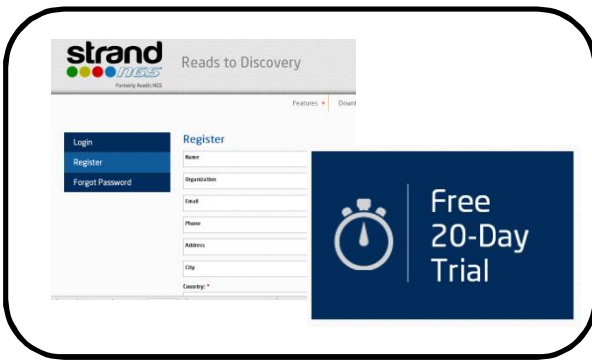
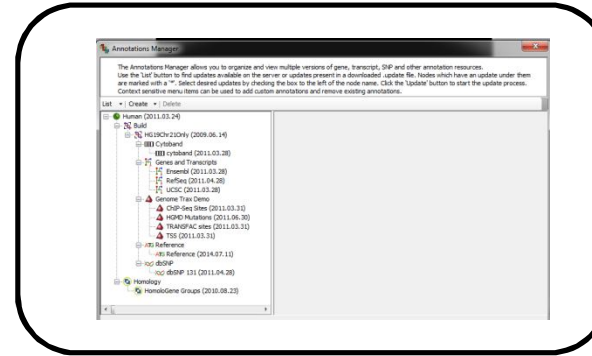
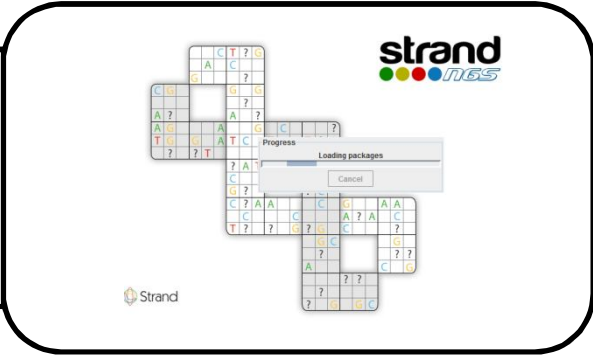


# Software Setup Guide



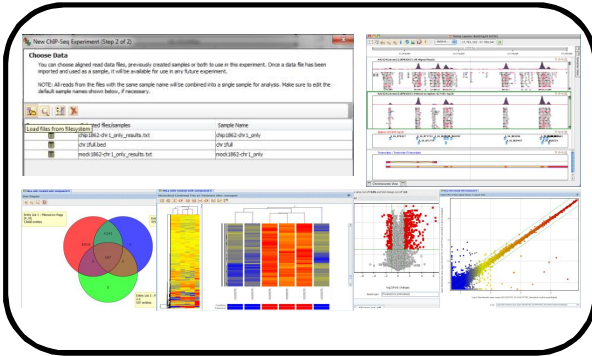
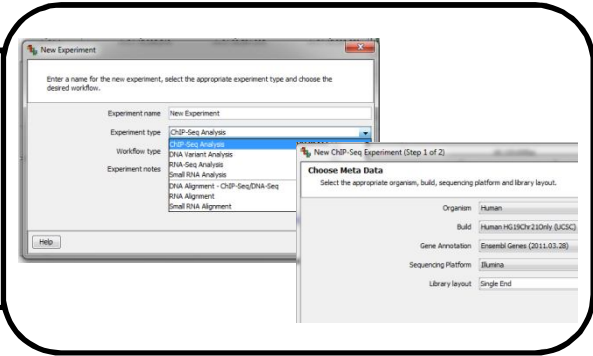
**Registration**  
Sign Up for an account in [www.strand-ngs.com](http://www.strand-ngs.com). Activate your account by clicking on activation link sent to your email id. Register for a free trial at <http://www.strand-ngs.com/ngs-free-trial>

**Install and Activate the Software**  
Download and run the Strand NGS installer for Windows/ Mac/ Linux from <http://www.strand-ngs.com/download/installers>. After installation, enter your license code(Order ID).  
License options: Free trial, Desktop/ Floating/ Server



**Download Annotations**  
Annotation Manager in Strand NGS has an extensive list of annotations for all standard organisms and some with multiple builds. To download, click on Annotation -> Annotations Manager->Choose the list ->From Server. User can also create custom annotations, if annotations for their organism of interest is not available

**Create New Project**  
To create a new experiment, specify the workflow (DNA, RNA, small RNA, ChIP, Methyl-Seq) and characteristics of your sequence data (organism, build, gene annotation, platform, library layout). Each project may contain several experiments. Multiple samples may be loaded under each experiment.



**Import Data, Analyze, Visualize and Interpret**  
Strand NGS supports data import in file formats – FASTA, FASTQ, SAM, BAM, ELAND, VAL and VCF. You can start analyzing your data, visualize and discover your objectives. The elastic genome browser, various visualization plots, and biological interpretation tools enable you to get publication quality data and assist in your journey from READS TO DISCOVERY.