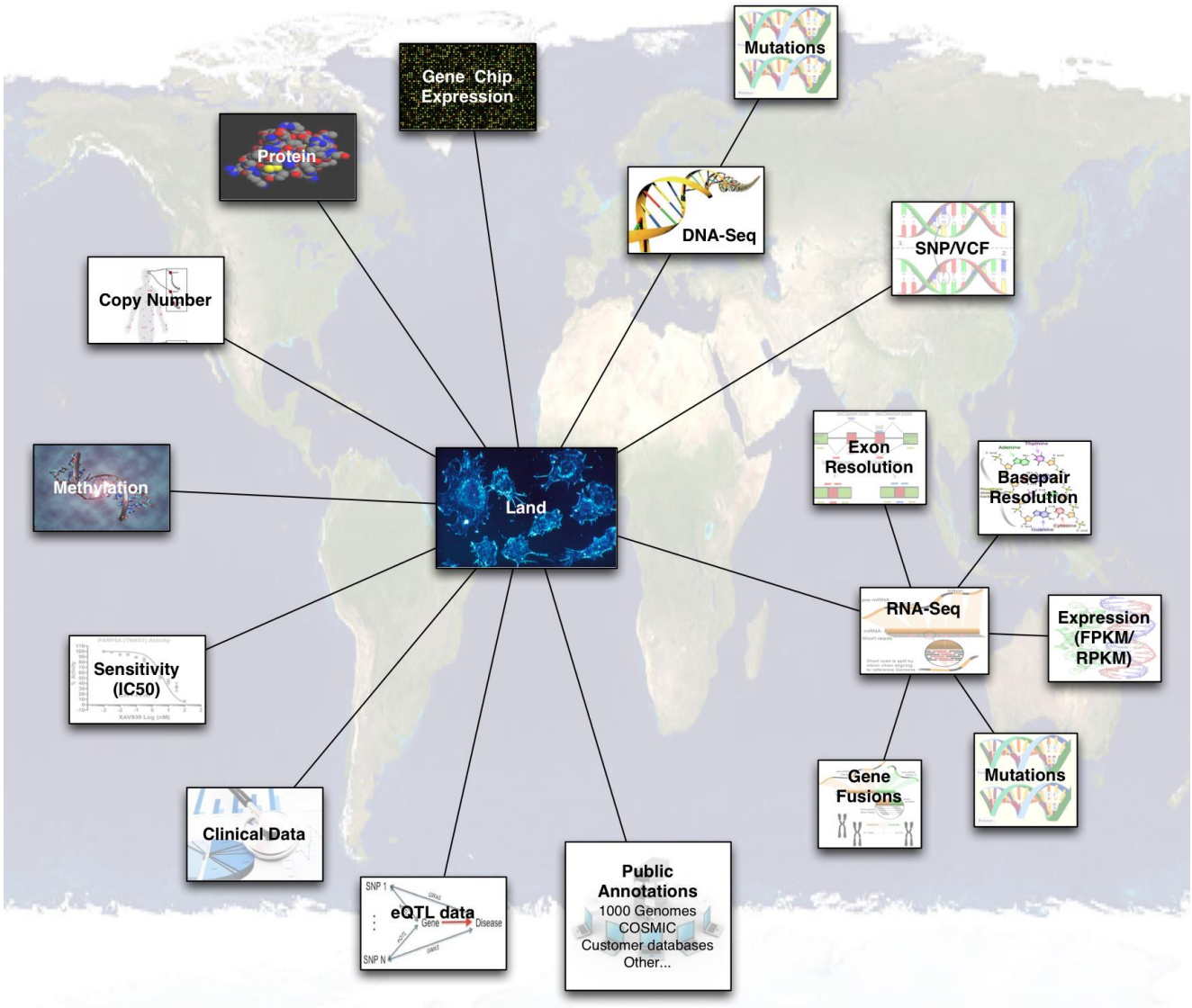
OmicSoft Corporation

Cancer Genomics Database, Bioinformatics, Next Generation Sequencing Data Solutions

ONCOLAND: INCORPORATING LARGE SCALE PUBLIC AND PRIVATE CANCER DATASETS

OncoLand is an Oncology database and visualization software that helps users explore public and private cancer genomics datasets using its "Land" technology, allowing researches to more readily power their research.

OncoLand is Omicsoft's flagship "Land". The "Land" technology is a next generation OMIC database storing genomics data in database files and different layers of indexes for genes/markers and samples. It is a revolutionary google-like storage for vector data. The goal of the Land technology is to provide fast data access for both samples and genes. OmicSoft uses the Land framework to deliver an increasing number of large datasets. Data types include: RNA-Seq, DNA-Seq, miRNA-Seq, Copy Number Variation, Gene Expression Chip, Protein Expression, Methylation and hundreds of clinical measurements.



Visit our OncoLand webpage http://www.omicsoft.com/oncoland-service/ and get a customized FREE trial. Or contact us at sales@omicsoft.com with any question.

Cancer Genomics Database, Bioinformatics, Next Generation Sequencing Data Solutions

- **Comprehensive:** Sample-centric view of genomics data and clinical data from multiple platforms

  More than 10 large public dataset Lands, including TCGA, CCLE, CGCI, ICGC, TARGET, Multiple Myeloma, GTEx, Blueprint and more.

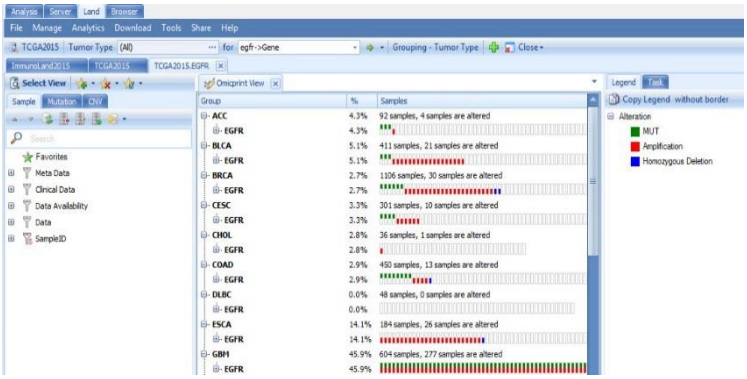
  More than 10 major genomic data types and hundreds of clinical measures
- **Controlled:** Standardized pipeline to process data and controlled vocabulary for clinical data
- **Integrated:** Integration with internal private datasets

  Integrate across public datasets (i.e GTEx vs TCGA)
- **Powerful:** Extended analytical capacity powered by Array Studio, Omicsoft's flagship product

  Built-in Genome Browser
- **Secured:** Trusted by increasing number of users from major pharma and biotech companies

Signature Land

- TCGA: The Cancer Genome Atlas is a comprehensive and coordinated effort to accelerate the understanding of the molecular basis of cancer through the application of genome analysis technologies. Led by National Cancer Institute (NCI) and National Human Genome Research Institute (NHGRI), TCGA currently includes more than 30 cancer diseases with more than 67,000 samples across 7 data types



DNA Alteration OmicPrint OmicPrint shows alteration (mutation and amplification/deletion) status across multiple genes, organized by tumor type, histologies, or any user-defined category.

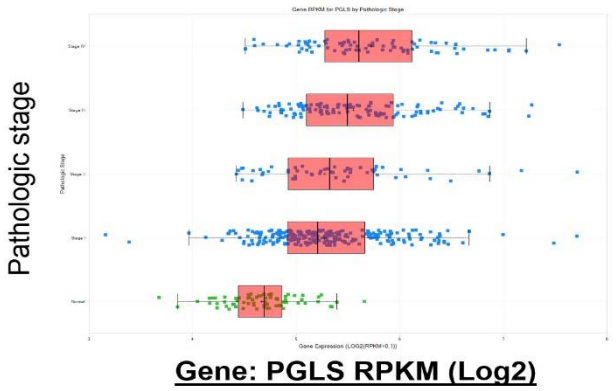
Example Questions

- Correlate mutation status to expression
- List top gene fusions in disease/study
- Detect exact fusion breakpoints for gene fusions
- Create cohorts and correlate to copy number, expression, and more.
- Expression pattern of gene of interest (RNA-Seq or chip-based)
- Mutation patterns or distributions (RNA or DNA level)
- Integrate Copy Number and Expression data
- Co-mutation frequencies
- Compare normal tissue distribution to tumor or cell line distribution

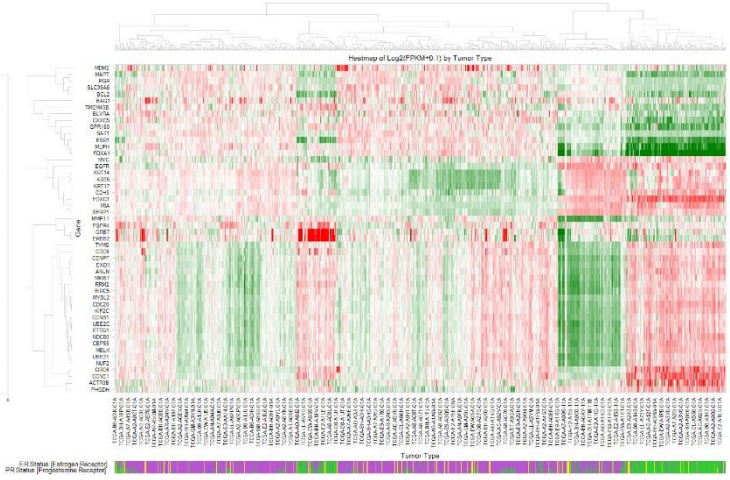
Integration of Copy Number and Expression (RNA-Seq) Plots for integration of copy number data and expression (chip-baesd or RNA-Seq), colored by tumor type, histologies, or any user-defined category.

Visit our OncoLand webpage http://www.omicsoft.com/oncoland-service/ and get a customized FREE trial. Or contact us at sales@omicsoft.com with any question.

Cancer Genomics Database, Bioinformatics, Next Generation Sequencing Data Solutions



Gene expression and pathologic stages in KIRC
Samples from high stage renal cell carcinoma show evidence of metabolic shift, for instance, up-regulation of the pentose phosphate pathway genes (e.g. PGLS)



PAM50 Breast Cancer Heatmap Visualization of the "PAM50" breast cancer genes in TCGA

Key Views	OncoLand
DNA-Seq and RNA-Seq Mutation	All Mutation Distribution and Landscape Somatic Mutation Distribution and Landscape Mutation Browser
RNA-Seq Quantification	Gene FPKM Transcript FPKM Genome Browser Exon Details Heatmap (Multiple Genes Search) Multigene Correlation (Multiple Genes Search) Exon Junction
RNA-Seq Fusion	Fusion Site, RPKM,Frequency and Browser Paired End Fusion
Expression	Summary of up- /down-regulation Expression Ratio
Protein	RPPA
Copy Number	Copy Number Log2 Ratio and Browser
Methylation	Methylation Beta Value
Integration Analysis	Mutation, CNV, Gene Expression, Protein Expression Two Way Association
Others	Clinical Data Survival Data Gene Annotation

Visit our OncoLand webpage http://www.omicsoft.com/oncoland-service/ and get a customized FREE trial. Or contact us at sales@omicsoft.com about any question.