



CASE STUDY

HANNOVER MEDICAL SCHOOL
RESEARCH CORE UNIT TRANSCRIPTOMICS

DELIVERING CORE TECHNOLOGIES RELIABLY AND AFFORDABLY

STRENGTHENED TRANSCRIPTOMICS ANALYSIS CAPACITIES AND CORE OMICS TECHNOLOGIES

Understanding how the genome is transcribed in different cell types and what changes occur when cells undergo a biological or chemical treatment leads to better insights into biology, the underpinnings of a particular disease, and possibly the success of a specific drug treatment.

Next-generation sequencing (NGS) and array technology – adopted increasingly by hospitals and medical systems across the globe – have revolutionized research and the diagnosis and treatment of human disease. As the use of this technology increases worldwide, the demand also grows for significant investments in analysis, expertise, software, and infrastructure to perform and maintain genomic analysis projects.

BLUEBEE

RCU

Transcriptomics

RESEARCH CORE UNIT TRANSCRIPTOMIC'S NEEDS

The Research Core Unit Transcriptomics (RCUT) is a central service unit at the Hannover Medical School (MHH) and provides transcriptomics-based analyses for over 100 research groups across 46 different departments. Major research areas focus on infection and immunity, transplantation and regeneration, and biomedical technology and implant research.

About a year ago, next-generation sequencing was added as a new service to both internal and external groups. Currently, analyses are performed for internal groups, using a pipeline-based approach on the well-established Tuxedo Suite for sequencing-based transcriptomics data. Further downstream analyses use commercial packages including Qluore Omics Explorer, GeneSpring Expression, Ingenuity Pathways Analysis, and Strand NGS.

Providing these services, however, requires properly configured computing power and an IT infrastructure that comes with ongoing maintenance needs. As a result, bioinformaticians who should be focused on complex data analysis are too often pulled away to solve IT infrastructure issues.

“ WE NEED HIGHLY SPECIALIZED PERSONNEL, DEDICATED AREAS AND PERMANENT MAINTENANCE SERVICES TO BE ABLE TO UTILIZE AN EFFICIENT NGS DATA PRODUCTION ANALYSIS PROCESS ”

THE NEED FOR DATA PROTECTION

“ EFFICIENT USER MANAGEMENT SUPPORTED BY APPROPRIATE PERMISSION SETTINGS IS ESSENTIAL WHEN HANDLING AND SHARING SEQUENCE DATA ”

Data security is integral to the RCUT since samples are processed across a broad range of different research groups and institutions. With the many internal and external customers and collaborations across those groups proper access control mechanisms need to be in place to prevent wrongful access or data loss.

THE NEED TO MANAGE DATA SURGES AND RELATED COSTS

Large sequencing projects now challenge our internal IT capacity of the RCUT facility to complete sequence data processing routines in an adequate time frame.

Outsourcing would also help with calculating and invoicing computing resources for cost estimation and assessments for external customers.

“ A PLATFORM THAT IS STRAIGHTFORWARD, INTUITIVE AND REQUIRES LITTLE TO NO TRAINING BY EXPERTS IS OF UTMOST IMPORTANCE ”

THE NEED TO OVERCOME THE BIOINFORMATICS BOTTLENECK

Due to the limited number of bioinformaticians and their expertise, the industry faces a bottleneck, and hence:

“ TO MAINTAIN OUR FULL COMPUTING POWER FOR MHH INTERNAL USERS, OUTSOURCING OF COMPUTATION MAY BE THE NEXT LOGICAL STEP PARTICULARLY FOR EXTERNAL CUSTOMERS ”

HOW BLUEBEE HELPS RCUT

With the increased prominence of “infection and immunity” research within the infectious disease research and therapeutic area, the MHH now emphasizes the need for the integration and development of OMICS technologies, called TRAINomics. The TRAINomics project is embedded into the TRAIN network serving as an infrastructural framework that connects translational research efforts of the MHH to its academic neighbors. The main goal of the collaboration is to provide quality OMICS-based technologies that reach the highest international standards and meets all of the customers’ demands.

In the context of the TRAINomics project, the Bluebee Genomics Platform may turn out as a “real game changer” with an intuitive interface and optimized RNA-seq pipelines, access to a flexible compute infrastructure and local data centers when needed, a multi-layered security system with user access and permission management, a budget management system, and an easy-to-use system for simplified results downloads for further downstream processing.

Next generation sequencing technology offers excellent access to clinically relevant genomics and its interrogation in the context of individualized infection medicine. Accordingly, plans to physically integrate some of the Omicsbased Core Units of the MHH (including the NGS Core Unit) directly into the envisaged Center for Individualized Infection Medicine (CIIM) will enable the use of highly efficient NGS technology approaches for researching individualized infection medicine and beyond.



RESEARCH CORE UNIT TRANSCRIPTOMICS OF HANNOVER MEDICAL SCHOOL (MHH)

LOCATION: Hannover, Germany

<https://www.mh-hannover.de/index.php?id=23882&L=1>

BASIC & TRANSLATIONAL RESEARCH

MHH STAFF: 7800

Projects and topics:

- It started in 2001 with the offering of one custom microarray.
- In 2012 the RCUT was formed offering full fledged transcriptomic analysis.
- Today the RCUT conducts transcriptomics analyses for over 100 research groups belonging to 46 different institutes and MHH departments.
- >5,600 microarray hybridizations performed, and >10,000 archived RNA samples from over 80 cell systems with over 80 different cell treatments.
- Since 2015, the RCUT provides total RNA sequencing (ribo-depleted), mRNA sequencing (polyA-enriched), and total RNA sequencing from small samples (1ng total RNA).

Resources:

- Microarrays: Agilent G2565C high throughput microarray scanner.
- Sequencing: Illumina NextSeq 500 & MiSeq; ThermoFisher Ion Torrent & SOLID 5500; Pacific Biosciences Sequel.

Data generation:

- For internal and external customers.



The Bluebee genomics platform supports cross-functional teams of life science researchers and clinicians by effectively centralizing and managing their genomics data processes and storage needs.

Bluebee accelerates genomics insights discovery via the delivery of optimized data analysis pipelines, employing both supercomputing and private cloud technologies. This results in a unique high performance cloud-based genomic analysis platform that enables efficient and affordable processing, and insight generation from ever-increasing genomic data.

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