

BioPhys

*Statistical Physics, Complex Systems,
Biological Physics, Precision Medicine*



BioPhys collaboration

Staff UNITO:

Michele Caselle

Matteo Osella

Postdoc:

Filippo Vale

Marta Biondo

PhD Students in Complex Systems for Life Sciences:

Silvia Lazzardi (III year)

Francesco Zirattu (II year)

Letizia Pizzini (II year)

PhD Student National Program in Artificial Intelligence:

Davide Pirovano (I year)

Several collaborators (wet labs, bioinformatics..)



Laura Cantini
ENS Paris



Enzo Medico
IRCCS Candiolo



Daniela Taverna
Francesca Orso
Mol Biotech Center, Torino



Marco Cosentino Lagomarsino
IFOM; UniMi



Andrea Riba



Antonio Scialdone

HelmholtzZentrum münchen
Deutsches Forschungszentrum für Gesundheit und Umwelt



Matteo Cereda
Hugef, Torino



Mattia Pelizzola

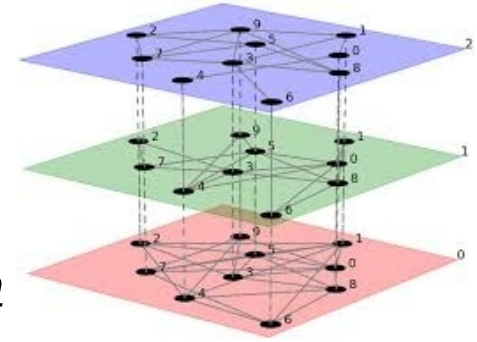


Research topics

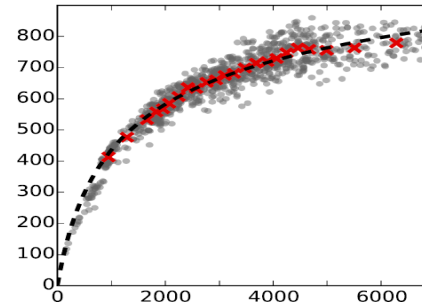
Different research topics:

Gene regulatory networks

*Structure and function of recurrent regulatory circuits;
Integration of different layers of regulation to identify
disease markers;
Tissue/cell-type/disease-type from RNA sequencing data*

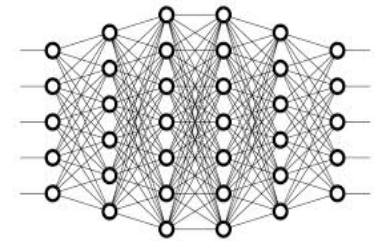


Universal Statistical laws in Molecular Biology



Machine Learning

*Role of data structure and neural network architecture
for performance*

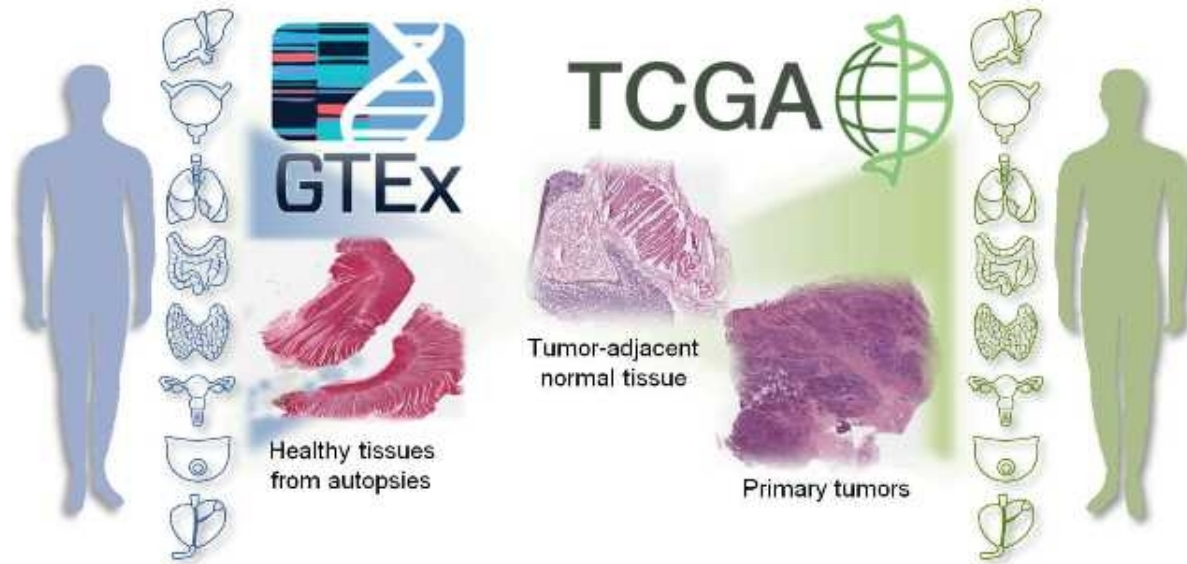


*Common denominator is the application of tools from stat phys and
stoch process theory to large-scale (Big?) data analysis.*

Main keyword: “Personalized Medicine”

Use of molecular data to fine tune therapeutic protocols

ML approach to the classification of expression patterns

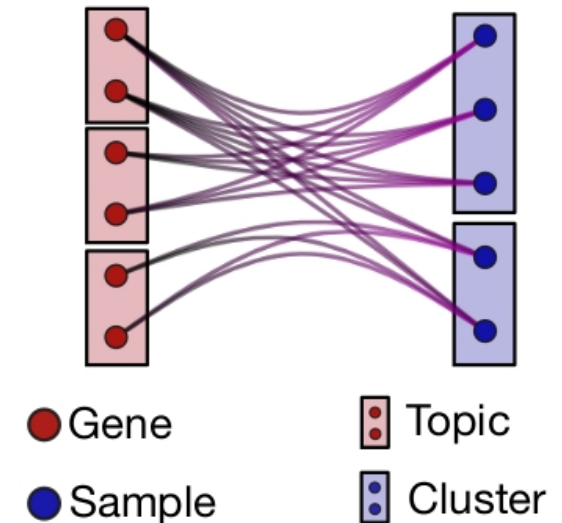


	samples				
	P1	P2	P3	P4	P5
genes	100	10	0	36	21
	45	0	6	124	0
	163	6	0	72	0
	43	32	12	0	2
	0	0	0	0	80

Classical questions:

Classify samples (e.g., healthy vs cancer)

Identify marker genes for classification

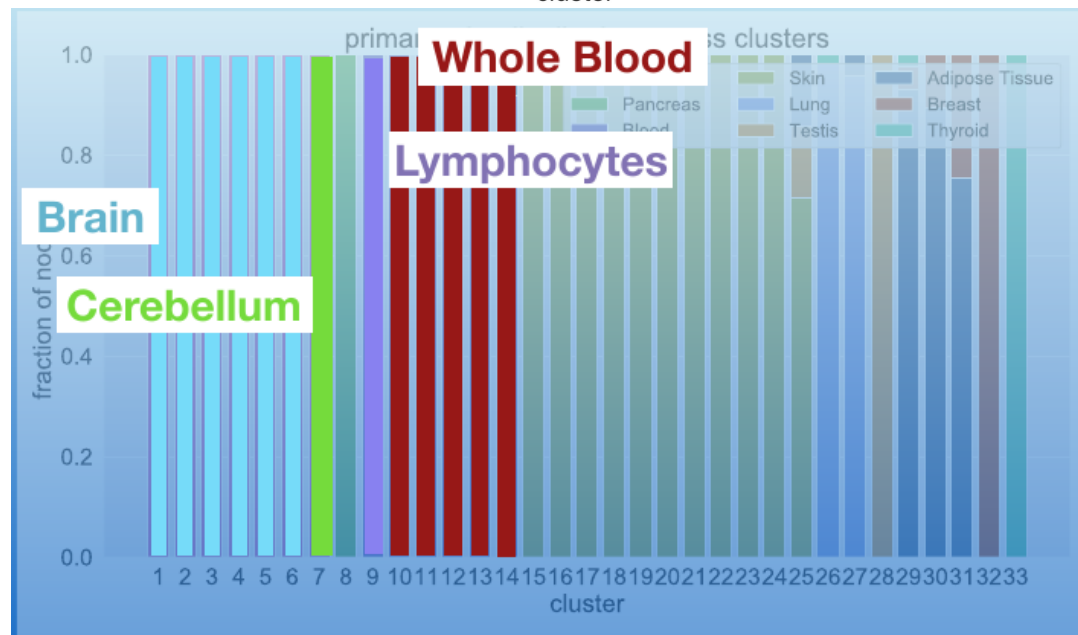
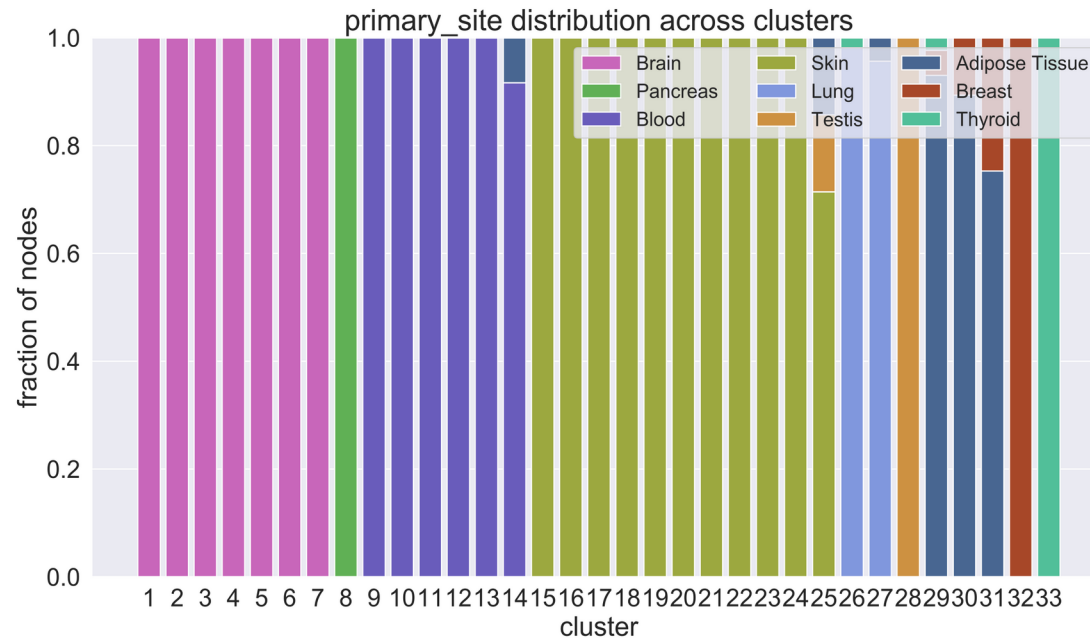


F. Valle, M. Osella and M.Caselle *Cancers* 2020, 12, 3799.

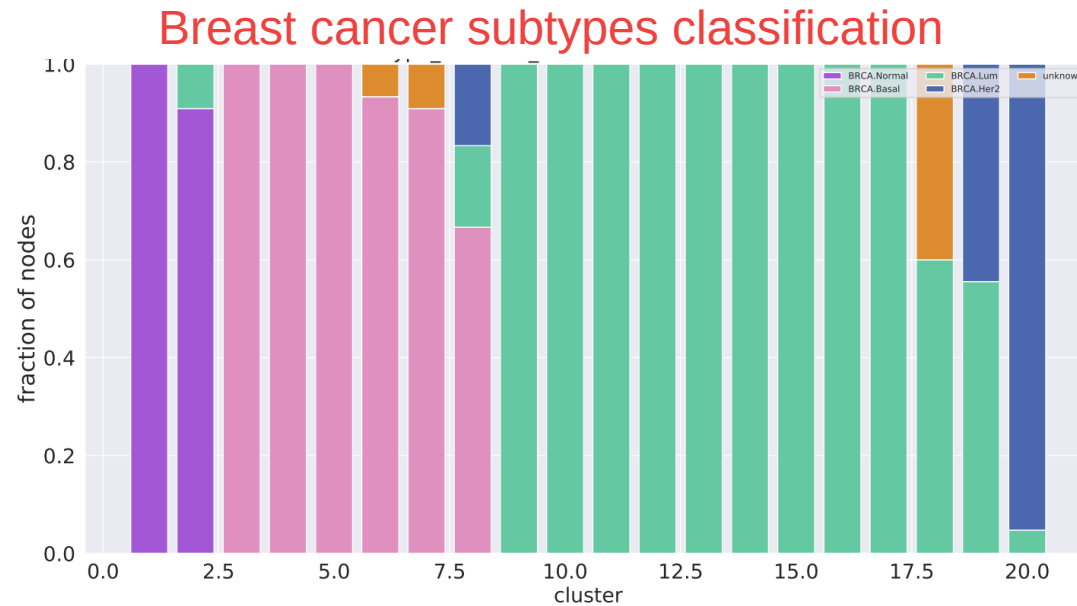
F. Valle, M. Osella and M.Caselle *Cancers* 2022, 14, 1150.

Topic structure of expression patterns

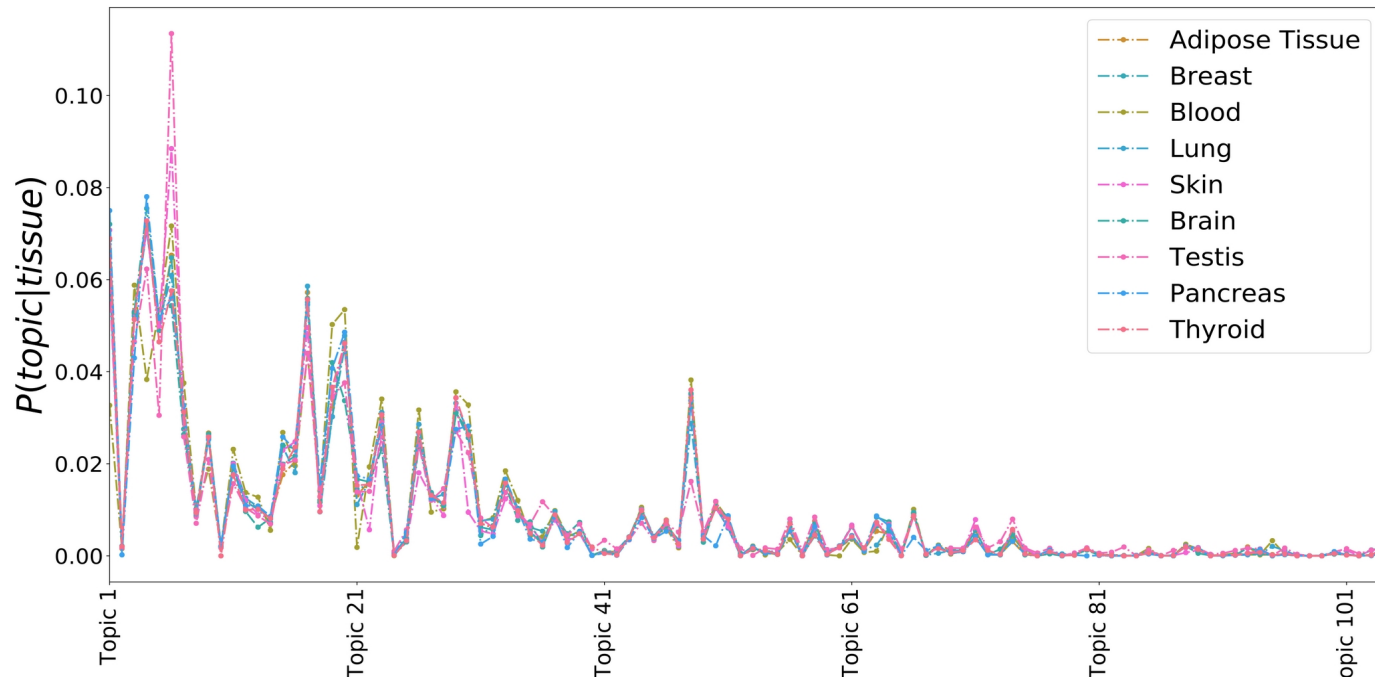
Topics are associated to tissue and sub-tissue organization



Application: classification of breast cancer samples



Classification based on global patterns rather than few markers...

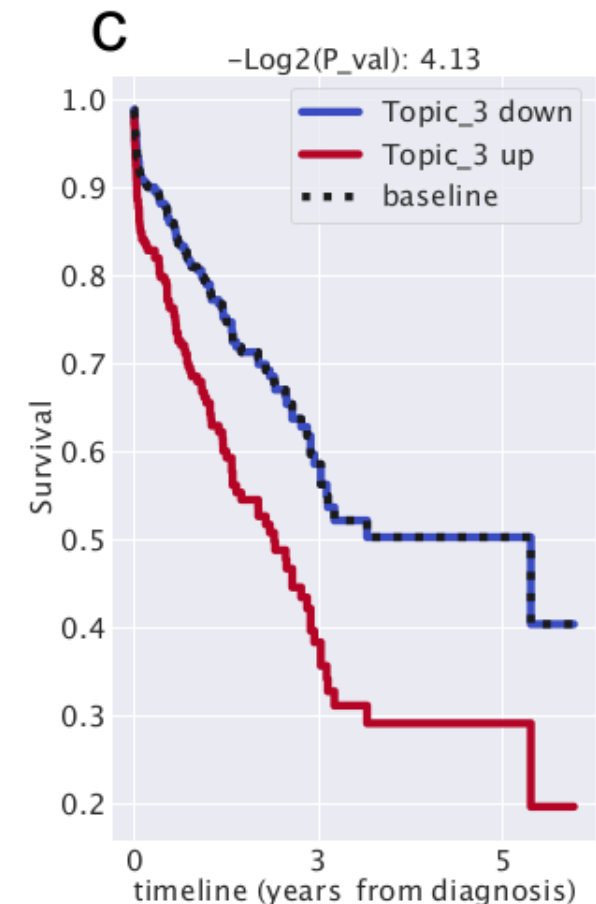
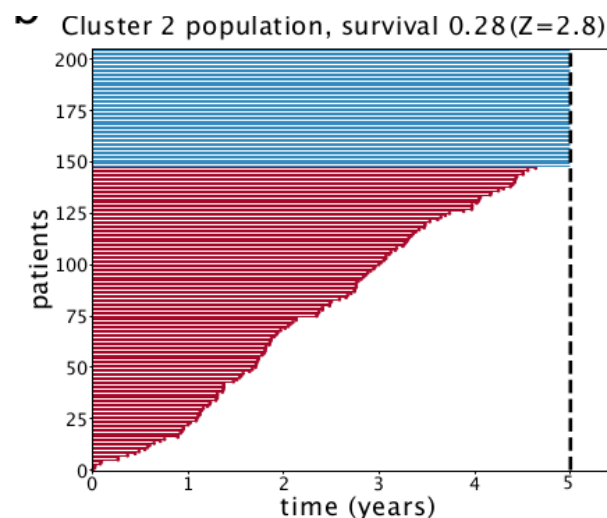


How can we use these results? Classify new samples, Identify clusters of patients with enhanced survival probability. Select group of marker genes

Framework: a “Precision Medicine” approach to Cancer. From the gene expression pattern of a given patient we may try to predict the survival probability, the risk of cancer insurgence or relapse and then fine tune the therapy .

a

real	BRCA.Lum	0.85	0.1	0.05	0
	BRCA.Basal	0	0.8	0.2	0
	BRCA.Normal	0	0.013	0.95	0.039
	BRCA.Her2	0.071	0.071	0.071	0.79
		BRCA.Lum	BRCA.Basal	BRCA.Normal	BRCA.Her2
		predicted			



BioPhys Group



