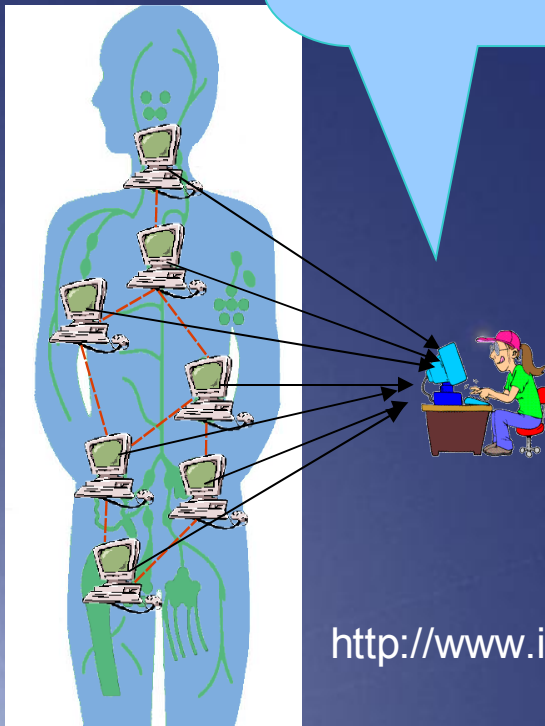


ImmunoGrid

The European Virtual Human Immune System Project

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? Antigen analyser
? Antigen processing simulator
? Infection simulator
? Cancer simulator
? Allergy simulator
? Vaccine designer
? Vaccine scheduler



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Why ImmunoGrid?

- ❑ The immune system (IS) is a **complex** and **adaptive** learning system that **protects** an organism from infectious diseases and cancers. Malfunction of IS may result in **autoimmunity** or **allergies**.
- ❑ The IS has an **immense diversity**.
- ❑ **Computational models** are ideal for compensating for the limitations of the experimental approaches in human.
- ❑ **Grid computing** enables modelling human IS at a natural scale.



What is ImmunoGrid?

- ❑ **ImmunoGrid** is a Specific Targeted Research Project (STREP) sponsored by the European Commission, 6th Framework Programme (**FP6-2004-IST-028069**).
- ❑ The project is a web-based implementation of the **Virtual Human Immune System** using **Grid technologies**. It integrates the simulation of immune system processes at **molecular**, **cellular** and **organ** levels.
- ❑ The set of tools have been validated with experimental data and will be disseminated to the users, such as **vaccine** and **immunotherapy** researchers and developers.



Developing Standards

ImmunoGrid develops and integrates the standards, based on the **IMGT-ONTOLOGY** concepts for:

- ☐ mapping genetic data,
- ☐ data representation of metabolic, regulatory and signal transduction networks,
- ☐ interchange format for interaction databases,
- ☐ annotation system for immune system, and relevant proteins.

ImmunoGrid also helps create the standards for:

- ☐ immunoinformatics course study,
- ☐ grid computing.



Molecular and System Level Models

Molecular level models simulate the immune system's sequence-based processing and discriminate self and non-self proteins at **molecular** level.

- e.g. T cell and B cell epitope prediction.

System level models describe processes at **cellular** and **organ** levels:

- immune response to viruses,
- analysis of MHC diversity under host-pathogen coevolution,
- B cell maturation,
- dynamic models that simulate both cellular and humoral immune responses.



Goals

- ❑ To use **bioinformatics** and **immunoinformatics** to interpret genome information related to immune system;
- ❑ To facilitate the understanding, description and prediction of **biological processes**, and generate new scientific **hypotheses**;
- ❑ To realise a **common shared resource** with significant potential for strengthening European research in **immunogenomics** and **immunomics**;
- ❑ To develop **cross-disciplinary research** supporting **medical biotechnology** and **computer science**.