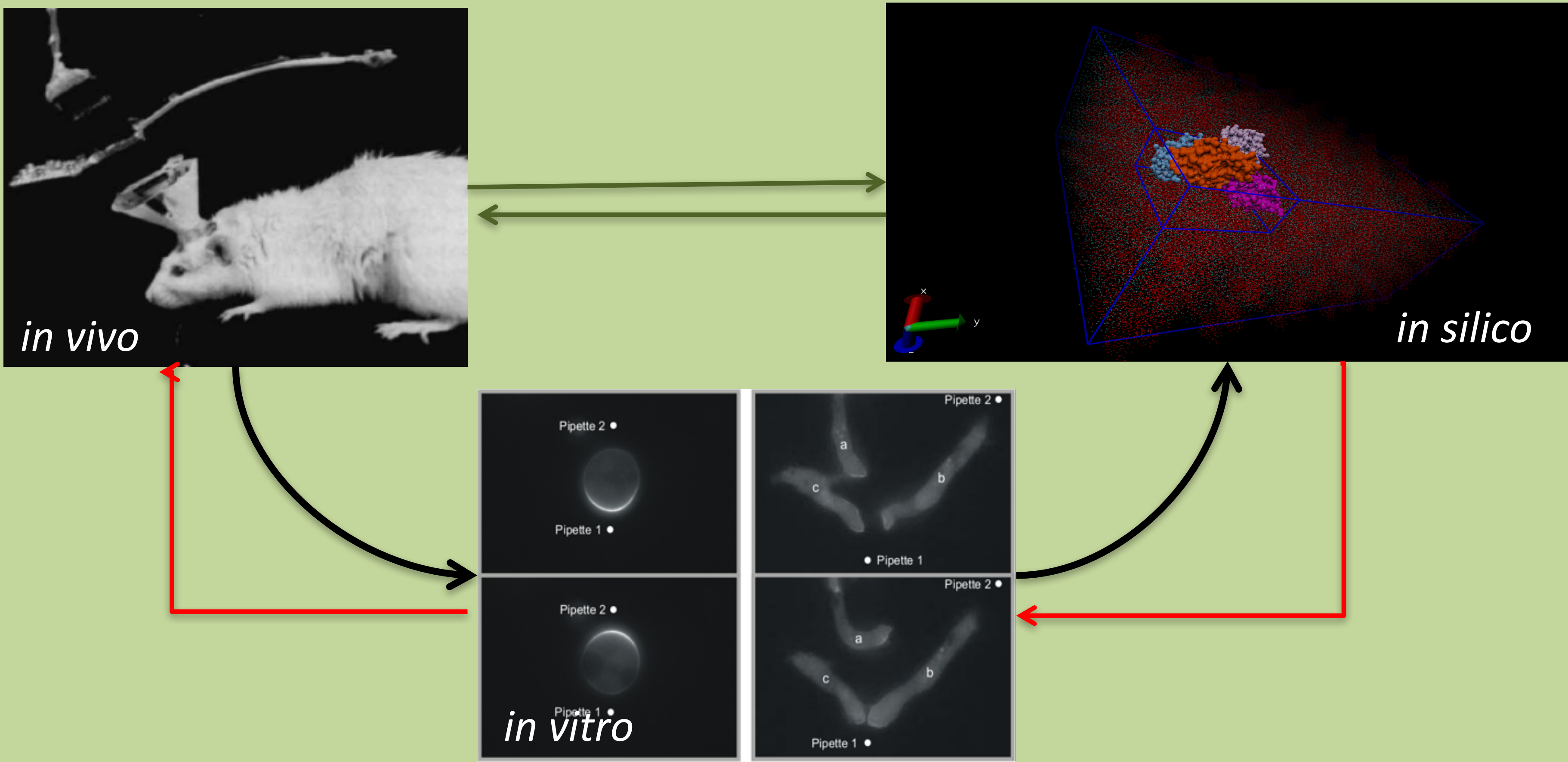
A summary of the BioPhys IS scientific activity

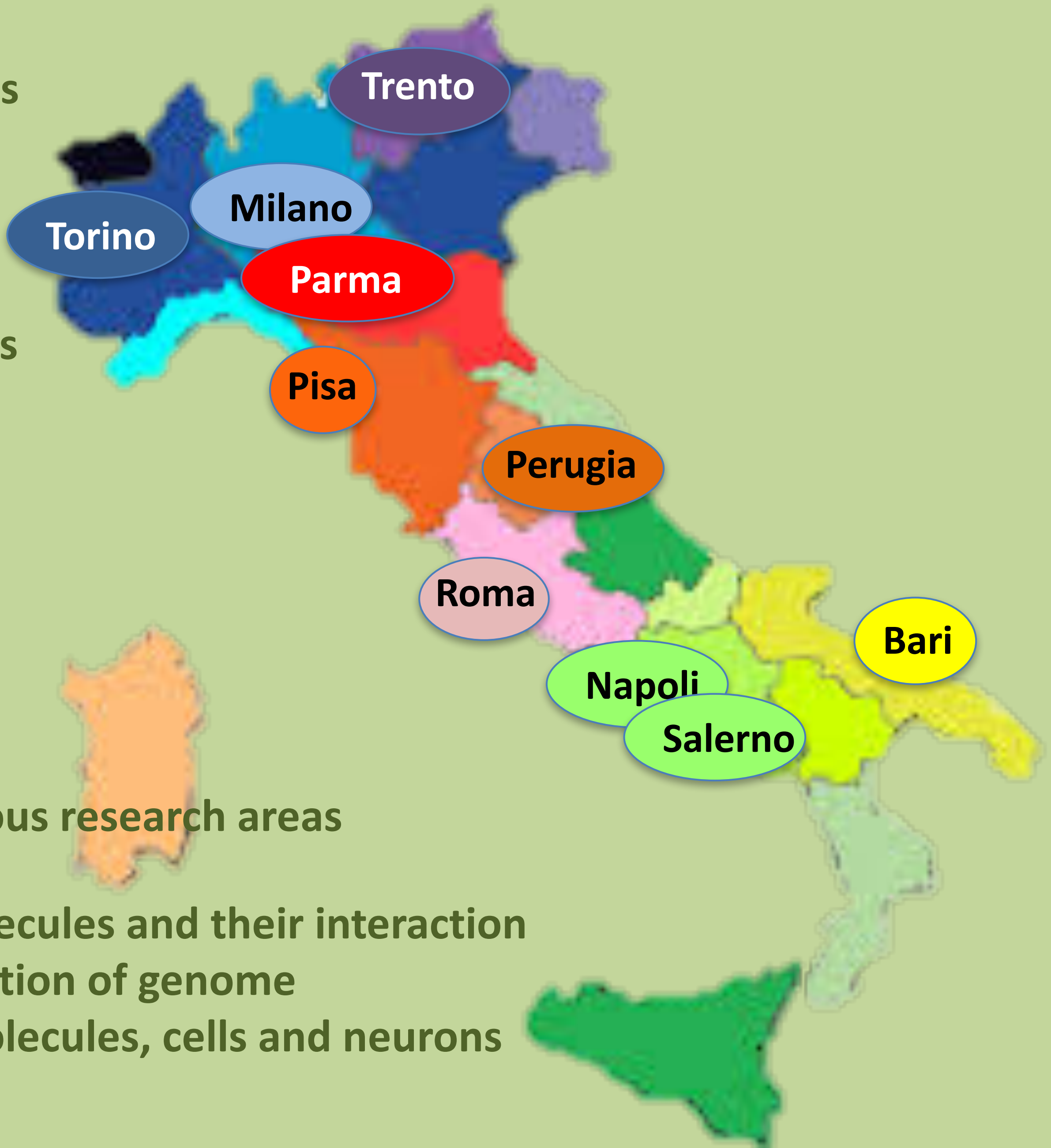
Silvia Morante

- Complexity
- Interdisciplinarity → Cross fertilization



National Coordinator: Mario Nicodemi

10 units spread out in 9 regions



Scientific activities in keywords

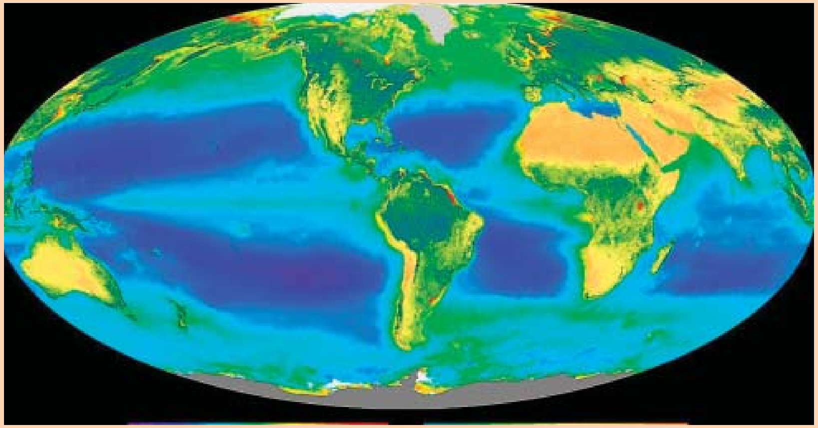
1) Statistical Mechanics
2) Computational Physics
3) Complex Systems
4) Biological Physics
5) Computational Biology

Scientific activities in the various research areas

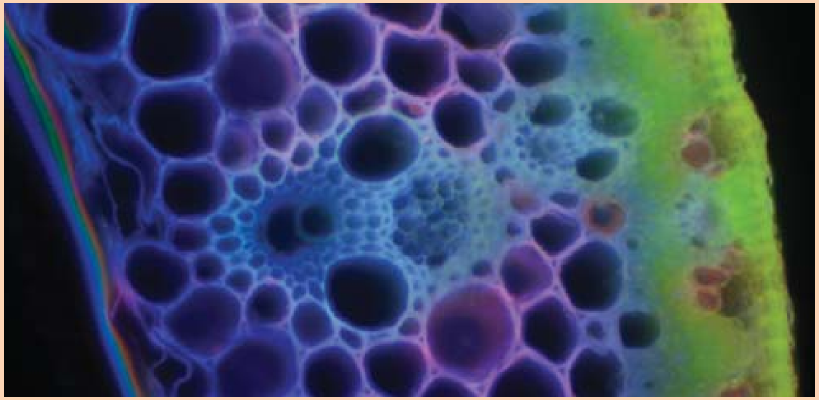
1) Characterization of biomolecules and their interaction
2) 3D organization and regulation of genome
3) Regulatory networks of molecules, cells and neurons

•••

Biophysics discovers how to modify microorganisms for biofuel (replacing gasoline and diesel fuel) and bioelectricity (replacing petroleum products and coal for producing electricity).



Biophysics discovers the biological cycles of heat, light, water, carbon, nitrogen, oxygen, heat, and organisms throughout our planet.



Biophysics harnesses microorganisms to clean our water and to produce lifesaving drugs.

Department of Theoretical Biophysics
Max Plank Institute – Frankfurt

CPLC
Center for the Physics of Living Cells

Department of theoretical Biophysics – Humboldt Berlin

Vrije University – Holland

Theoretical Physics: Theoretical Biophysics
Lund

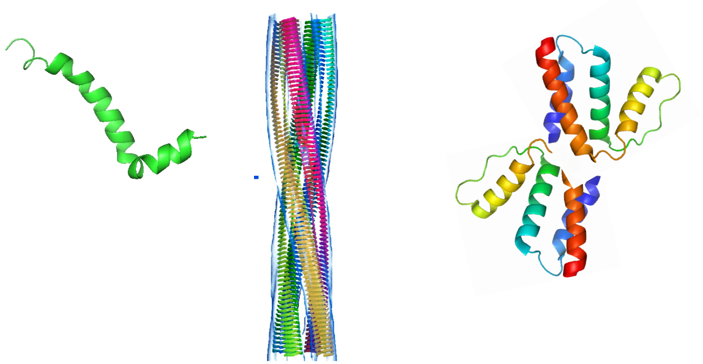
Stanford University School of Humanities and Sciences

Department of Applied Physics

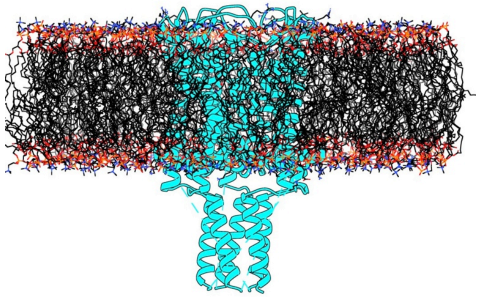
All content under "Experimental and Theoretical Biophysics"

Center for Theoretical Biological Physics (CTBP)
Houston, Texas

Peptides/proteins (RM-MI)

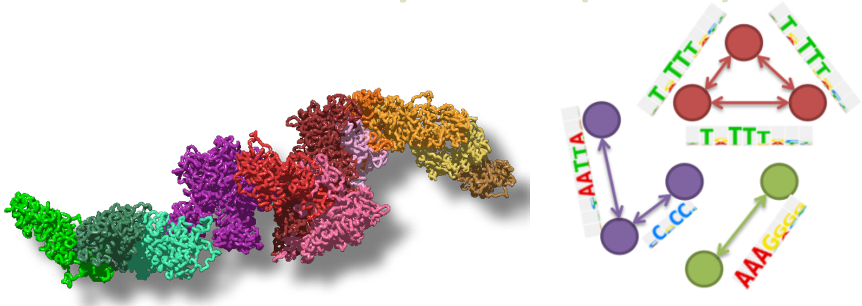


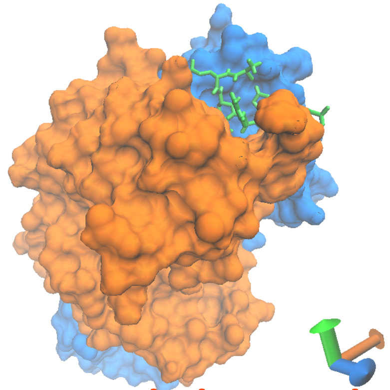
Folding/misfolding (aggregation)



Protein-membrane interaction (PI)

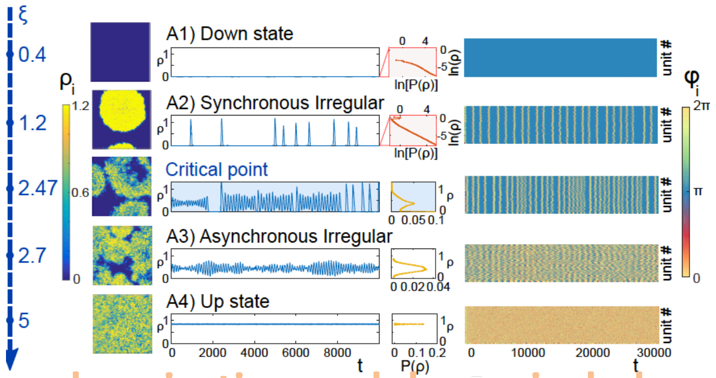
DNA structure & expression (NA-TO)



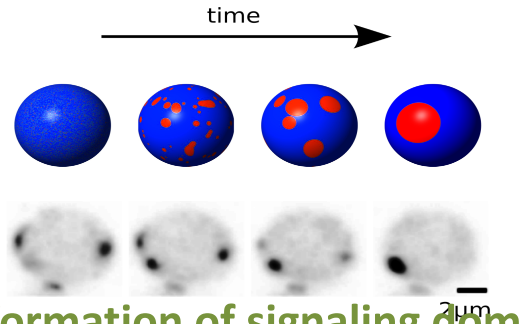


Peptide-Protein interaction (RM)

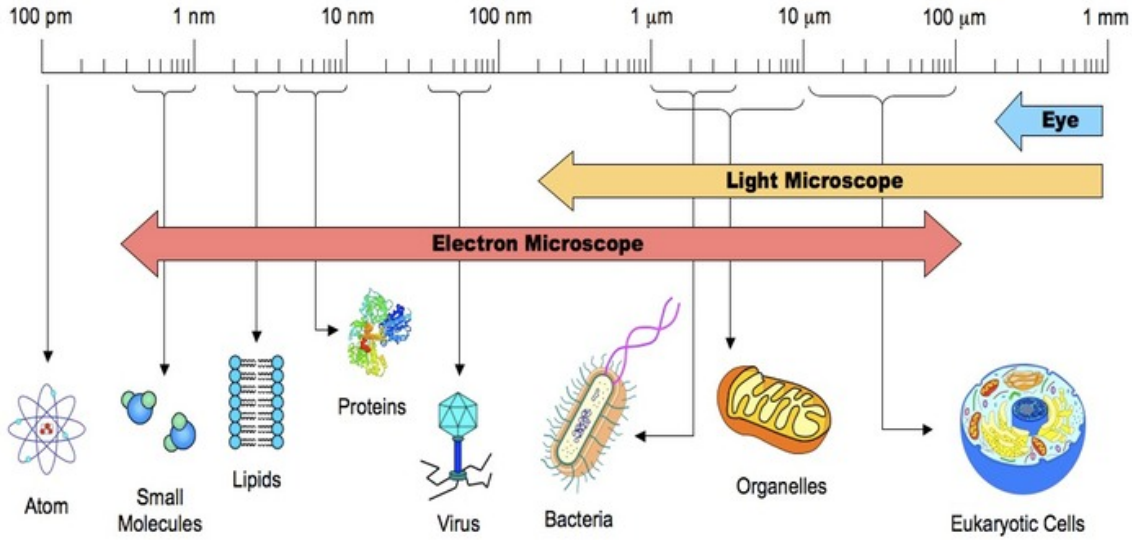
In vivo observation of critical phenomena (SA)

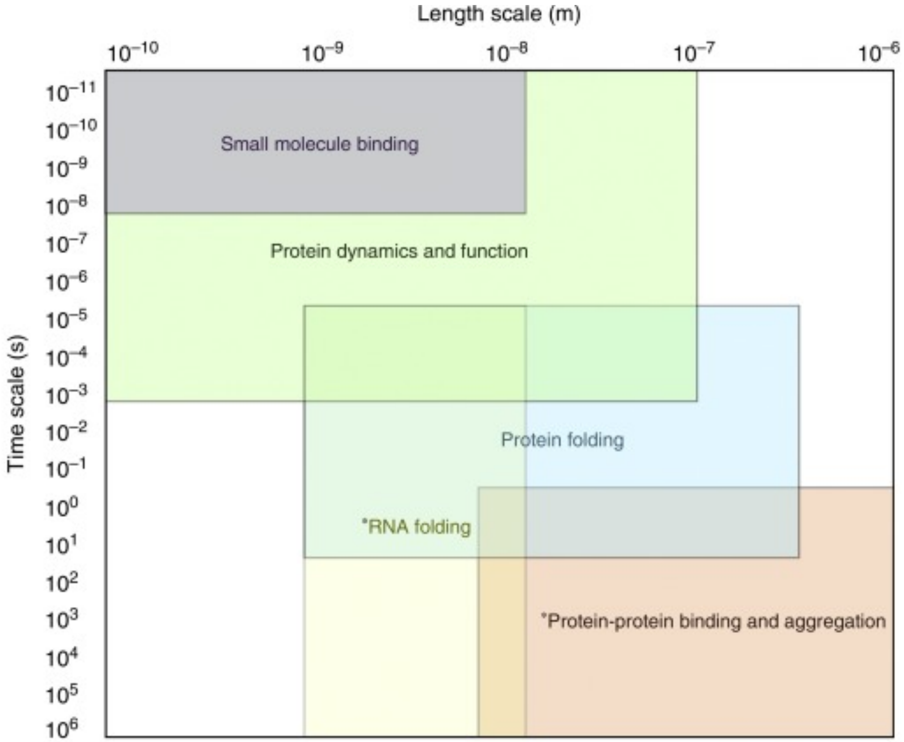


Synchronization and dynamical phase transitions in neural networks (PR)



Dynamic formation of signaling domains on cell membranes (TO)


100 pm
1 nm
10 nm
100 nm
1 μm
10 μm
100 μm
1 mm
Eye
Light Microscope
Electron Microscope
Atom
Small Molecules
Lipids
Proteins
Virus
Bacteria
Organelles
Eukaryotic Cells


Length scale (m)
10^-10
10^-9
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Time scale (s)
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10^-4
10^-3
10^-2
10^-1
10^0
10^1
10^2
10^3
10^4
10^5
10^6
Small molecule binding
Protein dynamics and function
Protein folding
*RNA folding
*Protein-protein binding and aggregation


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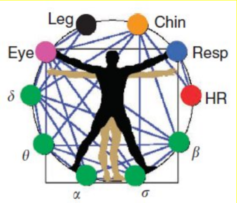
Bari (PI: Sebastiano Stramaglia)

NETWORK PHYIOSOLOGY: HEART-BRAIN INTERACTION

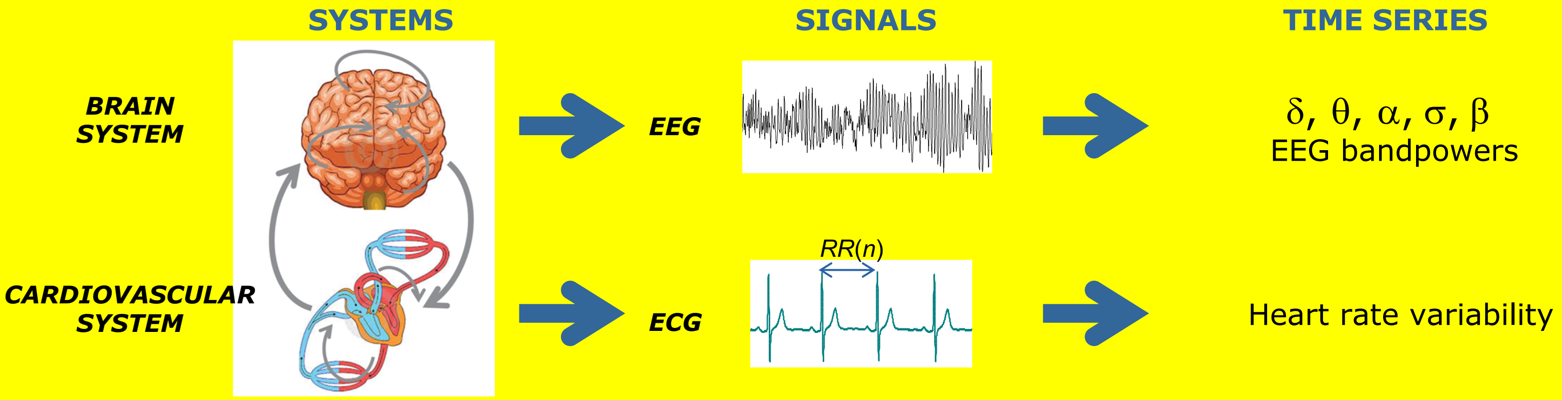
- **NETWORK PHYSIOLOGY:**

[Bashan A et al., *Nature Comm.* 2012]



Organ systems exhibit a degree of activity and interactivity depending on the physiological state

- **Brain-Heart interactions**



SYSTEMS | **SIGNALS** | **TIME SERIES**

BRAIN SYSTEM → ***EEG*** → $\delta, \theta, \alpha, \sigma, \beta$ EEG bandpowers

CARDIOVASCULAR SYSTEM → ***ECG*** → Heart rate variability

- **We have developed a new theoretical framework for multiscale analysis of Information Dynamics is introduced (Published in "*Uncovering brain–heart information through advanced signal and image processing*", Phil. Trans of the Royal Soc. A 2016)**

↓

- **Validation: simulated linear processes; Application: brain-heart interactions during sleep**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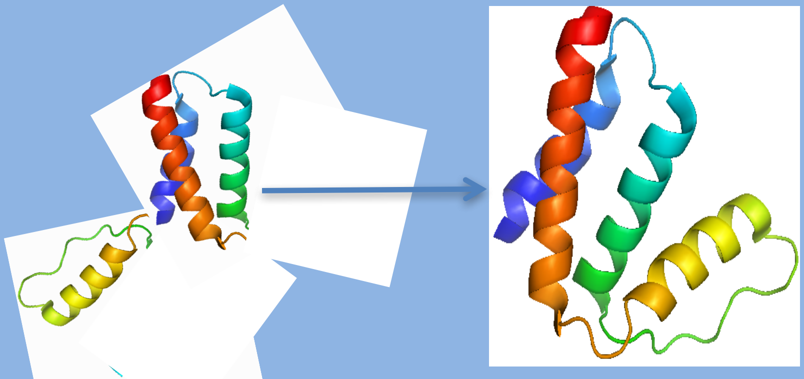
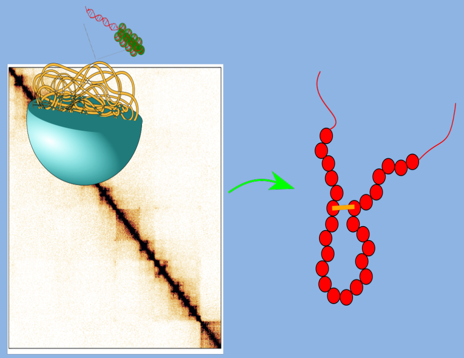
Milano (PI: Guido Tiana)

Main topics

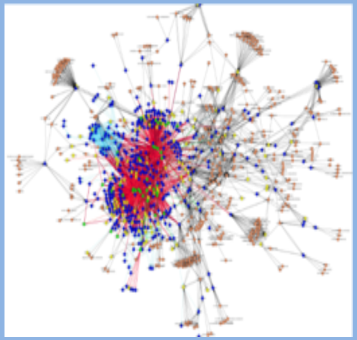


Conformational changes in proteins

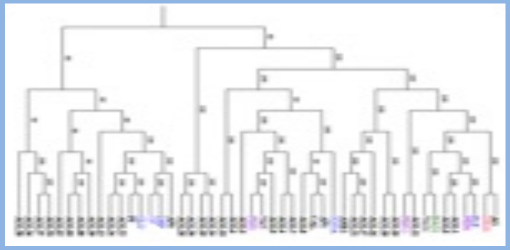


Conformational properties of chromosomes

Genetic networks



Molecular evolution



Methods

- Conformational sampling (Monte Carlo, etc.)
- Coarse-grained approaches (MaxEnt principle)
- MD simulations
- Dimensional reduction
- Replicas
- Inverse statmech models
- Differential equations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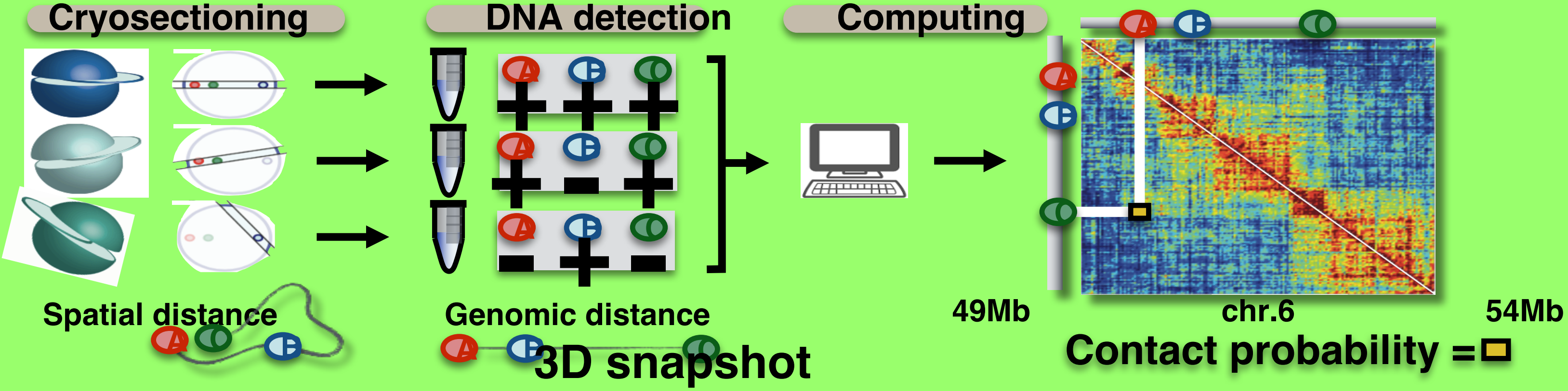
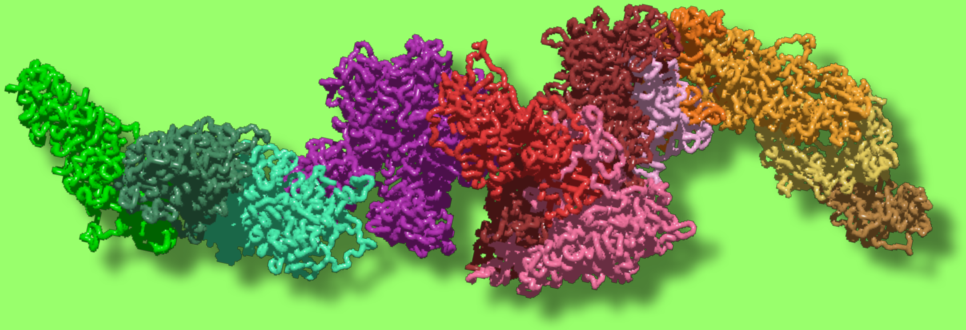
Napoli (PI: Mario Nicodemi)

The GAM technology (developed by Na group) probes, by sequencing DNA from nuclear sections, how **3D spatial proximity** is related to **co-segregation**



(Beagrie *et al. Nature* 2017)

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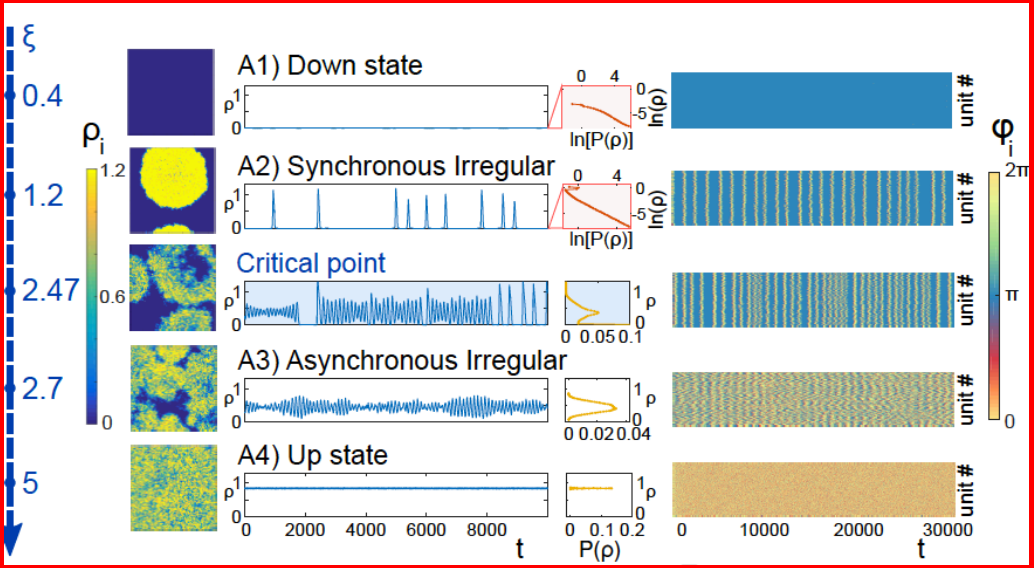
Parma (PI: Raffaella Burioni)

Expertize of the group:

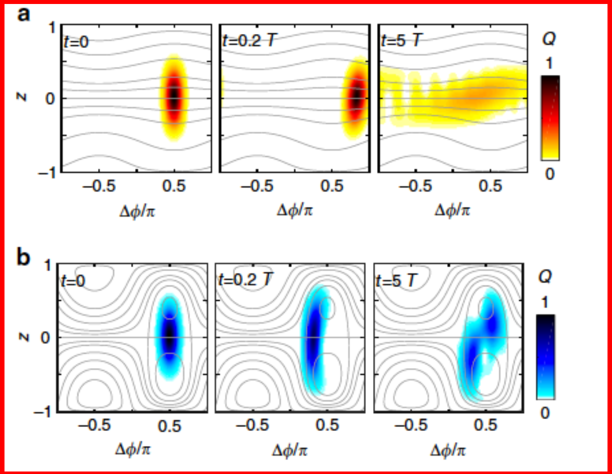
Complex Networks, Out of equilibrium Statistical Physics, Synchronization
Classical and Quantum Transport

Research Lines:

- Collective phases, Synchronization and dynamical phase transitions In neural networks and bistable biological systems
- Statistical Inference from dynamical signals in neural and biological systems
- Coherent transport and quantum effects in light harvesting complexes: Classical/quantum → Synchronization/Entanglement



S. Di Santo et al, PRL2017, and submitted



D. Witthaut et al, Nat. Comm. 2017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Pisa (PI: Giuseppe Brancato)

Development of Multi-scale Methods

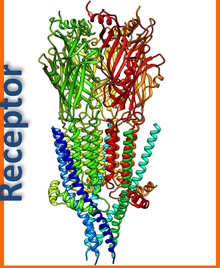
GLOB model for QM/MM MD simulations of complex systems in solution

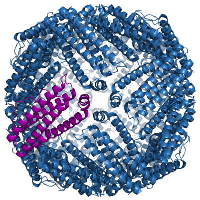
Bio-apps: Natural and Engineered Systems: Antimicrobial peptides; Peptides translocation through membranes; Ion transport in bio-channels and pores; Lipid dynamics in lipid bilayer; Engineered protein channels

Designing Novel Biosensors: Optical probes for imaging and sensing; Polarity and microviscosity sensors

gallery of recently investigated bio-systems

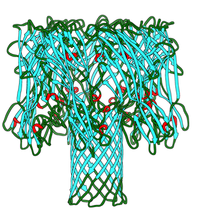
5HT3 Serotonin Receptor

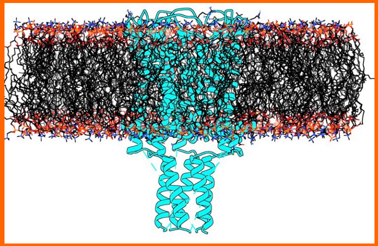




Ferritin

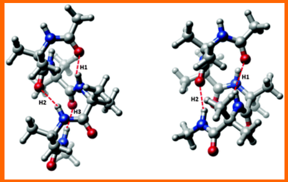
Hemolysin

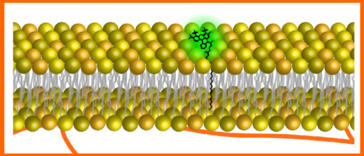




MscL channel

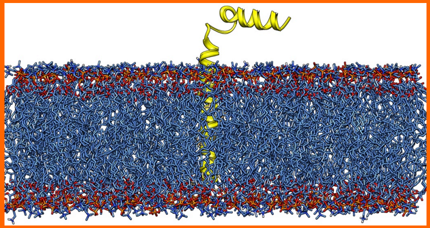
Aib-based peptides





Lipid Membranes

Fe-S cluster biosynthesis (IscS-IscU system)



Phospholamban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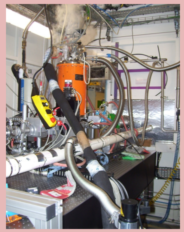
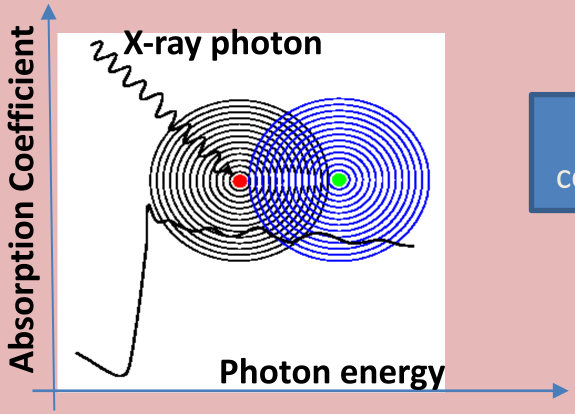
Roma(PI: Silvia Morante)

Experimental XAS spectra collection





Ab initio XAS spectra calculation

Classical MD configuration C'$_1$

Quantum Espresso

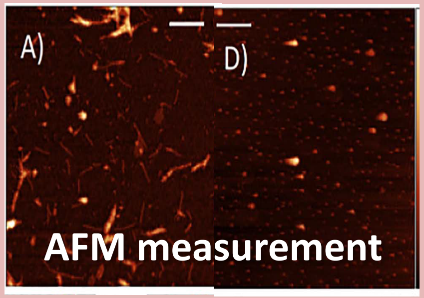
Atomic configuration C$_1$

Quantum Espresso XSPECTRA

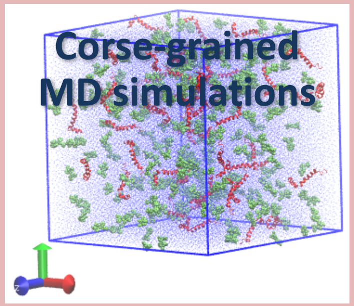
Spectrum S$_1$

G. La Penna *et al.* J. Chem.Phys. (2015), 143: 124508
F. Stellato *et al.* J. Chem.Phys (2018), to be submitted

Aβ-fibrils –amiloyd breakers interaction



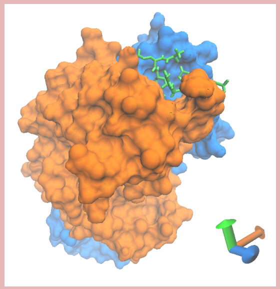
AFM measurement



Corse-grained MD simulations

F. Stellato *et al.*, BiophysChem, 229 (2017) 110–114

Aβ-peptide –antibody interaction



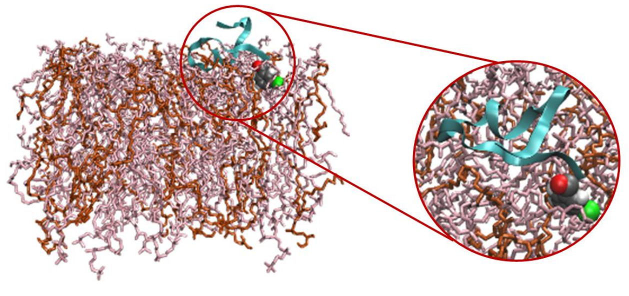
Classical MD

Umbrella sampling

ΔG

J. Sevigny *et al.* Nature, (2016) 537: 50–56
E. De Santis *et al.* (2018) to be submitted

Designing effective anticancer radiopepptidde carriers



E. Capozzi *et al., J.Chem.Theory & Comp.* (2017) to be published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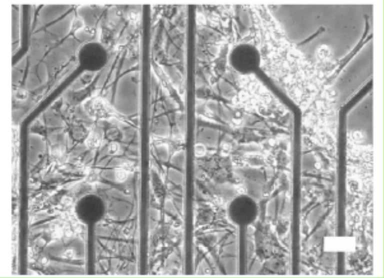
Salerno (PI: Silvia Scarpetta)

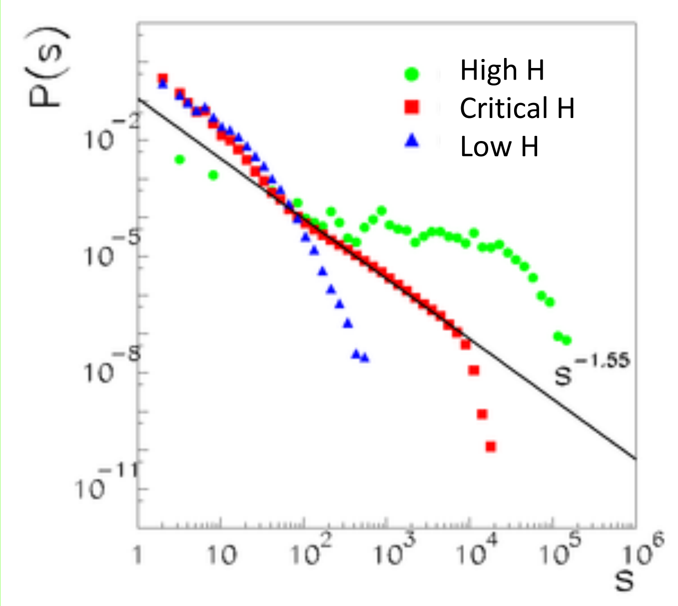
Critical phenomena in cortical neural dynamics

in-vitro and *in-vivo in* cortical recordings

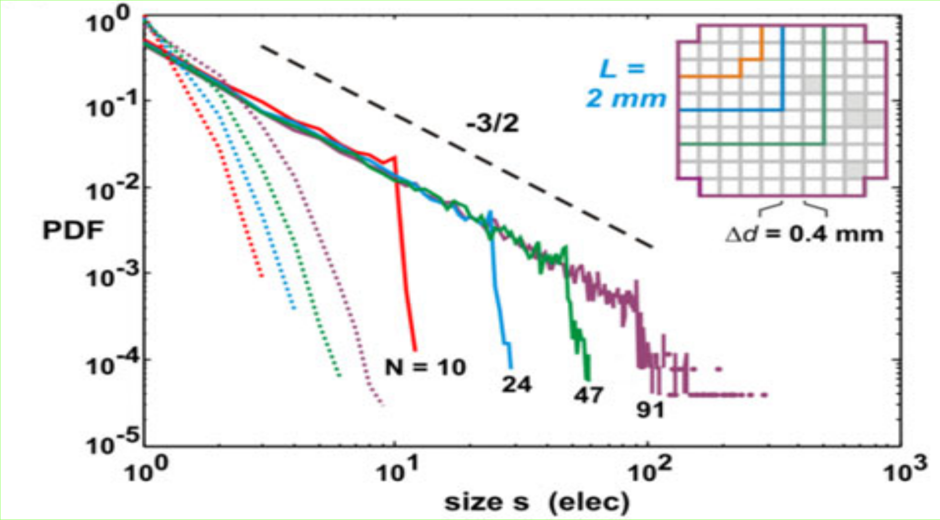


Collective dynamics → network of spiking units with structured connectivity → bridge between criticality and the need to have a reservoir of spatio-temporal metastable memories

Neural avalanches and critical behaviour



Power law organization of neuronal avalanche



- de Candia et al *Nat Sci. Reports* (submitted)
- L Minati, et al. Chaos 2016
- Lombardi, et al. Nat Sci Reports 2016
- P. Chialvo Plenz, PNAS 2009
- Plenz *Eur. Phys. J.* 2012;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Torino (PI: Michele Caselle)

Modeling the evolution of transcription factor binding preferences in complex eukaryotes

SCIENTIFIC REPORTS

Central Questions

- How Transcription Factor (TF) DNA binding preferences are organized?
- Which evolutionary forces shaped this organizations?

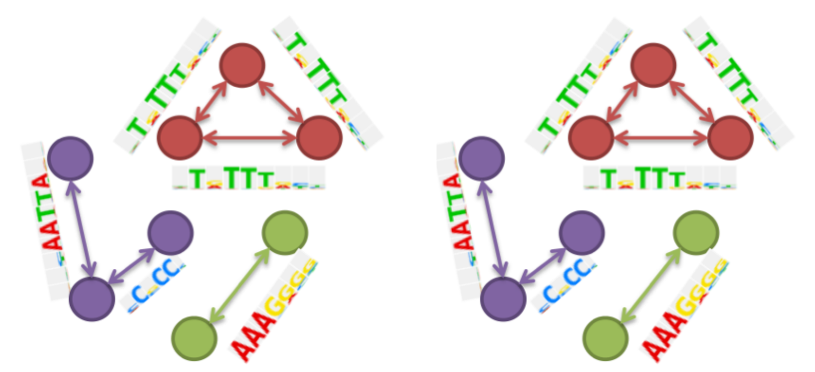
Tools

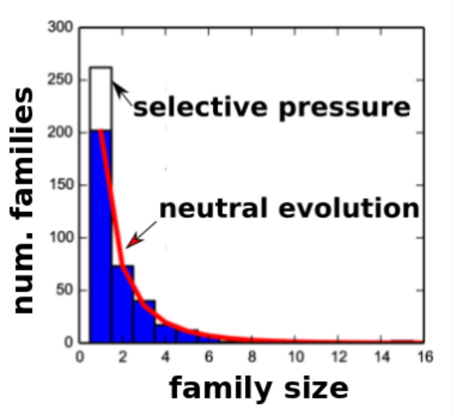
- Bioinformatics, network analysis and mathematical modeling

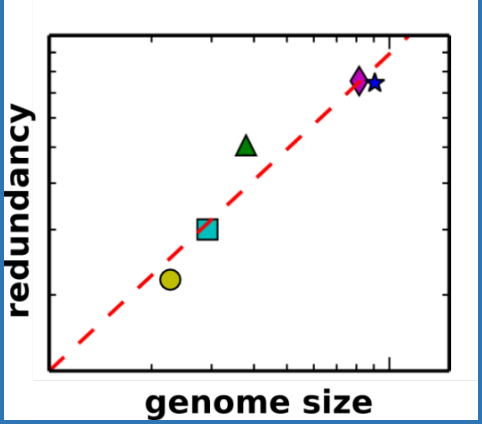
Main Result

- A general trend of neutral evolution of binding sites has been identified.
- Deviations from model predictions hint at selective pressure.
- Redundancy in TF regulation grows with the complexity of the organism

Antonio Rosanova, Alberto Colliva, Matteo Osella & Michele Caselle



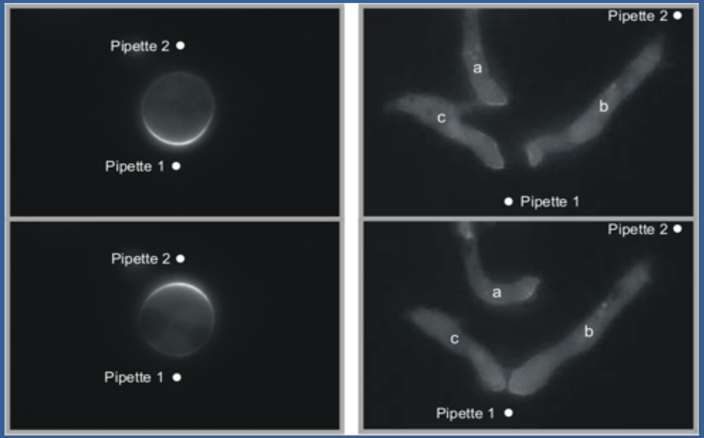


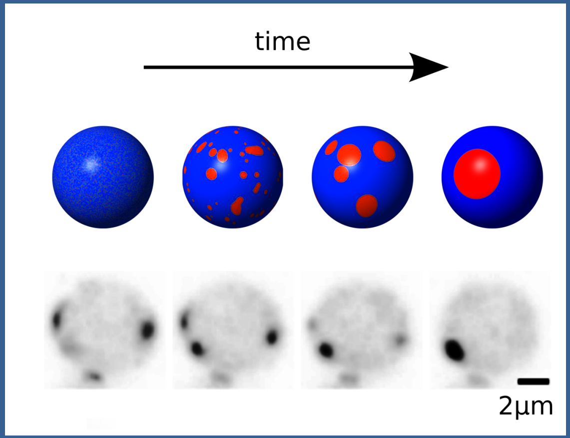


Torino Politecnico (PI: Andrea Gamba)

Dynamic formation of signaling domains on cell membranes

surface of living cells

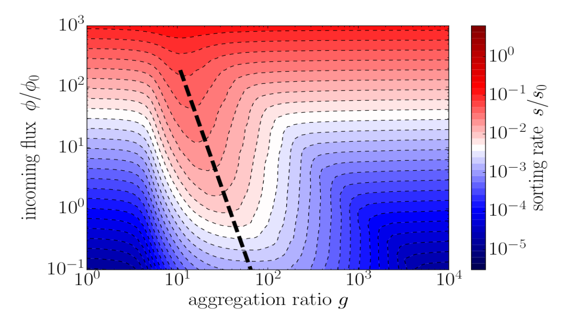


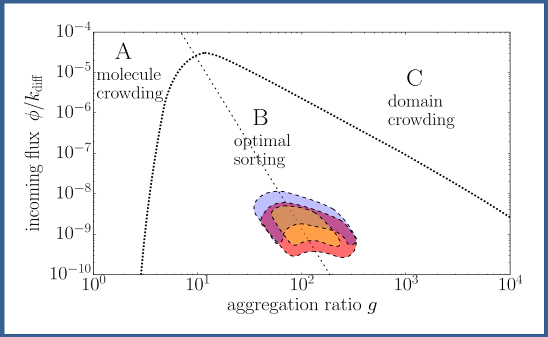


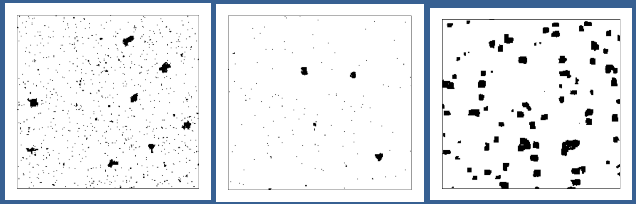
Enriched domain of specific protein are formed in response to stimuli→ a chemical compass

Signaling events studied by theory and numerical simulations of the stochastic reaction-diffusion process

Dynamic formation of signaling domains and sorting







Zamparo et al, Soft Matter 2015, 11, 838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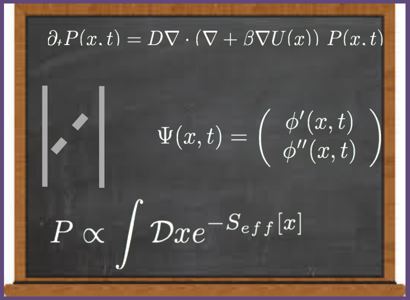
Trento(PI: Pietro Faccioli)

Trento Institute for Fundamental Physics and Applications

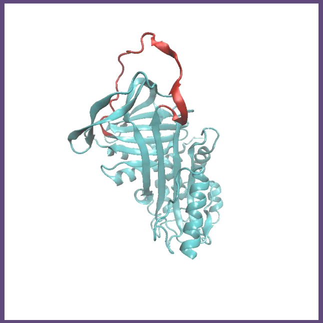
FOCUS:

Developing/applying techniques based on theoretical physics tools to study biomolecular systems.



Theory / method development

HPC



Biophysics/Mol. Biology

Starting grant
R. Potestio

Physics → Define a model → Solve Dynamics → Extract kinetics → Biology

coarse graining:
adaptive multiscale models

quantum excitations:
methods based on non-equilibrium QFT
conformational dynamics:
methods based on sampling stochastic path integrals.
Molecular dynamics simulations

Data reduction:
Renormalization Group based clustering

A few applications:
Allostery and membrane proteins, protein (mis)folding, viral caspids

THANK YOU

Bari: S. Stramaglia; G. Lattanzi; L. Angelini; N. Cufaro Petroni; J. Rasero Daparte
Milano: G. Tiana; R. Meloni; R. Capelli; F. Cola
Napoli: M. Nicodemi; C. Annunziatella; S. Bianco; A. Chiariello
Parma: R. Burioni; M. Casartelli; S. Wimberger; F. Pittorino; S. di Santo; E. Bertolotti; M. Tizzani
Perugia: S. De Lillo; D. Burini; D. Petturiti
Pisa: G. Brancato; V. Barone; G. Mancini; C. Balasubramanian; A. Muhammad; D. Di Maio
Roma: S. Morante; G. La Penna; V. Minicozzi; F. Stellato; E. De Santis; A. Dhar; G.C. Rossi
Salerno: S. Scarpetta; A. de Candia; L. de Arcangelis; A. Liccardo
Torino: M. Caselle; A. Gamba; A. Pelizzola; A. Colliva; A. Mazzolini
Trento: P. Faccioli; G. Lattanzi; G. Garberoglio; S. Orioli

DNA 3D structure

polymer physics models → chromosome folding
model to Hi-C/GAM data → 95% accuracy

(Chiariello et al. Nature *Sci. Rep.* 2016;
Barbieri *et al. Nature SMB* 2017)