Mining Transcriptomics Data
Genes up-regulated in mosquito tissues during Wolbachia infection

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Learning objectives
- Review the types of expression searches in VEuPathDB
- Run a direct comparison search in a microarray dataset

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Introduction

Wolbachia pipientis is a maternally inherited intracellular bacterium that is found in a wide range of arthropod species. It induces diverse reproductive abnormalities in its hosts. The virulent *Wolbachia* strain wMelPop has been introduced into the Dengue virus mosquito vector, *Aedes aegypti*, as a strategy to reduce disease transmission by shortening mosquito lifespan.

wMelPop grows to high densities particularly in the brain but also in the somatic tissues of its mosquito host. In this exercise, the goal is to find *Aedes aegypti* genes that are up-regulated in both head and muscle during infection with Wolbachia. Additionally, we want to determine possible functions shared by these genes.

The VEuPathDB VectorBase has data and informatics resources for vectors of human pathogens, including Aedes, Anopheles, Culex, Glossina, Ixodes, etc. VectorBase has a microarray data set that compares Wolbachia infected and uninfected mosquito head and muscle.

1. Navigate to VectorBase.org[1]

2. From the sidebar or header, search for "microarray" and click on Microarray Evidence
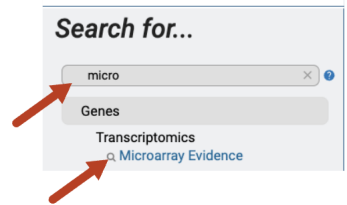
3. Identify the appropriate dataset titled 'Infection with a Virulent Strain of Wolbachia Disrupts Genome Wide-Patterns of Cytosine Methylation in the Mosquito Aedes aegypti (Ye et al.)' For this experiment, choose the Direct Comparison search.
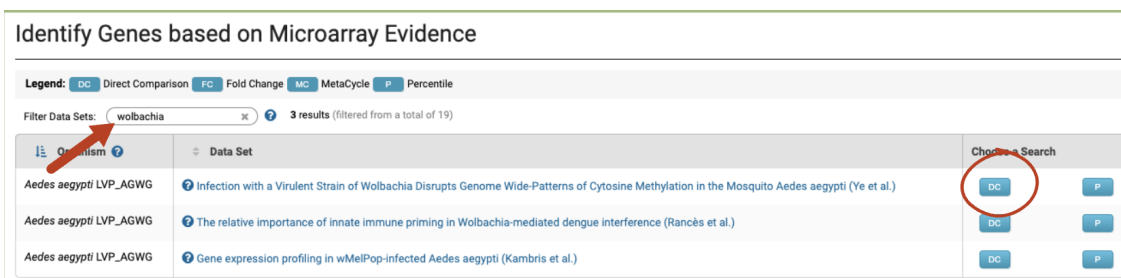

4. Configure the search to return genes that are up-regulated 2-fold in infected head vs. uninfected. How many genes did you get?

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[1] Note that this exercise uses VectorBase.org as an example database, but the same functionality is available on all VEuPathDB resources where this type of data is present.

5. Add a step to your search strategy to intersect with genes up-regulated in muscle
    a. Intersect your search result with another search that returns genes up-regulated 2 fold in infected muscle vs. uninfected. Your combined result will be genes that are up-regulated in both head and muscle in response to Wolbachia infection.
    b. How many genes did you get that are upregulated in both head and muscle in response to Wolbachia infection?
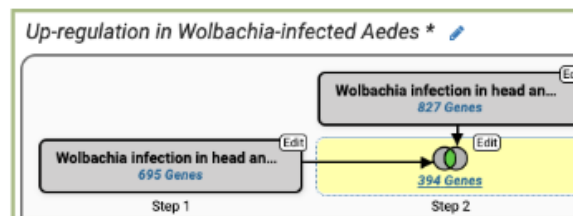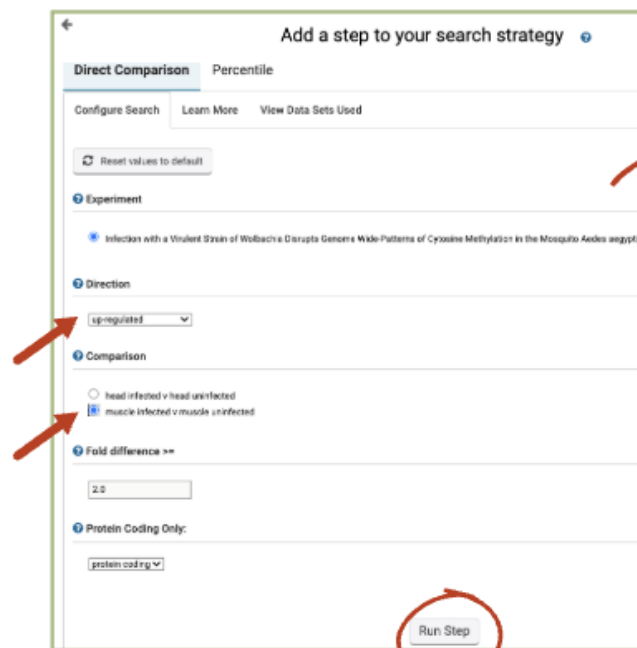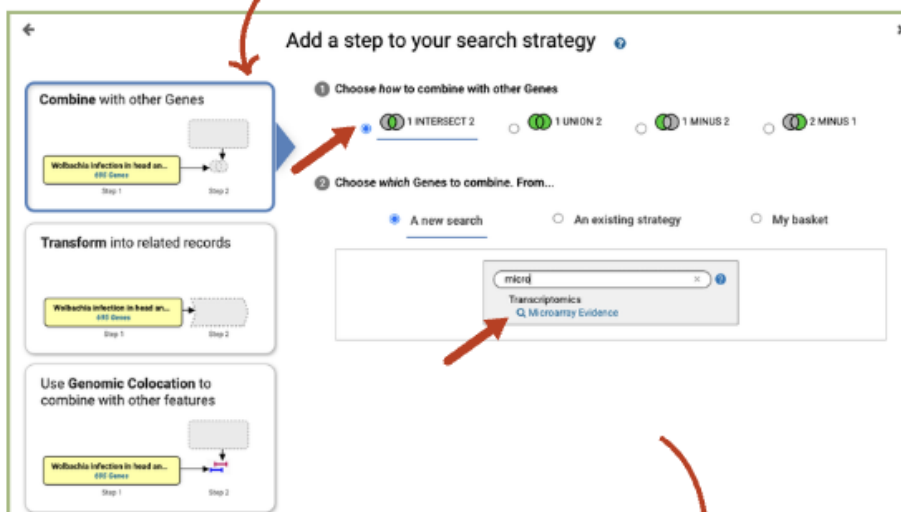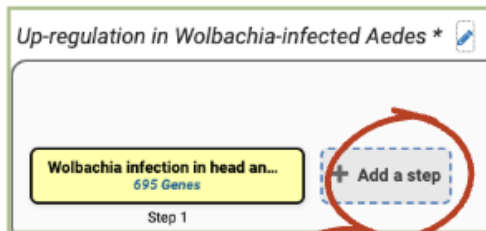
6. Explore the molecular functions of the up-regulated genes. Determine enriched Molecular Function Gene Ontology (GO) terms for the upregulated genes. Make sure you are viewing the combined result (the Step 2 result will be highlighted in yellow) and click Analyze Result to open the Enrichment Tool.

What gene functions are shared by the combined result? What biological role can you envision for these mosquito genes during the *Wolbachia* infection?

GO ID	GO Term	Genes in the bkgd with this term	Genes in your result with this term	Percent of bkgd genes in your result	Fold enrichment	Odds ratio	P-value	Benjamini	Bonferroni
GO:0003824	catalytic activity	3624	162	4.5	1.62	2.38	9.32e-14	1.57e-11	3.32e-11
GO:0008233	peptidase activity	647	54	8.3	3.03	3.69	1.38e-13	1.57e-11	4.93e-11
GO:0016787	hydrolase activity	1527	91	6.0	2.16	2.76	1.47e-13	1.57e-11	5.24e-11
GO:0004175	endopeptidase activity	473	45	9.5	3.45	4.17	2.06e-13	1.57e-11	7.42e-11
GO:0004252	serine-type endopeptidase activity	346	38	11.0	3.98	4.83	2.21e-13	1.57e-11	7.87e-11
GO:0008236	serine-type peptidase	372	39	10.5	3.80	4.59	4.66e-13	2.37e-11	1.66e-10