

New bioinformatics tool to visualize transcriptomes

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ZENBU, a new, freely available bioinformatics tool developed at the RIKEN Center for Life Science Technology in Japan, enables researchers to quickly and easily integrate, visualize and compare large amounts of genomic information resulting from large-scale, next-generation sequencing experiments.

Next-generation sequencing has revolutionized functional genomics, with protocols such as RNA-seq, ChIP-seq and CAGE being used widely around the world. The power of these techniques lies in the fact that they enable the genome-wide discovery of transcripts and transcription factor binding sites, which is key to understanding the molecular mechanisms underlying cell function in healthy and diseased individuals and the development of diseases like cancer. The integration of data from multiple experiments is an important aspect of the interpretation of results, however the growing number of datasets generated makes a thorough comparison and analysis of results cumbersome.

In a report published today in the journal *Nature Biotechnology*, Jessica Severin and colleagues describe the development of ZENBU, a tool that combines a genome browser with data analysis and a linked expression view, to facilitate the interactive visualization and comparison of results from large numbers of [next-generation sequencing](#) datasets. The key difference between ZENBU and previous tools is the ability to dynamically combine thousands of experimental datasets in an interactive visualization environment through linked genome location and expression signal views. This allows scientists to compare their own

experiments against the over 6000 ENCODE and FANTOM consortium datasets currently loaded into the system, thus enabling them to discover new and interesting biological mechanisms. The tool is designed to integrate millions of experiments/datasets of any kind (RNA-seq, ChIP-seq or CAGE), hence its name: zenbu means 'all' or 'everything' in Japanese.

ZENBU is freely available for use on the web and for installation in individual laboratories, and all ZENBU sites are connected and continuously share data. The tool can be accessed or downloaded from <http://fantom.gsc.riken.jp/zenbu/>.

"By distributing the data and servers we encourage scientists to load and share their published data to help build a comprehensive resource to further advance research efforts and collaborations around the world," explain the authors.

More information: Jessica Severin, Marina Lizio, Jayson Harshbarger, Hideya Kawaji, Carsten O Daub, Yoshihide Hayashizaki, the FANTOM consortium, Nicolas Bertin, and Alistair RR Forrest. "Interactive visualization and analysis of large-scale NGS data-sets using ZENBU". *Nature Biotechnology*, [dx.doi.org/10.1038/nbt.2840](https://doi.org/10.1038/nbt.2840)

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