofiler run

steinbock measure cells intensities              # regionprops, ...
steinbock measure dists border                   # centroid, ...
steinbock measure graphs dist --thres 4          # knn, ...
```

Discussion

- Viable solution?
- Missing functionality?
  - OME-TIFF export?
  - Spillover correction?
- CLI vs Jupyter notebook?
- Documentation (markdown)?
- HistoCAT-web integration?