KU Leuven Open Science Day

Implementing open science in a daily routine: Team contribution from the Laboratory for Translational Breast Cancer Research

François Richard¹

¹KU Leuven

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Abstract

The Laboratory for Translational Breast Cancer Research (LTBCR) was recently founded at KU Leuven in October 2018. Headed by prof. Desmedt, LTBCR aims at better understanding breast cancer (BC), especially: (i) its connection with adiposity; (ii) the mechanisms of progression that lead to metastases, (iii) the peculiarities of less frequent BC entities such as lobular and inflammatory BC. We investigate retrospective data and samples, set up clinical trials, and work with pre-clinical models through collaborations. We therefore collect a high number of samples and generate high amount of data and analyses on both collected samples and publicly available resources. To ensure a comprehensive open science approach, we are developing tools and a working environment that guarantee research integrity, reproducibility, and open access, while respecting GDPR.

Firstly, a common working environment has been implemented to allow all team members to work in a transparent manner, using KU Leuven drives, Google drives, and Slack. Secondly, considering bioinformatics, the versioning program Git has been implemented at a team level to share the code and to allow code peer reviewing. Thirdly, concerning samples and metadata encoding, LabCollector, a laboratory information management system, has been implemented. We made the system compliant with the UZ Leuven Biobank and all the samples are barcoded for comprehensive tracking. Fourthly, concerning clinical data, an eCRF has been designed in REDCap for each of our clinical studies. Data are programmatically imported whenever possible (laboratory values present in KWS for instance) and integrity checks have been implemented. Surveys used in the clinical studies have also been coded in REDCap, along with their score computation to be easily used and transferred to other projects.

The team is regularly trained to use all the aforementioned tools and we are now improving research reproducibility by integrating code ocean in our routine for bioinformatics analyses. A R shiny web platform will also be designed to allow browsing the results generated in some of our projects. Furthermore, we are working on facilitating the process of Data Transfer Agreement to make our research easily accessible to the scientific community after publication.

Slides

Visit the web version of this article to view interactive content.

Author biography

[François Richard](#) (KU Leuven) is a postdoc in bio-informatics at LTBCR, characterizing breast cancer progression and the connection with adiposity, as well as taking care of the bioinformatics, biostatistics, and open science practices of the laboratory. He obtained his master's degree in bioengineering from the University of Bordeaux (France) in 2012. During his PhD in protein sequences analysis, that he obtained in 2016 from the University of Montpellier (France), he developed tools to identify and characterize tandem repeats in proteins.