Visualizing Transcriptomics Data in Cancer

An Interview with Bridge Informatics & Qlucore CEOs: Dan Ryder & Carl-Johan Ivarsson

INTRODUCTION

In cancer research, understanding what's happening at the molecular level goes beyond DNA. Transcriptomics - studying RNA expression - provides a dynamic snapshot of cellular activity, offering crucial insights into disease progression and therapeutic targets.

In this Q&A, we sit down with Carl-Johan Ivarsson Founder & CEO of Qlucore, and Dan Ryder, Founder & CEO of Bridge Informatics, to discuss how transcriptomics data visualization advances cancer research.

DAN, CARL-JOHAN, CAN YOU PLEASE INTRODUCE YOURSELVES TO THOSE WHO DON'T KNOW YOU?

Dan: My name is Dan Ryder. I'm the founder and CEO of Bridge Informatics, a bioinformatics service provider that specializes in providing custom professional services and R&D software products that help life science companies translate data into biological results. I have a Ph.D. in Biochemistry and Molecular Biology and an MPH in Disease Control.

Carl-Johan: I'm Carl-Johan, and I'm the CEO and co-founder of Qlucore. My background is in software. I co-founded Qlucore with three colleagues to make complex biological data more accessible through intuitive visualization and analysis tools. Our mission is to empower researchers and clinicians with powerful yet user-friendly software to explore and interpret high-dimensional data.

WHAT SPARKED YOUR INTEREST IN TRANSCRIPTOMICS?

Dan: I've always been fascinated by the real-time snapshot of cellular activity transcriptomics gives us. It's essential for understanding disease mechanisms and finding potential therapeutic targets. We saw an opportunity to make transcriptomics data more accessible and user-friendly for researchers, so they can unlock its full potential without getting bogged down by complexity.

Carl-Johan: Exactly. Scientists need help navigating and visualizing complex transcriptomics data.

WHY IS TRANSCRIPTOMICS CRUCIAL FOR UNDERSTANDING CANCER, AND HOW DOES IT DIFFER FROM DNA ANALYSIS?

Carl-Johan: DNA provides a blueprint, but transcriptomics reveals real-time cellular activity. While mutations in DNA may predispose a person to cancer, RNA expression patterns show which genes are actively driving the disease. This makes transcriptomics a powerful tool for identifying biomarkers, understanding tumor heterogeneity, and even predicting patient response to therapies.

Dan: DNA is static - it tells us what could happen, but a global view or RNA, or transcriptomics - tells us what is happening in the cell at a given moment. This is especially critical in oncology, where gene expression can shift rapidly in response to treatment or disease progression. By integrating transcriptomic data, researchers gain a more comprehensive view of cancer biology.

WHAT ARE THE KEY CHALLENGES IN VISUALIZING TRANSCRIPTOMICS DATA?

Carl-Johan: One of the biggest challenges is the high dimensionality of transcriptomics data. It can exist in hundreds of dimensions, but we need to interpret it in a 2D or 3D space.

There's no one-size-fits-all solution, so we focus on enabling researchers to extract the most relevant insights for their specific questions. Our approach includes interactive filtering, dimension reduction techniques, and fast computational performance, ensuring users can explore data dynamically and intuitively while maintaining analytical rigor.

Dan: Another challenge is moving from bulk RNA sequencing, which provides an average expression across many cells, to single-cell RNA sequencing (scRNA-seq), which captures individual cellular differences and groups them into clusters based on an expression profile. This shift introduces new computational and visualization hurdles, as single-cell data is significantly larger than bulk RNA and requires specialized techniques to identify meaningful patterns.

WHAT ARE THE MOST EFFECTIVE VISUALIZATION APPROACHES FOR TRANSCRIPTOMICS DATA?

Carl-Johan: For larger non–single-cell datasets, Principal Component Analysis (PCA) plots are particularly effective. PCA is a natural method for dimensionality reduction that preserves as much variance as possible across the principal components. In many transcriptomics datasets, the first few components (often just two or three) can reveal key structures and patterns in the data. Once these underlying structures are identified, PCA plots can be complemented with other visualizations such as heatmaps, volcano plots, and violin plots, depending on the specific analytical goals.

For single-cell data, Uniform Manifold Approximation and Projection (UMAP) plots are often preferred. UMAPs are especially well-suited for capturing local and global structure in high-dimensional single-cell data.

Looking ahead, we expect that both PCAs and UMAPs will continue to play important and complementary roles in transcriptomics visualization, each offering unique strengths depending on the context.

Dan: As related to single-cell data, I'd just add that annotation is key. And in the case of annotation of cell clusters, visualization is so important to ensure it is done correctly and efficiently. Once this is done, my favorite follow up visualization is often a UMAP. This type of plot can be incredibly powerful to view your single cell data set. UMAPs start the journey and eventually make huge progress. With cancer properly annotated scRNA-seq data sets, you could track early-stage cancer development and progression, which is critical for refining treatment approaches and personalizing therapies.

WHAT'S NEXT FOR TRANSCRIPTOMICS VISUALIZATION IN CANCER RESEARCH?

Dan: Integration is the future. Combining transcriptomics with spatial omics, proteomics, and imaging data will provide a more holistic view of cancer biology. We're also seeing increasing adoption of cloud-based platforms that enable real-time collaboration and data exploration across research. My prediction is that at some point, most scientists will be using an LLM to quickly compare which integration algorithms give the best results.

Carl-Johan: As data expands with the use of single-cell, spatial single-cell, and multi-omics approaches, visualizations must evolve to capture and communicate these intricate layers of information in ways that directly support specific research questions. The next frontier will be creating tools that not only display these complex datasets but also allow researchers to interact with them in a meaningful way, offering deeper insights and enabling more precise discoveries.

WHY SHOULD A LIFE SCIENCES COMPANY CONSIDER USING SOFTWARE OR PARTNERING WITH A PROFESSIONAL SERVICES COMPANY, INSTEAD OF RELYING SOLELY ON IN-HOUSE DATA SCIENTISTS, TO HELP REALIZE THEIR VISION?

Dan: Bridge Informatics brings bench experience which helps us build custom software, and integrate them in ways that complements the capabilities of in-house teams. This collaboration allows companies to leverage external skills for handling complex data workflows, optimizing infrastructure, and building tailored solutions, all while allowing internal teams to focus on the science itself. Professional services help bridge the gap between vision and execution, ensuring that innovative solutions are implemented efficiently and effectively.

Carl-Johan: At Qlucore, we focus on providing software solutions tailored for academia and the life sciences industry. While in-house data scientists are critical for day-to-day operations, using software like Qlucore enables teams to work more efficiently and effectively. Our platform is designed to simplify complex data analysis by offering intuitive, interactive visualizations and supporting advanced techniques like PCA, UMAP, and multi-omics integration. This allows researchers to explore and interpret their data in real-time, reducing the time and expertise required to develop custom solutions. By leveraging our software, companies can quickly realize their vision without having to build these capabilities from scratch.

HOW CAN PEOPLE GET IN TOUCH WITH YOU IF THEY'RE INTERESTED IN WORKING WITH YOU?

Dan: Connect with me on LinkedIn or contact me via our website!
Carl-Johan: Connect with me on LinkedIn or visit our website.

CONCLUSION

Transcriptomics is transforming our understanding of cancer by revealing the functional impact of genetic alterations. As visualization tools evolve, they will continue to unlock new insights, helping researchers and clinicians make data-driven decisions for improved patient outcomes.

NEED HELP VISUALIZING YOUR OWN TRANSCRIPTOMICS DATA?

Our bioinformatics team works with cancer researchers to build scalable RNA-seq workflows and extract insights from complex datasets.

Visit bridgeinformatics.com to get in touch with us today.