

CCA Drylab vision document

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The Drylab is supporting all VUmc-CCA groups in the analysis of 'Big data' coming from the 'omics' sciences Genomics (DNA), Transcriptomics (RNA) and Proteomics (protein). To realize this support, the Drylab is building and running a hardware- and software-infrastructure to process and analyze these data and gives courses to teach the users how to use these services.

The Drylab aligns and collaborates with related initiatives on the national and international level. Notably it connects to the national CTMM-TraIT ('Translational research IT') initiative headed by Prof. Dr. GA Meijer.

Concept: Location of action of the Drylab: Shell model (see fig. 1)

- data is processed and interpreted where they are generated
- from inside to outside: from raw data processing to more sophisticated analysis/interpretation; low level to high level

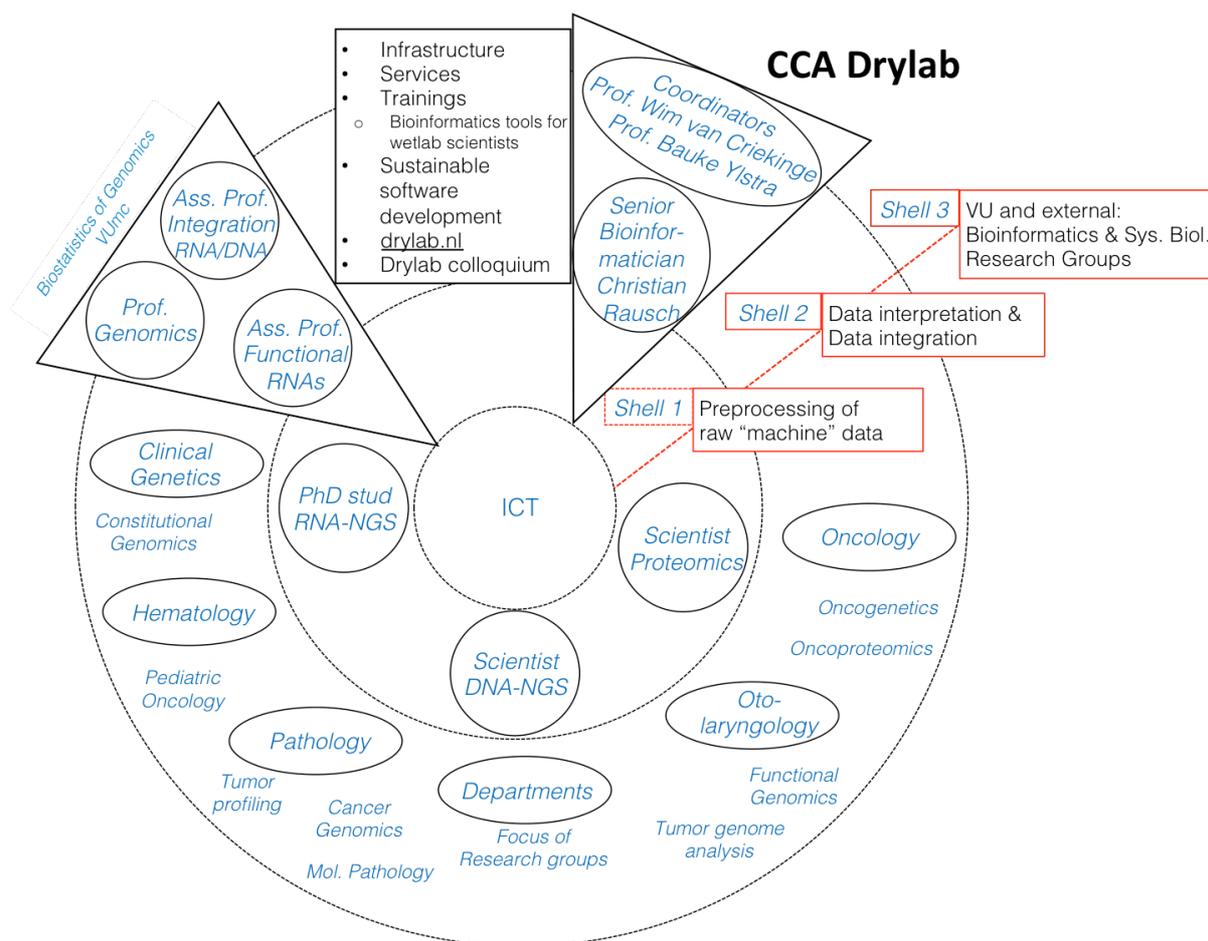


Figure 1: Shell model indicating where the CCA Drylab is acting

In practice, the main tasks and responsibilities are:

- Coordinate bioinformatics activities in the CCA;

- Christian is aligning with the CCA PIs to keep an overview of who is working on which bioinformatics questions and also to find out the bioinformatics needs. This is to help connecting people working on similar tasks, avoid parallel developments and make sure developed methods that are useful for more people are conserved and documented (software sustainability)
- Once a month a 'Drylab colloquium' is held, a forum to bring CCA researchers (Drylab users) and external or internal speakers together to discuss new developments and bioinformatics needs.
- An informal meeting of CCA bioinformaticians has been set up for exchange of knowledge and ideas (after the monthly Drylab colloquium)
- Provide bioinformatics services to CCA researchers AND
- Implement new and adapt existing data analysis workflows for (re)use by researchers;
 - 'services' typically mean software based services
 - these are set-up on demand if there are methods that are useful for several groups.
 - The drylab should not set-up new methods from scratch. These should be developed by/in collaboration with bioinformaticians in the CCA or outside and the Drylab can help in finding and connecting the right people. However adapting, generalizing and testing (e.g. benchmarking) of methods before making them available to more CCA users may be needed.
 - There should be a concrete use-case for every newly set-up method. The drylab support should lead to a tangible result. A measurable end-result can be e.g. a co-authorship on a publication.
- Develop and deploy bioinformatics IT Infrastructure
 - Analyse the current infrastructure needs
 - Focus on research needs but align with diagnostics needs, in particular Clinical Genetics department
 - Interact and negotiate with ICT department and CCA management for the bioinformatics needs of the CCA
- Provide training and support.
 - Practical hands-on bioinformatics trainings for CCA researchers and support during every day use.