
pIMZ

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pIMZ is a framework for python-based Imaging Mass Spectrometry (IMS) data analysis.

pIMZ focuses on a differential setting, where masses, specific to certain areas are obtained, which then serve as input for a cell-type detection framework and/or a differential expression setting.

pIMZ: an integrative framework for imaging mass spectrometry analysis

No idea what this framework does . . .

. . . it's not yet ready. But once it is, you will get to know a lot more here!

This is a “long description” file for the package that you are creating. If you submit your package to PyPi, this text will be presented on the [public page](#) of your package.

Note: This README has to be written using [reStructured Text](#), otherwise PyPi won't format it properly.

1.1 Installation

The easiest way to install most Python packages is via `easy_install` or `pip`:

CHAPTER 2

Indices and tables

- `genindex`
- `modindex`
- `search`