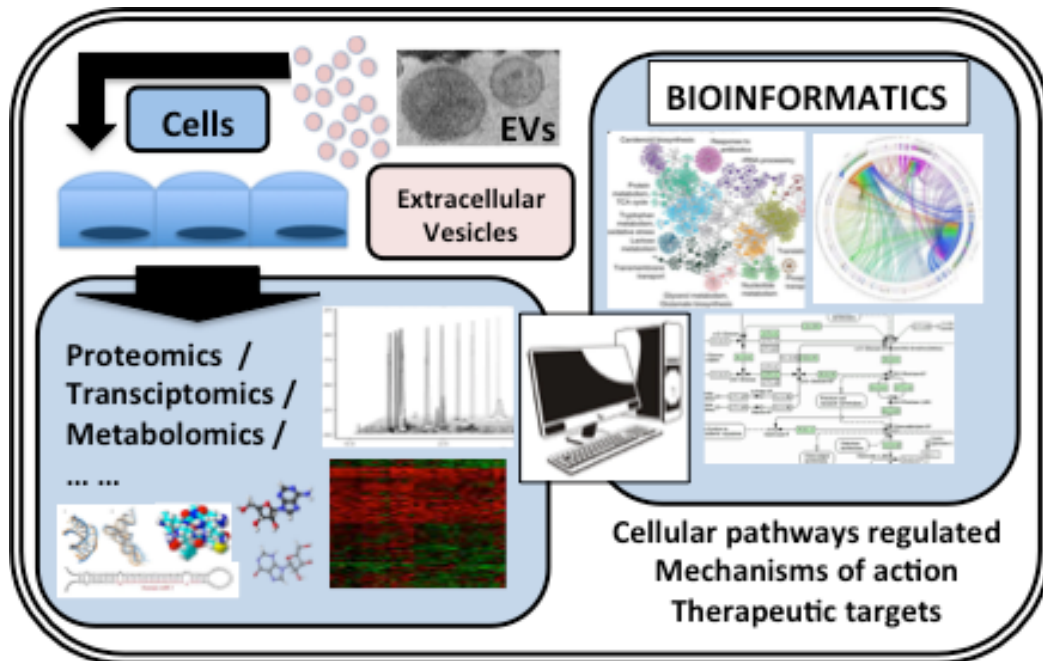<u>**PRACTICAL WORKSHOP**</u>

Bioinformatics Tools to study exosomes´ effects

DATE:

13-15 November, 2017

VENUE:

CIC bioGUNE, Derio (Bizkaia) SPAIN

<u>**Organizers:**</u>

JuanMa Falcón-Pérez / Félix Royo /Marc Clos
        Exosomes Lab. & Metabolomics Platform, CIC bioGUNE
Félix Elortza / Mikel Azkalgorta
        Proteomics Platform, CIC bioGUNE
Ana M Aransay / José Luis Lavin /Ana Rosa Cortazar
        Genome Analysis Plataform, CIC bioGUNE

<u>**Participation:**</u>
Teresa Sardon / Unai Cereijo (Anaxomics Biotech, Barcelona)

PRACTICAL WORKSHOP

Bioinformatics Tools to study exosomes´ effects

Program

Day 13	13:30	Welcome and registration.
	14:00	Overview of the course and experimental design of the proof of concept
	14:30	Introduction to Transcriptomics
	15:30	Introduction to Proteomics
	16:30	Introduction to Metabolomics
	17:30	Introduction to Systems Biology
	18:15	Group distribution
Day 14		9:00-18:00 including Lunch & Coffee-breaks

> ### *Practical session:*
> Working with the lists generated by proteomics and transcriptomics, containing the differential expressed proteins and genes of cells after the exposure to exosomes (EVs).
> Aspects that will be addressed during the day:
> 1) Pretreatment of the data. ID converters and search human homologues for mice protein and mRNAs.
> 2) Identification of messenger RNAs targeted by the microRNAs detected in Exosomes.
> 3) Protein-Protein interaction analyses.
> 4) Gene Ontology categorization.
> 5) Pathway enrichment analysis.

	21:00	Dinner
Day 15	9:00	All group exposed results
	10:30	Coffee
	13:00	Lunch
	15:30	Wrap-up and close

Schedule for Day 14.
9:00- 10:30.- **Session I**. ID converter tool and homologous searching tool.
10:30-11:00 coffee break
11:00-12:00.- **Session II.** Protein-Protein interaction
12:00-13:00.- **Session III**. mRNA targets of microRNAs
13:00-14:00.- Lunch
14:00-18:00. **Session IV**. Gene Ontology and Pathway enrichment analysis.

In session IV focused on Gene Ontology and Pathway enrichment analysis, the 20 participants will be divided in 4 groups, two groups will be working with the protein data and the other two groups with the RNA data. In all cases, each group will perform the following processes:
A) Gene Ontology categorization
B) Pathway enrichment analyses
C) Search for possible exosomal effectors

Software: Ingenuity Pathway Analysis (IPA), Cytoscape, STRING, DAVID, miRANDA, Scaffold, etc