A bioinformatics workflow for high-throughput, quantitative analysis of tumor cell invasion.

P. Masuzzo[1, 2,*], N. Hulstaert[1, 2], L. Huyck[2], C. Ampe[2], L. Martens[1, 2] & M. Van Troys[2]
[1] Department of Medical Protein Research, VIB, [2] Faculty of Medicine and Health Sciences, [2] Department of Biochemistry, Ghent University, A. Baertsoenkaai 3, 9000 Gent, Belgium - paola.masuzzo@ugent.be
* Corresponding Author

Keywords: *cancer cell invasion, bioinformatics, image analysis, data management.*

Abstract

Cell migration plays an essential role in physiological processes such as morphogenesis, immune function and wound healing, and has crucial implication in disorders, most notably in cancer metastasis. Mechanisms involved in deregulated cell migration are therefore attractive targets for therapeutic intervention. Yet screening drugs for such tentative targets requires high-throughput, quantitative analysis approaches. The most powerful such approaches are built on a platform of high-throughput *in vitro* cell-based assays, coupled to automated image acquisition and quantification strategies. However, the resulting large amounts of acquired data call for new management, storage, analysis and dissemination solutions.

We here therefore present a bioinformatics workflow for high-throughput, quantitative analysis of *in vitro* cell migration, with a focus on tumor cell invasion. The main two components of this workflow are the CellMissy[1] data management, storage, analysis and dissemination software, and the CELLMIA automated image analysis software. First, CellMissy captures the detailed annotation of biological conditions during experimental set-up: cell types, treatments, extracellular matrix components are all specified and stored in a relational database. CELLMIA then processes the acquired phase contrast time-lapse images of cells invading 3D matrices to track individually migrating cells as well as collectively invading cell populations. The output of this processing is subsequently fed into CellMissy for storage, (semi-)automated data quality control, inspection, and statistical analysis using pluggable methods. CellMissy can also provide XML output files as well as PDF reports for dissemination purposes.

With the ability to process 96 samples per run, our automated workflow provides a high-throughput system for the quantitative characterization of cancer cell invasion, enabling direct comparisons of different biological conditions in terms of (drug) treatments, dosage response and matrix properties.

[1] Masuzzo et al., Bioinformatics 2013 - 29:2661-3. https://cellmissy.googlecode.com