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http://www.virtualplant.org

VirtualPlant enables biologists to mine lists of genes, microarray experiments, next-generation sequencing data and gene networks to address biology's grand challenge questions. VirtualPlant achieves this by enabling researchers to integrate, analyze, and visualize genomic data in a systems biology context. VirtualPlant simplifies data analysis by integrating the tools into a single platform. The unique "gene cart" functionality enables iterative data analysis and suggest additional more functional to the single size of the rounds of experimentation.

Please see the following manuscript for details and example case studies: Katari et al. "VirtualPlant: a software platform to support systems biology research." Plant Physiol. 2010 Feb;152(2):500-15.



Tair 10 and other versions: The Arabidopsis annotation has been updated to Tair 10. A feature in the gene cart allows users to convert their gene lists from an older version of Tair to the newer version



Multi-Species: VirtualPlant can support any number of species or ecotypes. Rice is already available and we are in the process of supporting more sequenced plant

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Comparative Analysis: Currently users can align their sequencing using Blast to identify putative orthologs based on top match. Other methods and databases will be supported in the near future.

VirtualPlant 1.0.0.8 Bl Please enter the sequence or sequences below FASTA ONCBI Accession ONCBI GI d a file with the sec Browse... E-value cutoff e -s all 🗘 h ALIGN

COMING SOON

ECOTYPES METAGENOMICS

VirtualPlant Development Team attending the meeting: Email: virtualplant-discuss@googlegroups.com



Biomaps: The gene set enrichment tool, now has an interactive graph written in Flash with the ability to save the GO-heirarchy image as a high quality figure.



GeneSect: A new tool that uses non-parametric randomization test to determine whether overlap between two gene sets are significant.



Genesect: Z-score (number of standard deviations)

	A: ATGE7 (286)	B: ATGE8 (289)	<u>C:</u> ATGE8 (178)	D: ATGE8 (99)	
A: ATGE7 (286)		<u>32.1</u>	20.4	<u>1.6</u>	Overrepresented
B: ATGE8 (289)			6.0	24.7	Green: Z-score >5
<u>C:</u> <u>ATGE8</u> (178)				<u>1.5</u>	Red: Z-score <5
<u>D:</u> <u>ATGE8</u> (99)					

RNA-seq: A new tool is being developed where users can submit the read counts for each gene in the genome and then use tools such as edgeR to determine differentially expressed genes

upload a file that contains counts of reads matching a gene. Each column is a different sample and each row is a gene. The alues are the amount of reads matching each gene per sample. Please do not normalize the data before uploading. The ex data will be seed in your cart as an ma-seq exertioner, which will allow you to run future analysis.

Step 1 of 2: Name and Describe the Experiment						
Name:	RNA-SEQ EXPERIMENT					
Description:	DIFFERENTIAL GENE EXPRESSION DETERMINED USING DESEQ					

Browse... Continue to Step 2 >>