Quick overview

Academic Qualifications

Medical University of Vienna — **Austria**
Research Internship — *2019–present*
Project title: Genetic variants identification of individuals wit autoimmune diseases and its relation with autophagy.

National Autonomus University of Mexico (UNAM) — **Mexico City**
PhD candidate in Biomedical Sciences — *2015–present*
Project title: Computational identification of drug targets associated with specific pathways for treating molecular subtypes of breast cancer.

Autonomous University of Aguascalientes — **Aguascalientes, México**
Medical Doctor — *2008–2015*

Michoacana University — **Michoacán, México**
Two years in Bachelor of Mathematics — *2006–2008*

- Some formal mathematical education.
- MD (general practitioner) with clinical experience.
  - Now could be useful for interpretation
- Education in genomics / computational biology
  - Genomic data analysis

Main projects

- Drug repurpousing in breast cancer subtypes
  - RNAseq and Microarray data
- Variant identification in drug induce phospholipidosis
  - Exome-seq and RNAseq.

“For this project we are looking for:”

A) The generation of an atlas of human normal CNS development and its analysis.

B) the mapping of normal brain development data onto our rich set of brain tumor data.

C) the establishment of a single nucleus DNA methylation analysis protocol

How does my profile match with that tasks:

- Genomic data analysis. No experience in single nucleus methylation (C), but experience in:
  - RNAseq, NGS, Microarrays and some trainnig in ChIP-seq
- Interpretation of the data:
  - A) Generation of a Normal CNS development atlas
    - Anatomy, Embriology , Phisiology.
  - B) The mapping of normal brain development data onto our rich set of brain tumor data

Other coincidences:

- Research interests in computational oncoepigenomics[1]:
  - Experience in genome-wide DNA sequencing, RNA-seq, some training on ChIP seq.
  - Identification of drug targets based on high dimensional biological data to improve treatment decisions.
  - Experience with oncology classificators based on HTBD

- Identification and characterization of novel genetic alterations.
  - Your particular interest is in pediatric gliomas of different stages
  - Drug screen and preclinical experiments

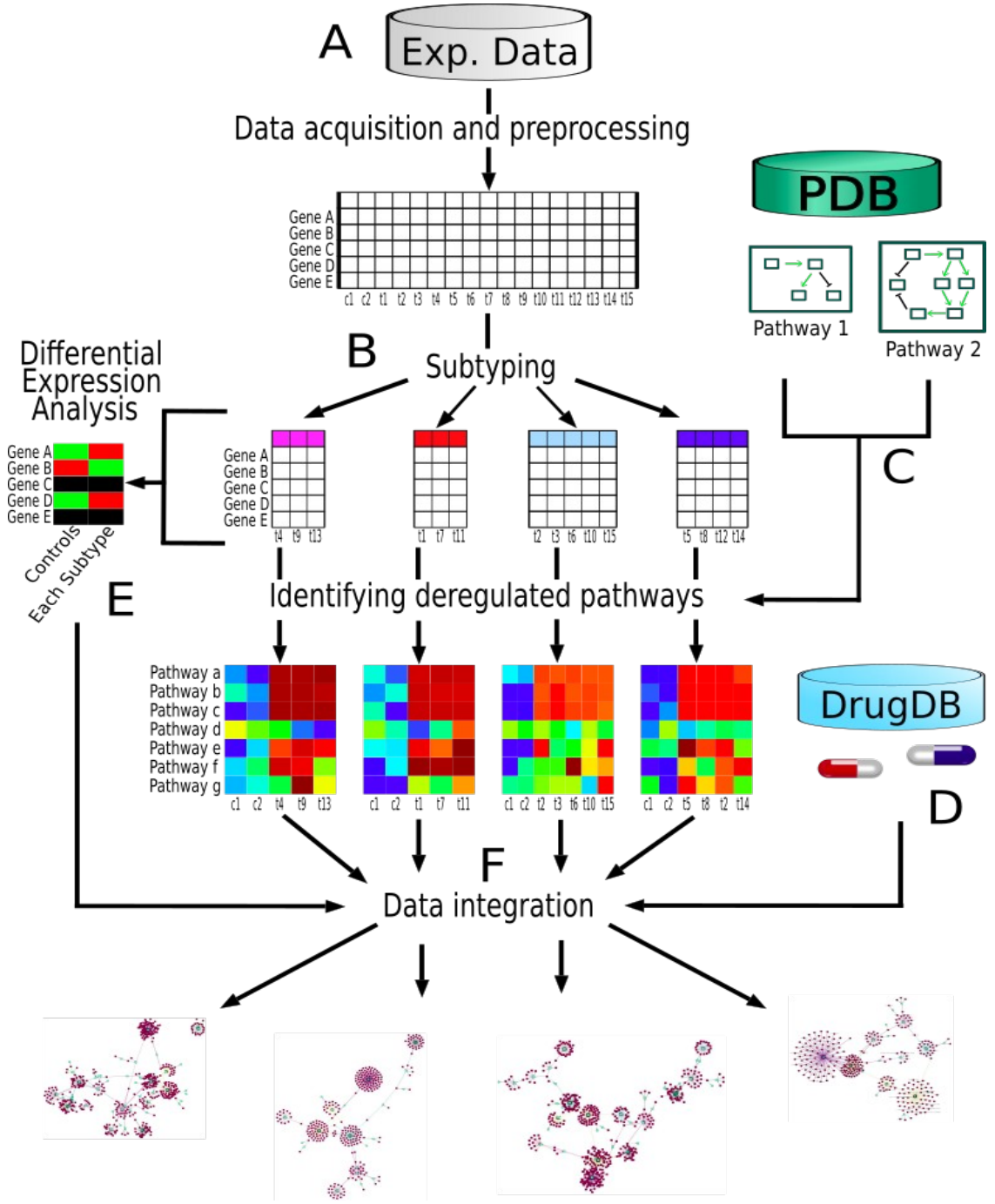
1.- http://pediatric-neurooncology.dkfz.de/index.php/en/research/pediatric-neurooncology/bioinformatics

Thank you

Doctorate Project

- Objective

  Identify new associations between pharmacological targets and their respective pathways to each breast cancer molecular subtype



Results

A) We identified the **most deregulated pathways per breast cancer subtypes.**

B) We proposed associations between deregulated pathways their pharmacological targets.

C) We prioritized pharmacological targets according to the deregulation level of the target, type of drug-target interaction, if the drug leads to "homestatic" expression levels of the target, and features of drug. Finally, we got a list of targets and drugs per breast cancer subtype.

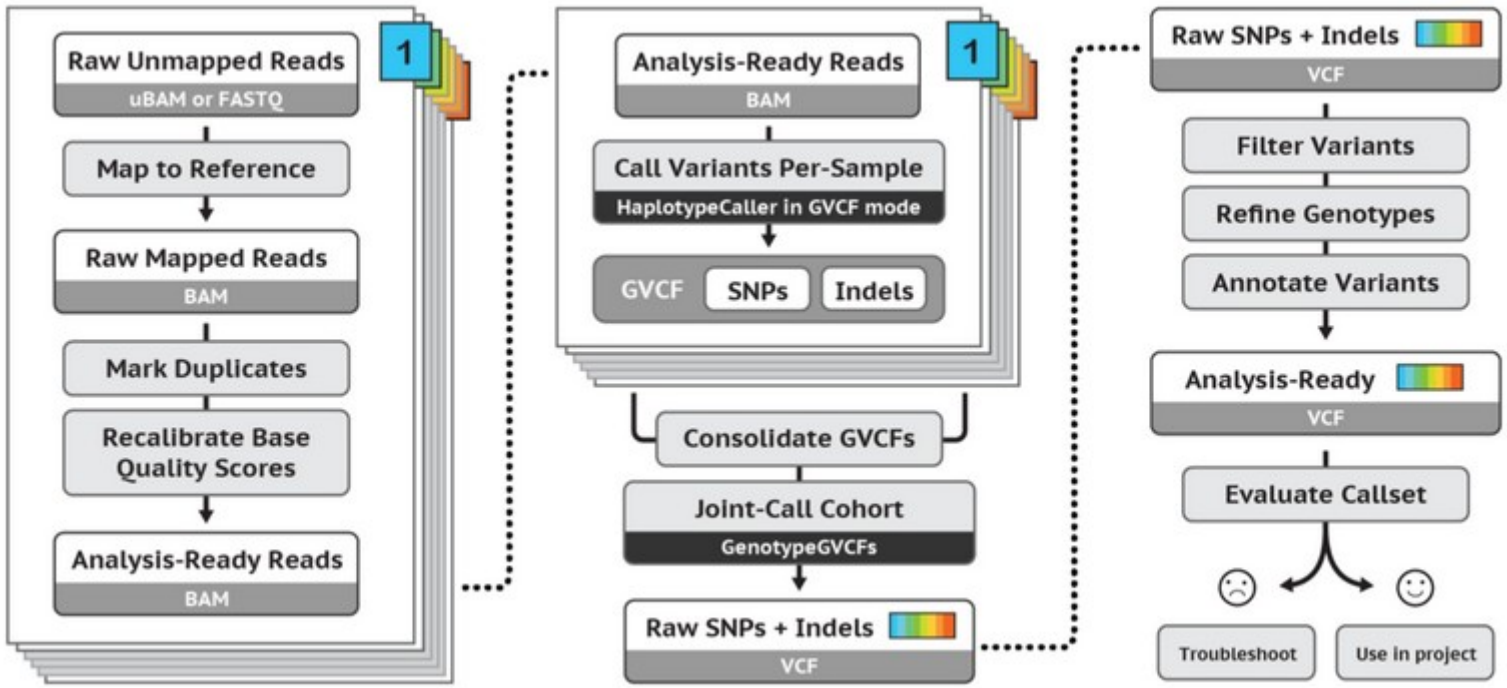
D) With the available information, and calculated features we built up a new database.

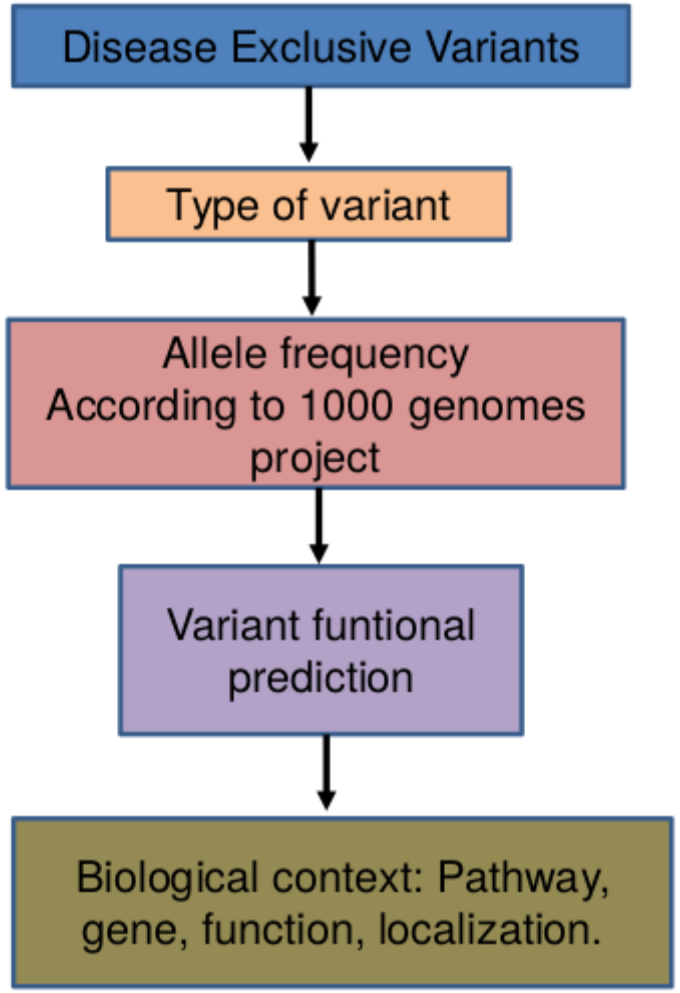
E) We propose a proof of concept to extend this methodology to individuals (personalized level).

Validation in process

In colaboration with Alejandro-Sweet-Cordero group (molecular oncology initiative, University of California at San Francisco).

Drug induced phospholipidosis





Assumptions

- Assumptions
  - The variant is **only present** in the disease phenotype and not in the controls.
  - **The variant type** is important. Our variant has a relevant functional implication in its gene/pathway and probably we are dealing with a non-conservative variant.
  - **Rare variant**. The variant that we are looking for doesn‘t have a high prevalence across the populations.
  - The variant maybe plays a role in the pathways related to lysosomes or their metabolism.

Tools in which I have some experience

- Construction of coexpression networks and Gene regulatory networks: ARACNE

- Network analysis and visualization: Cytoscape, NetworkX (Python package), igraph (R package).

- Analysis of drug-Perturbation networks: DeMAND

- Experience in these technologies: , RNA-seq, RNA-Microarrays, Exome-seq, ChIP-seq

- Programming lenguages R (training for bioconductor packages development), python, BASH, java.

- Experience also in: git, docker, hadoop

- Linux server administration:

DNA methylation-based classification of central nervous system tumours

- Why random forest? Did you try other algorithms?

Category 3 reflects the fact that WHO grading cannot be fully recapitulated by methylation profiling for several classes. Further data is required to assess if the methylation classes of this category may provide a more robust means of prognostication than histology alone, as has been demonstrated for several other classes 4,9,11. **In category 4,** the WHO entity boundaries are not identical to the boundaries of the methylation classes. Until additional data on the exact boundaries become available, this category should be critically discussed in the clinical context and orthogonal testing should be undertaken whenever possible. **Category 5** represents putative new entities that are currently not recognized by the WHO, and while limited data on these cases is currently available, the biological rationale for a novel class was considered strong.

The Landscape of genomic alterations across childhood cancers

"To assess the status of druggability of childhood cancers, the cohort (n = 675 with full genomic information; WES-only, n = 39; see Methods) was screened for potentially druggable events19(PDEs, that is, alterations in 179 genes with a directly or indirectly targeted treatment currently available or under development"

- When you detect the Potentially Druggable Events (PDE) and their related pharmacological targets, Did you perform a priritization of them?