



Zenon Bio's NGSSuite is a novel data analysis service to provide next generation short read sequencer users with rich biological findings.

Computational analysis of Digital Gene Expression data

The high throughput next generation sequencers provide a very powerful instrumentation for sequencing short nucleic acid fragments. Combining next generation sequencing with SAGE resulted in previously unprecedented robustness, comparability, and richness of expression profiling data.

The emerging new experimental technology has already tended to be a very serious rival of microarrays in transcriptomics as it offers distinct advantages including better coverage, the ability to measure low-abundance genes and to find unknown transcripts.

Similarly to other high throughput technologies the major bottleneck of DGE studies is the extraction of easily interpretable biologically relevant information from the huge amount of data accumulated even by a single experiment.

The raw experimental output must be further processed and additional biological information from different external resources has to be associated with the tags.

ZenonBio Ltd as a member of a large scale EU6 project investigating the zebrafish transcriptome landscape in different pathological conditions acquired substantial expertise in this problem including the storage, analysis and statistical description of DGE libraries containing millions of sequence tags.

About Digital Gene Expression (DGE)

DGE - Digital Gene Expression (or DeepSAGE) is a novel fully quantitative gene-expression profiling approach utilizing serial analysis of gene expression (SAGE) method together with next generation short read sequencers like Genome Analyzer (Illumina) or SOLiD (Life Technologies).

The SAGE approach involves end tagging of cDNA fragments and producing short sequence tags that can be identified and counted after sequencing.

Zenon Bio has developed many tools for different aspects of this task like correlation analysis of parallel libraries, identifying tags with significantly altered expression; mapping tags to transcript databases or mapping tags to genome and provides data analysis service to the research community.

Service summary

- Tag library quality check
- Basic descriptive statistics of the libraries
- Mapping tags to a transcript database available in public databases
- Mapping tags to custom transcript database provided by customer
- Mapping tags to genome
- Summary statistical statement about the mapping results
- Providing extra confidence information about tag mapping events
- Filtering subsets of data in tag libraries according to customer defined aspects
- Comparing tag libraries and identifying tags showing significant change
- Summary statistical statement about the significant tags

For more information please contact us at:

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