

Cytomine main documentation



Welcome to the Cytomine main documentation.


It is recommended to start by reading the main [Cytomine overview page](#) for a short introduction on Cytomine main concepts.

Then the documentation is organized in four main sections below for administrators/operators, developers, data/computer scientists, and end-users.

For testing the Cytomine platform, you can either:

1. Install a Cytomine instance on your own computer (laptop/desktop), on a server at our own site (intranet-only or worldwide internet access), on in the cloud, or
2. Access our demo instance available here: <http://demo.cytomine.be/> (see [Cytomine User Guide](#) for usernames/passwords or request a personal account).
3. [Contact us](#) for hosting/installation options.


Operations



Documentation for **administrators/operators**:

- Install Cytomine on Linux
- Install Cytomine on MacOS
- [OLD] Install Cytomine v1.1 on Linux
- Backup and restore data


Developments



Documentation for **software developers**:

- How to install a Cytomine development environment
- Global architecture: Implementation overview & paradigms
- Data model: main packages
- Extension: How to extend Cytomine core, development guidelines & tools

Data & algorithms



Documentation for **data /computer scientists**:

- Data access and interoperability (RESTful API): How to import/export data
- How to install the Cytomine Client and Data Mining Package
- Available algorithms for image retrieval, segmentation, classification, ...
- Extension: How to add and execute new software/script /algorithms

Contact us:

E-mail: info@cytomine.org

Users



Documentation for **end users**
(**biologists,...**):

- Cytomine User interface guide
- Scientific papers using Cytomine

Github: <https://github.com/cytomine> (Official version) and <https://github.com/cytomine-uliege/> (ULiège research latest developments)

Main website: <http://www.cytomine.org/>

Cite our work:

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10.1093/bioinformatics/btw013.