

# Interdisciplinary consortia for the study of pandemics

**CICbiomaGUNE**  
CENTER FOR COOPERATIVE RESEARCH IN BIOMATERIALS

**CICbioGUNE**  
MEMBER OF BASQUE RESEARCH  
& TECHNOLOGY ALLIANCE

**CIC nanogUNE**  
NANOSCIENCE COOPERATIVE RESEARCH CENTER

**ikerbasque**  
Basque Foundation for Science

**(bcam)**  
Basque center for applied mathematics

**dipc**

**CFM**  
Centro de Física de Materiales  
Materials Physics Center

**biodonostia**  
osasun ikerketa institutua  
instituto de investigación sanitaria

**POLYMAT**  
Basque Center for  
Macromolecular Design and Engineering

**eman ta zabal zazu**  
Universidad del País Vasco  
Euskal Herriko Unibertsitatea

---

## About us

2020 saw many historical events that will impact our society in the years to come. Among them the SARS-Cov-2 pandemic redefined the role of Science in the society. Despite many warnings over the last decades on pandemic risks, countries found themselves unprepared to face this new threat. The resulting emergency status, resulting in lockdowns of large segments of our societies, has pushed many scientists from all fields to come together and join their expertise to find new solutions in the shortest possible time. Around the world, multiple large consortia are combining computational and experimental methods and propose new potential drugs against the SARS-Cov-2. Their success proves the effectiveness of creating interdisciplinary teams of like-minded scientists to tackle the current pandemic.

In the Basque Country many scientists with a broad range of expertise, working in different research centers have answered the call to arms investing their experience and knowledge on key aspects of the fight against the pandemic. In May 2020 the time was ready to create a local community of scientists to consolidate the knowledge acquired and create a team that would combine such a knowledge and foster synergetic collaboration thinking ahead of future challenges.

The objectives of **Interdisciplinary consortia for the study of pandemics (ICSP)** is to keep an active discussion on subjects related to pandemic prevention and response. We also aim at promoting local and international collaboration to further develop the seeds that were planted in the past months. We propose to slowly let our local community grow inviting like-minded scientists from all

fields. Finally, we intend to engage in scientific outreach activities towards the general public and policy makers.

The current key topics covered by our team are detailed below.

---

## Key topics

Our community currently covers four main areas of expertise: pathogen detection, drug repurposing, drug design, and epidemiology.

### Pathogen Detection

Pathogen detection is key at all stages of a pandemic. Initially it allows to identify quickly the individuals that are carrying the disease and isolate them. During the pandemic it allows to monitor the progress and focus the medical care.

In our group we specialize in the following approaches to detection:

- **Methods:**
  - **Protein cluster**
  - **Gold nanoparticles**
  - **Surface**
  - **Antibody**
  - **PCR**
- **Target**
  - **Virus surface**
  - **RNA**
  - **Antibody**

## ***Detection teams' structure***

### **Drug Repurposing**

In case of a quickly spreading of a disease for which there is no effective therapy the standard methods of drug development and clinical testing could be too slow to guarantee an effective response. Drug repurposing aims at looking through existing database of molecules approved for human therapy and test if they have any effect on the new target.

In our group we specialize in the following approaches to repurposing:

- **Methods:**
  - **Computational screening:** Large scale docking of FDA approved molecules.
  - **Binding assays:** Experiments aimed at measuring the binding affinity of the FDA approved molecules on the target.
  - **Structural biology:** Structural characterization of the binding of FDA approved molecules.
- **Targets:**
  - **S protein:** One of the Sars-Cov-2 surface proteins key for the binding to the host cells.

## ***Repurposing teams' structure***

### **Drug design**

A new disease needs a new cure. There are many methods to develop new drugs and often needs adaptation to new target disease. Moreover, new methods could provide unforeseen solutions and, in a timescale, more compatible with a state of emergency.

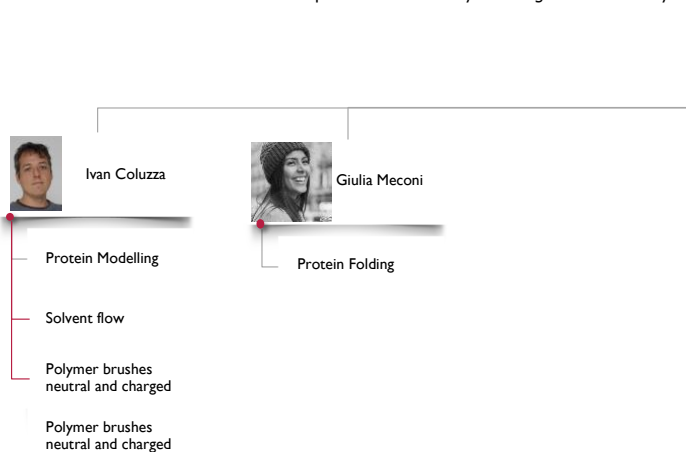
In our group we specialize in the following approaches to drug design:

- **Methods**
  - **Peptides:** Design small peptides targeting either the host cell receptors or the viral proteins blocking infection.
  - **Computational design**
  - **Computational screening**

- **Ligands**
- **Structural biology**
- **Targets**
  - **S protein**
  - **Protease**

## *Drug Design teams' structure*

**AUTOMATED PROTEIN ANNOTATION:** Protein Functional regions result from an evolutionary process leading to specific patterns of amino acids tailored to the activity of the biomolecule. The identification of residues directly responsible for functionality has been obtained with large scale mutation experiments where the effect on the protein function is tested against each alteration. We have developed a tool to identify such regions without any knowledge of the biological role of the protein.



## **Multiscale Mathematical Modelling**

With the SARS-CoV-2 coronavirus pandemic, we have witnessed the recognition of the importance of rigorous mathematical models as major players in understanding the dynamics and evolution of the pandemic. They have also proved to be of invaluable help as (evidence-based) guidance tools for the governments' decision-making process and the management of healthcare resources. The

mathematical models develop and refined during the current crisis will be essential in a future pandemic to guide lockdown policies and hospital organization. Mathematical models also play an important role in molecular simulation, including simulation of proteins, binding and drug screening, and Artificial Intelligence tools have proved to be very useful in the fight against the pandemic.

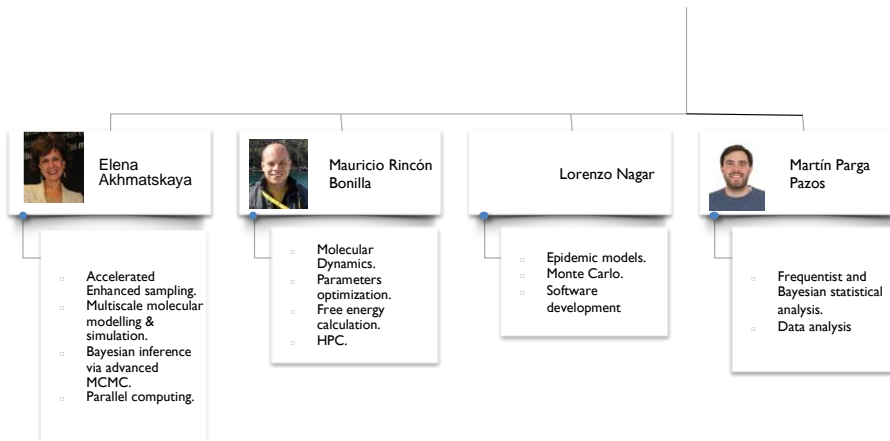
In our group we specialize in the following approaches to epidemiology:

- **Methods**
  - **Advanced mechanistic and mechanistic-statistical models for the transmission of infectious diseases.**
  - **Nonlinear dynamics and spatially extended stochastic processes**
  - **Bayesian model calibration.**
  - **Probabilistic screening.**
  - **Multiscale molecular simulation.**
  - **Binding free energy calculation.**
  - **Stochastic ABM.**
  - **Discrete Element Methods - stochastic pedestrian dynamics.**
  - **Smoothed Dissipative Particle Dynamics.**
  - **Machine learning techniques.**
- **Target**
  - **Advanced modelling of epidemic outbreaks and spread of disease: prediction and control**
  - **Main protease (Mpro).**
  - **SARS-CoV-2-S - ACE2 complex.**
  - **Nonlocal models of pathogen spreading using Agent-Based Models.**
  - **Modeling infection spreading coupled with pedestrian flow.**
  - **Multiscale modelling of clotting.**
  - **Analysis of RX images to detect COVID-19.**
  - **Analysis of COVID-19 Mobile App datasets.**

# Multiscale Mathematical Modelling teams' structure

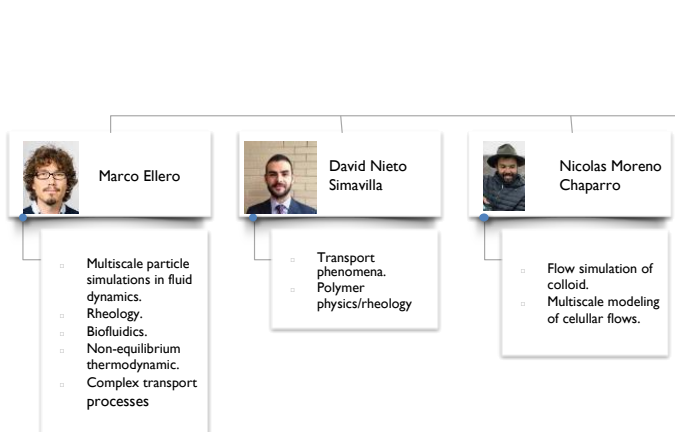
## MODELLING AND SIMULATION IN LIFE AND MATERIAL SCIENCES

Our goal is to obtain biological information from the stability boundaries of population dynamical equilibria in a two-parameter space. To enable efficient detailed simulations of extremely large and complex systems which are not possible with conventional simulation methods. Methods include integral equations, semigroup theory and numerical curve continuation. Molecular dynamics, Monte Carlo, stochastic thermostats and shadow Hamiltonians.



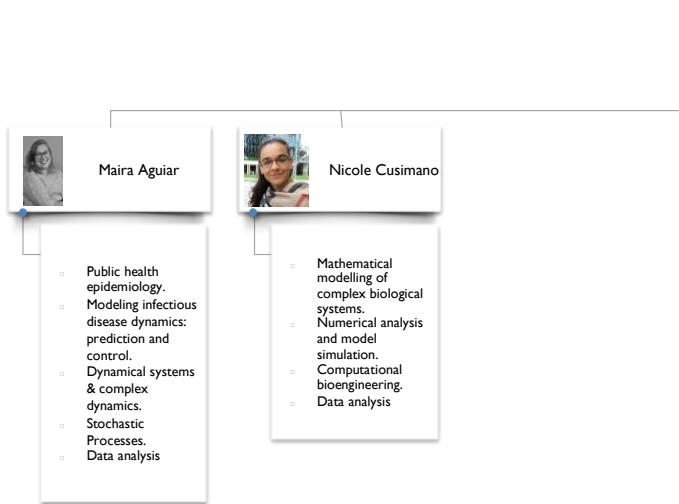
## CFD MODELLING AND SIMULATION

Our goal is to develop novel, advanced numerical methods and simulation tools to solve mesoscopic and macroscopic fluid dynamic problems. We combine best numerical approaches on continuum macroscopic scales (Smoothed Dissipative Particle Dynamics, Discrete Vortex Hydrodynamics, Finite Volumes), on mesoscopic scales (Smoothed Dissipative Particle Dynamics, Brownian Dynamics, Lagrangian Particle Tracking) as well as best computer science techniques (C++, massively parallel MPI, etc.).



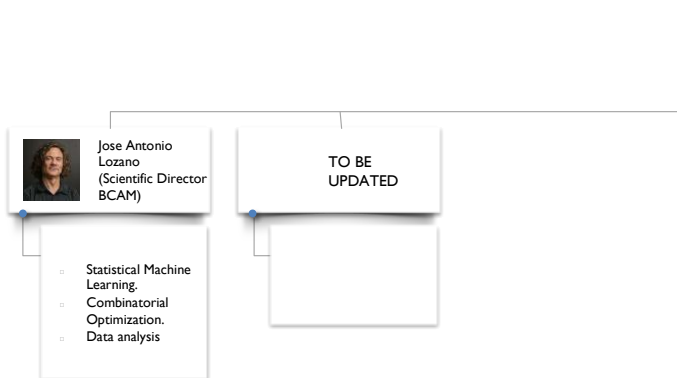
# MATHEMATICAL AND THEORETICAL BIOLOGY

With a highly interdisciplinary team, our research addresses significant mathematical problems and fundamental questions in medicine and biology. Using methods from nonlinear dynamics, bifurcation analysis, dynamical systems theory, stochastic processes and biostatistics, our work focuses on the development of theoretical methods, modeling and simulation techniques and its practical applications in life sciences, covering topics on population dynamics, eco-epidemiology, public health epidemiology, physiological and medical systems, molecular and antigenic evolution and evolutionary dynamics, as well as methodological topics in natural sciences and mathematics.



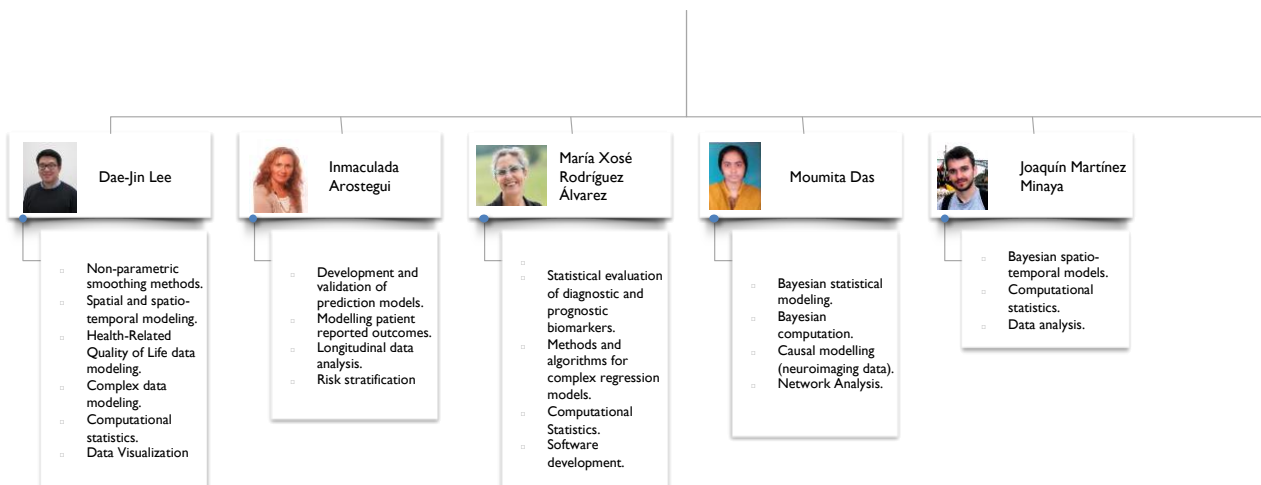
# MACHINE LEARNING

The objective is to design new methods for learning probabilistic graphical models in general, and Bayesian networks in particular. These methods will be a hybrid between classical operations research techniques and metaheuristic methods. We apply the developed techniques in the solution of real data analysis tasks. We combine many mathematical methodologies. First of all are probability theory and statistics. The final objective is to learn a probability distribution. It also deals with graph theory as probabilistic graphical models are represented using graphs. A third topic used in the area is optimization. Most of the processes are based in optimizing a score, and therefore the area of combinatorial optimization, in particular is basic for the topic.



# APPLIED STATISTICS

Our goal is to develop innovative statistical methods, computational algorithms and visualization tools for the analysis of complex data sets from different and diverse sources. We have particular interest in semi-parametric regression, multidimensional smoothing, (Bayesian) hierarchical models, mixed and random effects models, spatial and spatio-temporal modeling, functional data analysis, computational statistics, and data visualization tools.



# Transmission

Identify the means of transmission of a pathogen is a key step in containing a pandemic. With the current Sars-Cov-2 outbreak we are still not sure about the method of transmission or the virus survival time on surfaces.

In our group we specialize in the following approaches to transmission:

- **Methods**
  - **Physical virology**

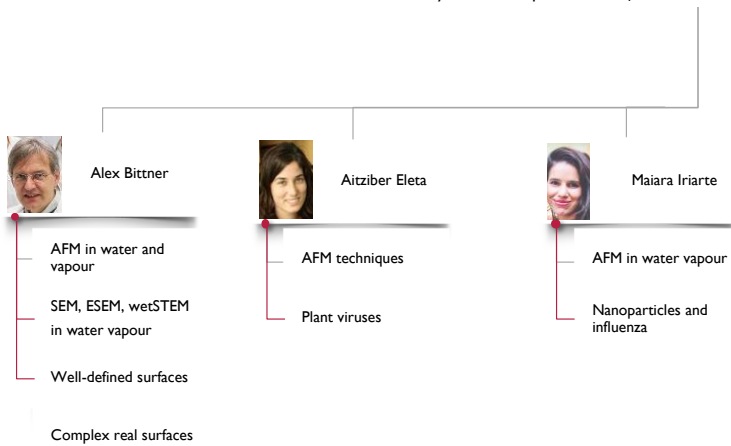


- **Targets**
  - **Influenza Virus**

## ***Transmission teams' structure***

### **PHYSICAL VIROLOGY:**

Some viruses complete all of their "life cycle" in vivo. Others, especially those responsible for respiratory infections, have to "survive" on surfaces or in air for some time. The Bittner group images viruses on defined surfaces, in a defined environment (temperature, humidity) with scanning probe and with electron microscopy methods. The aim is understanding the physicochemical basics of "virus survival". We have obtained many results for plant viruses, and have recently moved to influenza and models of influenza.



---

## Members

Maira Aguiar, UPV/EHU-BCAM  
Elena Akhmatskaya, UPV/EHU-BCAM  
Ignacio Arganda-Carreras, EHU/UPV  
Inmaculada Arostegui, UPV/EHU-BCAM  
Oksana Azpitarte, UPV/EHU  
Ana Beloqui, Polymat-UPV/EHU  
Aitor Bergara, UPV/EHU-DIPC  
Alexander Bittner, CIC nanoGUN  
Mauricio Rincón Bonilla, UPV/EHU-BCAM  
JJ Gomez Cadenas, DIPC  
María M. Caffarel, IIS Biodonostia  
Marcelo Calderón, Polymat-BERC  
Ivan Coluzza, CIC BiomaGUNE  
Aitziber López Cortajarena, CIC BiomaGUNE  
Fernando Cossio, EHU/UPV  
Nicole Cusimano, UPV/EHU-BCAM  
Moumita Das, UPV/EHU-BCAM  
David De Sancho, DIPC/EHU  
Marco Ellero , UPV/EHU-BCAM  
Fernando López Gallego, CIC BiomaGUNE  
Marek Grzelczak, DIPC  
Raul Perez Jimenez, CIC nanoGUNE  
David Rodriguez Larrea, UPV/EHU-CSIC  
Dae-Jin Lee, BCAM  
Aritz Leonardo., UPV/EHU-DIPC  
Xabier Lopez, UPV/EHU  
Jose Antonio Lozano , UPV/EHU-BCAM  
Óscar Millet, CIC BioGUNE  
Joaquín Martínez Minaya, UPV/EHU-BCAM  
Francesc Monrabal, DIPC  
Nicolas Moreno, UPV/EHU-BCAM  
Ricardo Díez Muiño, DIPC  
Lucinda Mulko, Polymat-BERC  
Lorenzo Nagar, UPV/EHU-BCAM  
Dina Niculaes, CIC BiomaGUNE  
Gonzalo Jiménez Oses, CIC BioGUNE  
David Otaegui, IIS Biodonostia  
Martí Parga Pazos, UPV/EHU-BCAM  
Iván Rivilla, DIPC\_UPV/EHU  
Maria X.(Coté) Rodriguez, BCAM/Ikerbasque  
Óscar Rodríguez, CFM  
Luca Salassa, DIPC  
David Nieto Simavilla, UPV/EHU-BCAM  
Neha Tiwari, Polymat  
Maia G. Vergniori, DIPC