
RAPPORT D'ACTIVITE 2017

ACTIVITY REPORT 2017

LAST NAME : CZERWIŃSKA

FIRST NAME : URSZULA

TEAM : Computational Systems Biology for Cancer

0 – MISSION DESCRIPTION 2017:

PhD candidate. My doctoral project engages collaboration between Systems Biology (Emmanuel Barillot) and Immunology teams (Vassili Soumelis) at Institut Curie. In this project, we will develop and apply the *advanced methodology of signal deconvolution* to decipher sources of signals shaping *transcriptomes* (global quantitative profiling of mRNA molecules) of *tumor samples*, with a particular focus on *immune-related signals* in the context of the tumour environment.

1 – ACHIEVEMENTS 2017:

Projects:

1.1 PhD project: DECONVOLUTION OF CELL AND ENVIRONMENT SPECIFIC SIGNALS AND THEIR INTERACTIONS FROM COMPLEX MIXTURES IN BIOLOGICAL SAMPLES

Supervisors: A. Zinovyev, V. Soumelis

Immuno-oncology remains a focal point of cancer research. Recently, there have been numerous publications related to the main topic of my PhD project: the immune infiltration of tumours. Our specific goal is to analyse transcriptome of tumour samples and infer composition of immune infiltration: deconvolute the mixed signals of different cell type in tumour microenvironment (TME).

In 2017, at first, I worked on simulated data that could be used as a “ground truth” data for our project. The issue turned out to be quite a complex one and is still under development. Secondly, I performed bibliographic study to formalise state of art of gene expression deconvolution in mathematical terms. The summary of this work will be a part of a chapter of my PhD thesis. Then mainly, we worked on standardized definition of pipeline of data treatment that will be published in a form of R package.

In April 2017, I successfully passed through thesis advisory committee. Perspectives and development of the project were assessed as highly satisfactory. The report and the assessment can be provided on the request.

In July 2017 I presented my work in a form of a poster at ISMB 2017 in Prague and subsequently at Data Science Summer School at l'Ecole Polytechnique in September 2017. The poster can be seen online: <https://drive.google.com/file/d/0BwbuCoLN00xpekloa3lvdUxKOUe/view>.

I completed numerous hours of various training (compulsory and facultative). The FdV ED474 doctoral school officially validated the second year.

Paris Descartes attributed me 'Mission d'enseignement' of 64 hours at Faculté de Pharmacie de Paris Descartes in the department of Mathematics, Statistics and Informatics.

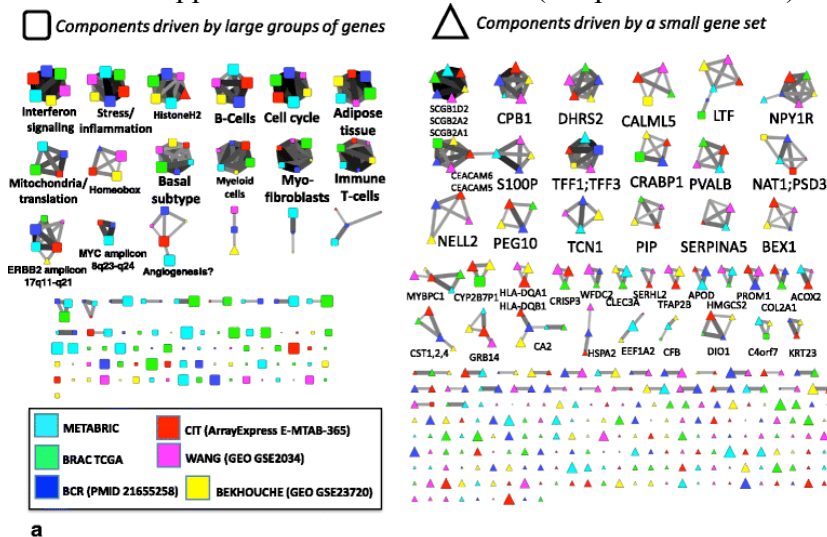
1.2 Determining the optimal number of independent components for reproducible transcriptomic data analysis

Collaborators : Ulykbek Kairov, Laura Cantini, Alessandro Greco, Askhat Molkenov, Emmanuel Barillot and Andrei Zinovyev

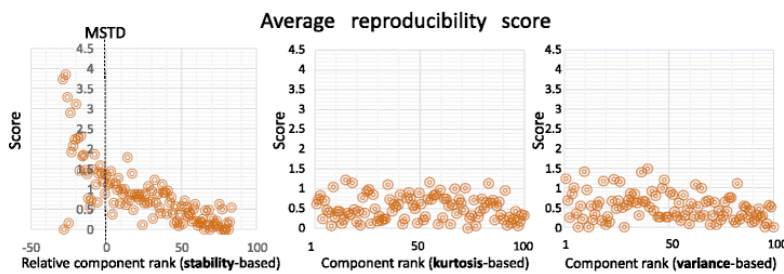
In this project the main goal was to define an optimal number of components for ICA that would be the most reproducible between different datasets.

My contribution was restricted to time benchmarking of ICA algorithm on R and MATLAB platforms, correction of the manuscript, checking reproducibility of obtained results through repeating established pipeline.

Publication appeared in BMC Genomics (see publication list)



a



b

Fig 3. Analysis of component reproducibility in independent datasets.
(from Kairov U & Cantini L et al. BMC Genomics. 2017)

1.3 Single cell data analysis for Immune Map

Collaborators : Maria Kondratova , Inna Kupersein, Andrei Zinovyev

I explored Tirosh et al. publication of single-cell composition of metastatic melanoma, using their population of macrophages and natural killer cells. Using ICA and literature based gene-sets, we have discovered functional groups within the cell population, highlighting possible functional polarisation of immune cells.

In 2017 we refined results and added to the manuscript additional elements. Manuscript of this work is in preparation coordinated by Inna Kuperstein.

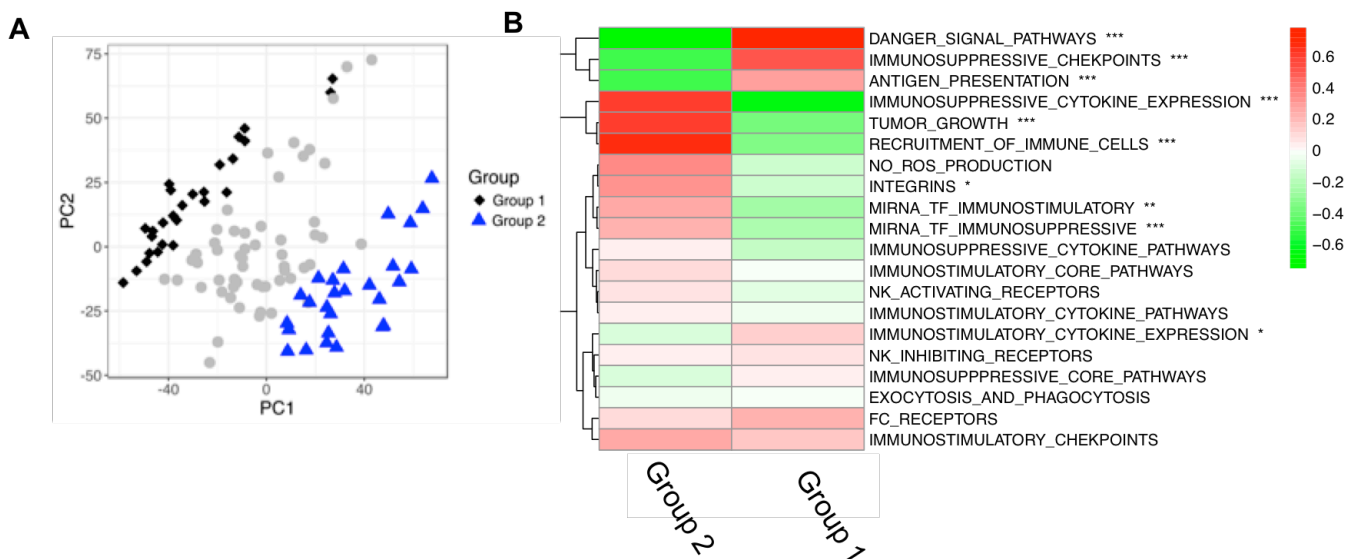


Fig. Enrichment of subgroups of macrophages in innate immune map (MK) A: Single cell data of macrophages (Tirosh et al.) was analysed with ICA and PCA algorithms. Extremes of two groups kept for further analysis. B: the mean value of expression of 50% of genes present in each module of the map was used to compute an average score for each group and each map module. T.test p.value were used to assess the significativity of the score difference between two groups.

1.4 DC cells heterogeneity

Collaborators : Vassili Soumelis, Paula Michta, Floriane Noel, Andrei Zinovyev

In 2016, I did supplementary analysis using ICA and ROMA module activity. I identified set of pathways that allow separation of DC subsets in an unsupervised manner. The manuscript of this work was initially accepted to Nature Immunology and then rejected because of reviewers' doubt concerning the experimental part of the work. I contributed to revision of the paper (before the rejection) and I will follow participate in the new submission.

1.5 Wikipedia protein-protein network

Collaborators : Andrei Zinovyev, Laura Cantini, Luca Albergante, José Lages, Dima Shepelyansky

Team of physicistes in Toulouse established an efficient way to compute reduced Google Matrix. In collaboration with them we obtained reduced Google matrix for Wikipedia pages of protein entries.

The project is in its initial phase. So far we focused on comparison of computed Wikipedia network with different properties and a protein-protein interaction database (SIGNOR)

Quality and reproducible research:

- Evernote posts of daily activity – I document for myself and my supervisor my everyday progress;
- writing readable code with comments/ .Rmd files – I put a lot of effort documenting my scripts and putting in an online repository, for some projects (like 1.5) we work on code that is stored in git system (BitBucket);
- writing R package – I am writing an R package that will allow anyone reproduce my analysis and apply to his/her needs

2 – PERSPECTIVES 2018:

1.1 In 2018 I will write the thesis and defend it. I will finish writing the package and related publication.

1.3 I will contribute in submission and revision of the publication

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1.5 We will infer interesting characteristics of the “Wikipedia protein network”. We will write a publication on the topic.

3 – ELEMENTS STATISTIQUES / STATISTICS:

3.1 – TRAINING AND COURSES DELIVERED 2017:

Titre / Title : Mission d’enseignement : UFR Pharmacie, Statistique Informatique

Date : 1/09/2017-30/06/2018 (64h)

Lieu / Location : Faculté de Pharmacie de Paris de l’Université Paris Descartes, 4 av de l’observatoire, 75006 Paris.

Organizers : Chantal Guihenneuc, Chantal.guihenneuc@parisdescartes.fr

Audience : Pharmacy Students

3.2 – TRAINING RECEIVED 2017:

Titre / Title : HackinScience Python course

Date : 16-20 January 2017

Lieu / Location : CRI Montparnasse

Organizers : Hackinscience (Antoine Angot, Julien Palard)

Titre / Title : "Construire et activer son réseau dans le cadre de sa recherche d'emploi"

Date : 13 January 2017

Lieu / Location : Paris Diderot

Organizers : CFDiP (teacher: Barbara Filler)

Titre / Title : "Comment décrocher votre futur emploi "

Date : 12 January 2017

Lieu / Location : Paris Diderot

Organizers : CFDiP (Adoc Talent Managment)

Titre / Title : " Big dive "

Date : 19 June – 21 July 2017

Lieu / Location : Turin, Italy

Organizers : TOP-IX

3.3 – PUBLICATIONS (Format Pubmed) 2017:

Type : article, abstract, book chapter

Status : published / in press / revised / submitted / in preparation

3.3.1 – ARTICLES 2017:

Type : article

Status : published

[The inconvenience of data of convenience: computational research beyond post-mortem analyses.](#)

Azencott, C. A., Aittokallio, T., Roy, S., Norman, T., Friend, S., Stolovitzky, G., ... & DREAM Idea Challenge Consortium.

[Nat Methods](#). 2017 Sep 29;14(10):937-938. doi: 10.1038/nmeth.4457.

(among collaborators)

[Determining the optimal number of independent components for reproducible transcriptomic data analysis.](#)

Kairov U, Cantini L, Greco A, Molkenov A, **Czerwinska U**, Barillot E, Zinovyev A.

BMC Genomics. 2017 Sep 11;18(1):712. doi: 10.1186/s12864-017-4112-9.

[Reconstruction and signal propagation analysis of the Syk signaling network in breast cancer cells.](#)

Naldi A, Larive RM, **Czerwinska U**, Urbach S, Montcourrier P, Roy C, Solassol J, Freiss G, Coopman PJ, Radulescu O.

PLoS Comput Biol. 2017 Mar 17;13(3):e1005432. doi: 10.1371/journal.pcbi.1005432. eCollection 2017 Mar.

Type : article

Status : submitted

A blood biomarker detecting severe disease in young dengue patients at hospital arrival.

Nikolayeva, I., Bost, P., Casademont I., Duong V., Koeth F., Prot M., **Czerwinska U.**, & ... Schwikowski B. (2017)

3.3.2 – BOOK CHAPTERS 2017: *not applicable*

3.3.3 – TICK BOX I HAVE UPDATED THE U900 WIKI WITH MY PUBLICATIONS: ☐ **yes**

3.4 – PARTICIPATION TO CONFERENCES 2017:

3.4.1 – TICK BOX I HAVE UPDATED THE U900 WIKI WITH MY CONFERENCES: ☐

yes

Young Researchers in Life Science conference

15-17/05/17, Paris, France

Czerwinska U., Barillot E., Vassili S., Zinovyev A. DECONVOLUTION OF CELL AND ENVIRONMENT SPECIFIC SIGNALS AND THEIR INTERACTIONS FROM COMPLEX MIXTURES IN BIOLOGICAL SAMPLES

Talk

FdV PhD school retreat

8-11 June 2017, Porquerolles, France

Czerwinska U., Kairov U., cantini L., Greco A., Barillot E., Vassili S., Zinovyev A. Computational deconvolution of mixed signals in tumor microenvironment using Independent Components Analysis

Poster

ISMB/ECCB conference

22-25/07/17, Prague Czech Republic

Czerwinska U., Kairov U., cantini L., Greco A., Barillot E., Vassili S., Zinovyev A. Computational deconvolution of mixed signals in tumor microenvironment using Independent Components Analysis

Poster

DS3: Data Science Summer School

28/08/17 – 01/09/2017 Ecole Polytechnique, Massy Palaiseau, France

Czerwinska U., Kairov U., cantini L., Greco A., Barillot E., Vassili S., Zinovyev A. Computational deconvolution of mixed signals in tumor microenvironment using Independent Components Analysis

Poster

3.5 – INVITATION TO SEMINARS 2017:

not applicable

3.5.1 – TICK BOX I HAVE UPDATED THE U900 WIKI WITH MY SEMINARS: ☐ *not applicable*

3.6 – ORGANISATION OF EVENTS 2017:

3.6.1 – ORGANISATION OF CONFERENCES 2017

not applicable

3.6.2 – ORGANISATION OF SEMINARS 2017 :

3.7 – PUBLIC OUTREACH 2017:

Personal blog: <http://urszulaczerwinska.github.io/thoughts/> & urszulaczerwinska.github.io/works

3.8 – BOARD MEMBERSHIP:

conseil de laboratoire : PhD representative

3.9 – PRIZES AND NOMINATIONS 2017:

none

4.0 – GRANTS AND COLLABORATIONS 2017:

4.0.1 – NATIONAL, INTERNATIONAL INDUSTRIAL COLLABORATIONS 2017 :

Collaboration with Immunology team (Vassili Soumelis) at Institut Curie through doctoral project.

4.0.2 – GRANTS OBTAINED 2017 :

FdV 474 ED, travel grant of 1000 eur

Aviesan PhD grant for 3 year of PhD (till November 2018)