Application BASTRI

Fiches Equipes

SISTM (SR0575YR)

Statistics In System biology and Translational Medicine

SISTM ▯ SISTM (SR0678GR)

Statut: Terminée

Responsable : Rodolphe Thiebaut

Mots-clés de "A - Thèmes de recherche en Sciences du numérique - 2024" : *Aucun mot-clé.*

Mots-clés de "B - Autres sciences et domaines d'application - 2024" : *Aucun mot-clé.*

Domaine : Santé, biologie et planète numériques
Thème : Neurosciences et médecine numériques

Période : 02/04/2013 -> 31/12/2015
Dates d'évaluation :

Etablissement(s) de rattachement : <sans>
Laboratoire(s) partenaire(s) : <sans UMR>

CRI : Centre Inria de l'université de Bordeaux
Localisation : Centre Inria de l'université de Bordeaux
Code structure Inria : 091058-0

Numéro RNSR : 201321095C
N° de structure Inria: SR0575YR

Présentation

The team is devoted to the development of statistical methods for the integrative analysis of data in medicine and biology. Thanks to the technological improvements, clinical and biological research is generating massive amounts of data. Of importance are the "omics" data such as genomics (gene expression) and proteomics but also other types of data, for which modern technologies have strongly increased the amount of information (e.g. medical imaging, cell counts). The challenge is to analyze these BIG DATA to answer clinical and biological questions by using appropriate statistical methods. With data on the machinery of a cell to the clinical status of individuals in any circumstances including in clinical trials, new tools are needed to translate information obtained from complex systems into knowledge. This has led to the field of "systems biology" and « systems medicine » by extension, which naturally takes place in the context of translational medicine that links clinical and biological research. The statistical analysis of these data is facing several issues: • There are more parameters (p) to estimate than individuals (n) • The types/nature of data are various • The relationship between variables is often complex (e.g. non linear) and can change over time To tackle these issues we are developing specific approaches for these questions, often related to immunology. The methods are mainly based on either mecanistic modeling using differential equation systems or on statistical learning methods. The general paradigm of our approach is to include as much information as available to answer a given question. This information comes from the available data but also from prior biological information available defining the structure of the model or restricting the space of the parameter values. We develop and apply our methods mainly for applications belonging to clinical research especially HIV immunology. For instance, several projects are devoted to the modelling of the response to antiretroviral treatments, immune interventions or vaccine in HIV infected patients.

Axes de recherche

Axis 1: Mecanistic modelling Axis 2: High dimensional data

Relations industrielles et internationales

- Vaccine Research Institute (Labex Hôpital Henri Mondor, Creteil) - Immunobiology department, Institute of Child Health, University College London - Statistical Center for HIV/AIDS Research & Prevention (SHARP), Vaccine and Infectious Diseases Division of the Fred Hutchinson Cancer Research Center - Department of Systems and Computational Biology at Albert Einstein College of Medicine, New York - School of Mathematics and Physics at the University of Queensland

Contact

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En savoir plus

- Site sur inria.fr
- Site du responsable
- Derniers Rapports d'Activité : 2016 , 2017 , 2018 , 2019 , 2020 , 2021 , 2022 , 2023 , 2024

Documents sur la structure

- Intranet
- Privés

Décisions

- 9324 (02/04/2013) : création
- 9325 (02/04/2013) : nomination responsable
- 10129 (01/04/2014) : prolongation

Localisation

- **Adresse postale :** Centre Inria de l'université de Bordeaux 200 Avenue de la Vieille Tour 33405 Talence France
- **Coordonnées GPS :** 44.808, -0.6