Motivation

### Subject "Post-Doc Application (Anders group)"

Dear Dr. Simon Anders,

I am Engineer in Biology. My first experience with computing using biological data, was done when I had a huge mass spectrometry data to analyze during my PhD (Toxico-Proteomics). Since, I started to spend more time in computing and tested several language as regexp, bash, C, Perl, python to response to biological questions. Finally, I found that R is the most adequate for the biology. The statistics are fundamental to make a sens to crude and heterogeneous biological data. It is an object-oriented scripting language that combines:

1. A user interface with a few basic menus and extensive help facilities,
2. An enormous set of functions for classical and modern statistical data analysis and modeling,
3. A graphics functions for visualizing data and model output,
4. And now with Shiny package, R can get web application with high performance as JavaScript, html and css.

These advantages are useful for integrate and visualize multi-omics cancer genomics data. For that, I started to develop package as [canceR](http://www.bioconductor.org/packages/release/bioc/html/canceR.html) and [CancerPortal](https://github.com/kmezhoud/CancerPortal). canceR is a graphical user interface dedicated to biologists without programming skill and want to analyze, explore, and modeling the cancer genomics data.

CancerPortal is more light package. It is a web application based on [Shiny](http://shiny.rstudio.com/). The power of cancerPortal is the freedom to get a multitude of computing and modeling methods depending on heterogeneous variables and have delicate graphs. This work is in progress and available in my [github](https://github.com/kmezhoud/).

Also, I participate to [collaborative](https://github.com/vjcitn/biocMultiAssay) work that have in part the same goal of your group. This is a Bioconductor multi-assay interest [group](https://groups.google.com/forum/" \l "!forum/biocmultiassay) from multiple countries. It is the welcome of all people interested in analysis of multi-assay cancer genomic experiments as gene expression, copy number, methylation, somatic mutation, microRNA. This group is animated by Dr. Levi Waldron (see references).

This is a great opportunity for me to be part of your group that would improve my work and expend my knowledge. We can develop new ways to enrich cancer genomics data and elucidate significant biological knowledge. I believe that my background and skills will prove to be an effective match for your qualifications.

I believe that I will be an excellent fit for this position. My resume contains additional information on my experience and skills. I would appreciate the opportunity to provide any further information on my candidacy. I can be reached via my home phone at 00216-25-909-901 or by email at: [kmezhoud@gmail.com](mailto:kmezhoud@gmail.com).

Thank you for your time and consideration. I look forward to speaking with you about this exciting opportunity.

Yours Sincerely

Karim Mezhoud

# Karim Mezhoud

Cancer, Data Visualization

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## Currently

I'm a research assistant in Nuclear Science Center of Tunisia. My main goal is to assess the risk of Low radiation exposure of Radiobiologist workers in Hospitals, Airport or other work places that have ionizing Rays. The Synopsis of my work is to predict the OMICS frontiers of healthy and cancer patients using Multi-Assays of genomics data. I'm developing tools to explore, visualize and interpret available Studies from public repositories as cBioPortal.

### Previous interest

Microcystin is a cyanotoxin that can be found in sea foods. It is hepato-toxic and can induce liver cancer. I worked on it to elucidate the molecular mechanisms to induce cancer using Proteomics techniques (*in vivo* Assays (Fish, Rodent)), 2D SDS-PAGE, LC-MSMS, bioinformatics).

## Education

2013- **elearning** Bioinformatics, Biostatistics, System Biology, Biomedical system, and Integrative Biology.

2013 **Faculté des Sciences de Tunis** Habilitation (HDR)

2003-07 **Museum National d'Histoire Naturelle (Paris, France)** PhD Proteomics

2002-03 **Museum National d'Histoire Naturelle (Paris, France)** DEA in Ecosystems and toxins interactions

2001-02 **National Veterinary School of Alfort (Paris, France)** Master in Total Quality and Management

1995-00 **National Agriculture Institute of Tunisia** Engineer in Food Technologies

## Selected Publications

2014 **Karim Mezhoud**, Amina Sakly, Hassen Ben Cheikh, Mouldi Saïdi, and Marc Edery. Radiobiology Worker Risk Assessment Using Stress Indicators and Proteomics. *Int. J. Low Radiation* Vol.9, No.3, 2014.

2013 **Karim Mezhoud** Graphical identification of cancer-associated gene sub-networks based on small proteomics data sets. *OMICS: A Journal for Integrative Biology* 2013 17(7): 393-397.

2011 **Karim Mezhoud**, Puiseux-Dao S., Edery M., Toxins and stress in fish: proteomic analysis and response network. 2011 Review, *Toxicon*, 57(7-8), 959-969.

## R Packages

**canceR** A Graphical User Interface for accessing and modeling the Cancer Genomics Data of MSKCC.

**CancerPortal** is a Shiny App to explore interactively Multi-Assay of Cancer Genomic Data.

## Technical skills

R | Statistics | LaTeX | Github | GNU/Linux | Bash | regex | Inkscape | Proteomics | Biochemistry | Mass Spectrometry.

## Language

French | Arabic | English

## References

Levi Waldron works at CUNY School of Public Health at Hunter College 2180 3rd Ave Room, 538 New York, NY 10035 [levi.waldron@hunter.cuny.edu](mailto:levi.waldron@hunter.cuny.edu)

Paul Shannon Fred Hutchison Cancer Research Center, Bioconductor Core team, Seattle, 98109, United States, [pshannon@fhcrc.org](mailto:pshannon@fhcrc.org)

Tim Triche Jr. works at University of Southern California, [ttriche@usc.edu](mailto:ttriche@usc.edu)