steinbock

A dockerized multi-channel image segmentation framework

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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*.

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?