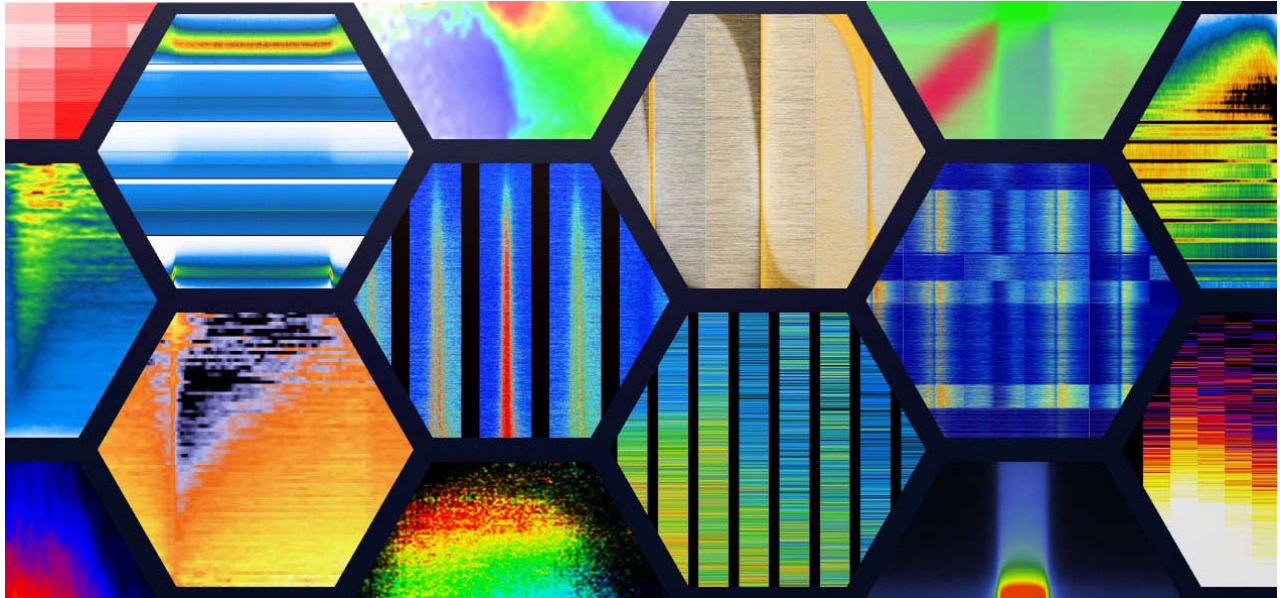# An interactive environment for agile analysis and visualization of ChIP-sequencing data

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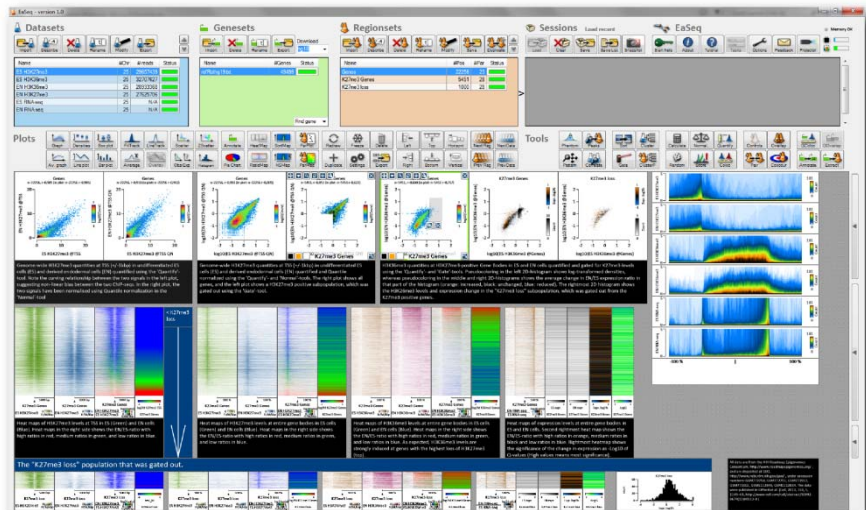
A selection of the many visualization options in EaSeq

- Made for life scientists – point and click interface, no coding or scripting
- Quick, Interactive, and genome-wide visualization and exploration of data
- Integrate e.g. ChIP-seq, expression, and DNA-methylation data
- No need for servers – EaSeq is free and runs on an ordinary Windows PC
- Automatic documentation of analyses – writes legends and methods.
- Versatile - more than 20 tightly integrated tools

Uses:

Visualizing genome-wide location and differences of polycomb proteins (*Dietrich et al., PLoS Genet, 8, 3, 2012*). Integration of RNA-seq and ChIP-seq from parkinsonian mouse striatum. (*Sodersten et al., PLoS Genet, 10, 9, 2014*). Peak-finding, annotation, controls, and colocalization of β-Catenin. (*Funa et al., Cell Stem Cell, 16, 2015*). Meta-analysis, in silico screening, and large-scale visualization, (*Lerdrup et al., Nat Struct Mol Bio, 2016*)

Screenshot from the program