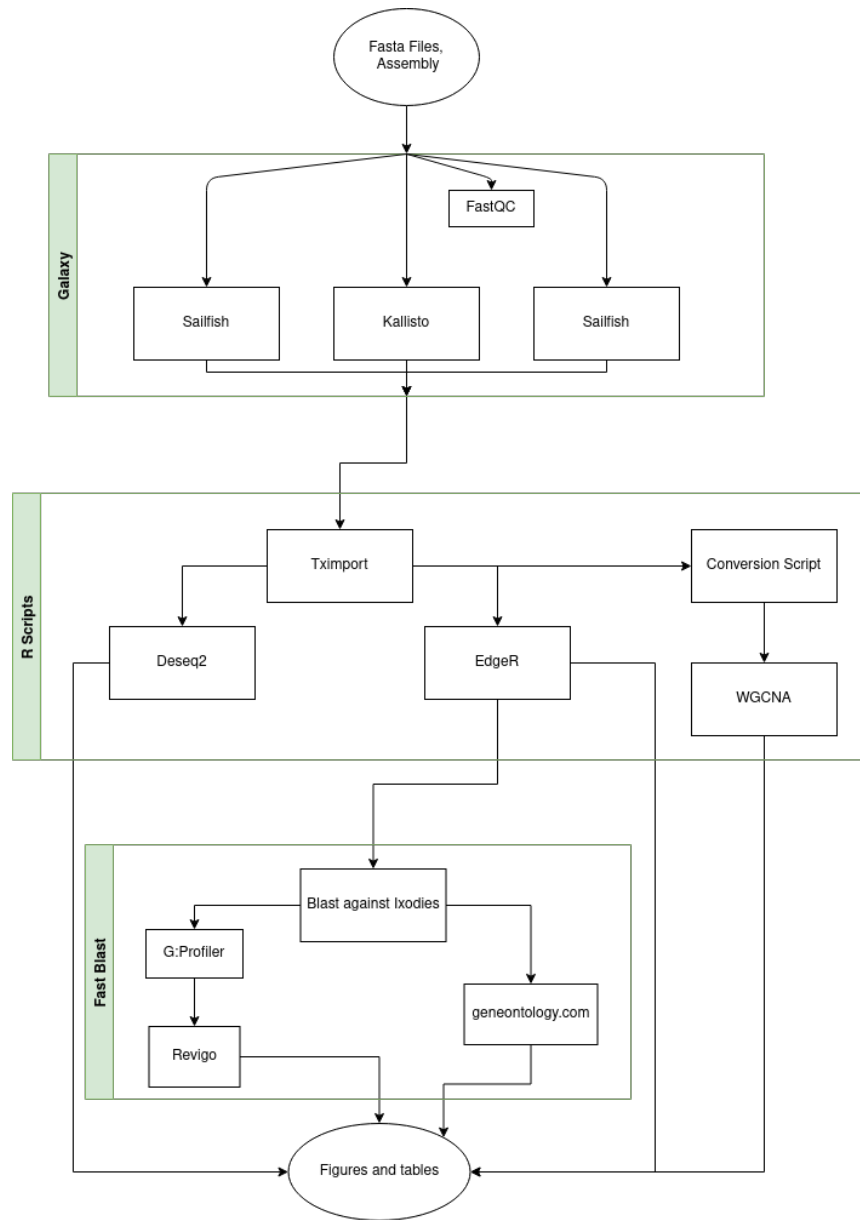


Contents

1	Abstract	2
2	Introduction	2
3	Methods	2
3.1	Transcriptomic Workflow Overview	3
3.1.1	Quantification	3
3.2	Differential expression analysis	4
3.3	WGCNA	4
3.4	GO analysis	4
3.4.1	Blast	4
3.4.2	GProfiler	4
3.4.3	Revigo	4
3.4.4	Geneontology.org	4
4	Results	4
4.1	Figure 1: methods comparison between EdgeR and Deseq2 . .	5
4.2	Figure 2: Perm and Deet repellency and survival	5
4.3	Figure 3: Leg vs Body general (control)	5
4.3.1	TODO supplemental tables	6
4.4	Figure 4: Leg vs Body Specifics overlap with Ixodies	6
4.5	Figure 5:Response to DEET In Leg and Body	6
4.5.1	Body	7
4.5.2	Leg	7
4.5.3	TODO supplemental tables	7
4.6	Figure 6: Response to PERM in Leg and Body	8
4.6.1	Body	8
4.6.2	Leg	8
4.6.3	TODO supplemental tables	9
4.7	Figure 7: WGCNA	9
4.8	Figure 8: Overlap Between the response, body and leg	9
4.9	Figure 9: Time Course Legs	9
4.9.1	DEET	9
4.9.2	PERM	10
4.10	Figure 10: Time Course Body	10
4.10.1	DEET	11
4.10.2	PERM	12

5	Discussion	12
1	Abstract	
2	Introduction	
3	Methods	

3.1 Transcriptomic Workflow Overview



3.1.1 Quantification

The Raw high-throughput RNA-sequencing data from each trial were saved as individual FASTQ files. The FASTQ files were uploaded to the Galaxy

platform (usegalaxy.org) where the quantification occurred. First, Galaxy's 'FastQC' tool was used to determine the quality of the raw data and to mitigate the effects of amplification bias (**insert settings here**). The Kmer test within 'FastQC' was enabled and set at a length of 7bp. Following this initial quality-check, the raw files were trimmed with 'Trimmomatic' using its default settings (**description**). FastQC was run on the trimmed files to confirm its quality.

After the data was trimmed, transcript abundance quantification was performed by the Galaxy's 'Sailfish quant' tool using the default settings (**description**).

3.2 Differential expression analysis

DESeq2(**Reference**) and EdgeR(**Reference**) were used to test for differential expression between the legs, body, and pesticide treatment (Deet and Perm). The differential analysis becomes more reliable when the results of the similar tools are compared.

3.3 WGCNA

3.4 GO analysis

3.4.1 Blast

3.4.2 GProfiler

functional enrichment analysis. The output from Blast is sent to GProfiler. The GProfiler output is sent to revigo.

3.4.3 Revigo

The R script output of Revigo generates tree-maps of the genes.

3.4.4 Geneontology.org

The output of blast is sent to Geneontology.org

4 Results

4.1 Figure 1: methods comparison between EdgeR and Deseq2

This figure compares the expression data that is present in both EdgeR and Deseq2. The P value is small, indicating that EdgeR and Deseq2 have similar results.

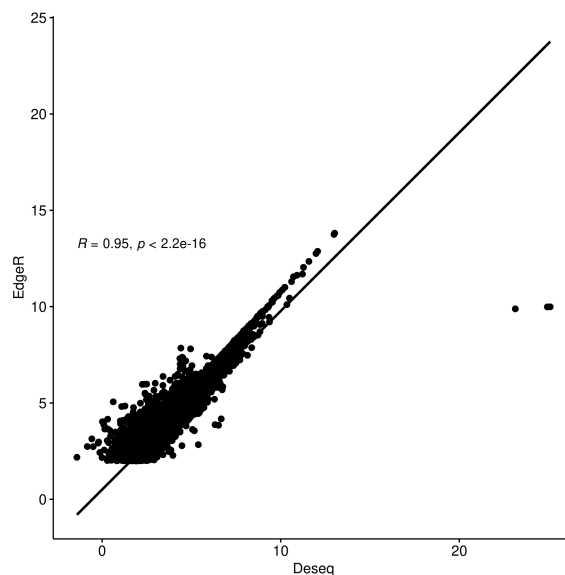


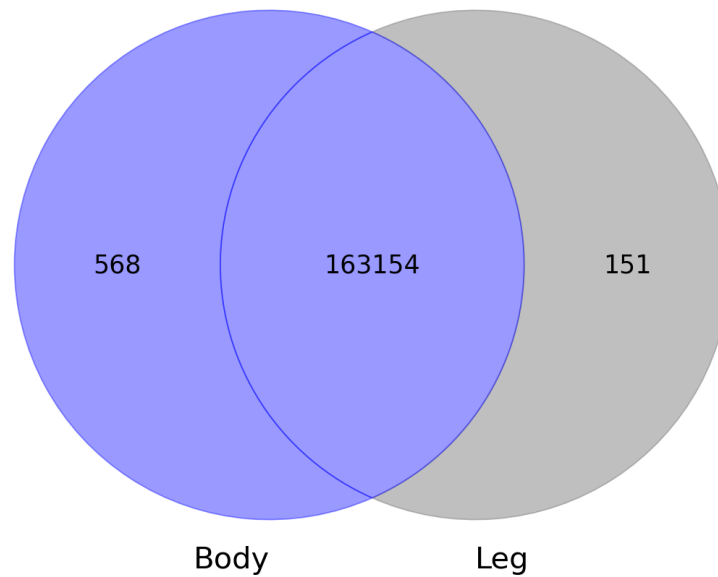
Figure 1: The quantification files were run through both EdgeR and Deseq2. Each axis plots the expression values as given by its respective title.

4.2 Figure 2: Perm and Deet repellency and survival

4.3 Figure 3: Leg vs Body general (control)

This figure compares the genes up-regulated in the body and leg compared to the total number of genes from the sample.

Leg vs Body



4.3.1 TODO supplemental tables

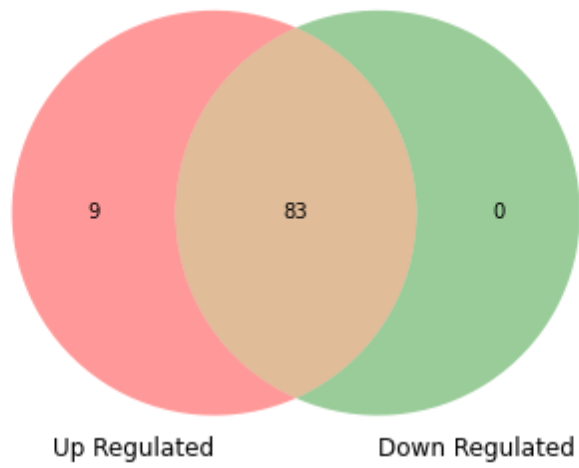
4.4 Figure 4: Leg vs Body Specifics overlap with Ixodies

Refer to paper in google drive. Discussion.

4.5 Figure 5: Response to DEET In Leg and Body

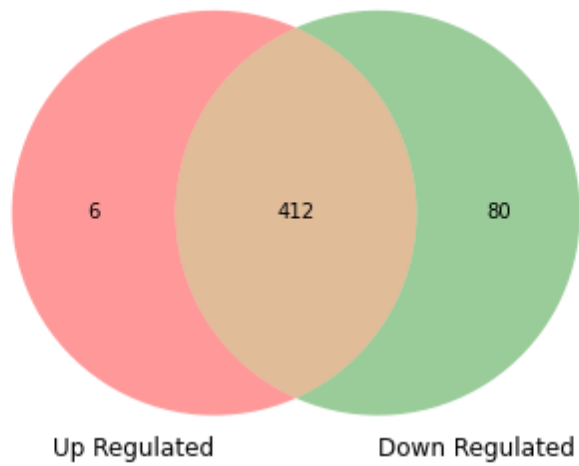
4.5.1 Body

Deet Expression in Body Genes



4.5.2 Leg

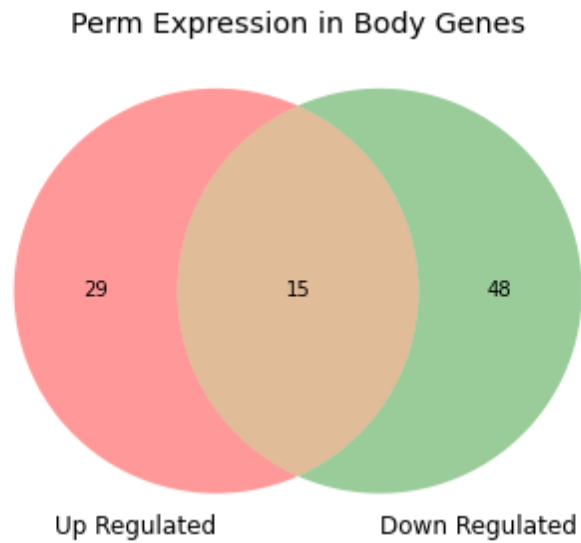
Deet Expression in Leg Genes



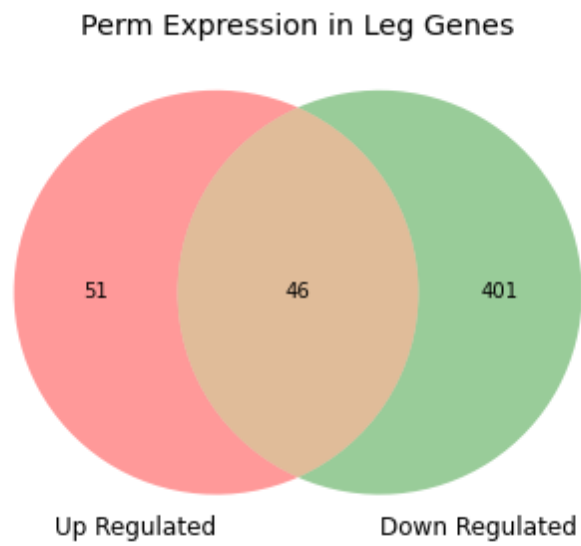
4.5.3 TODO supplemental tables

4.6 Figure 6: Response to PERM in Leg and Body

4.6.1 Body



4.6.2 Leg



4.6.3 TODO supplemental tables

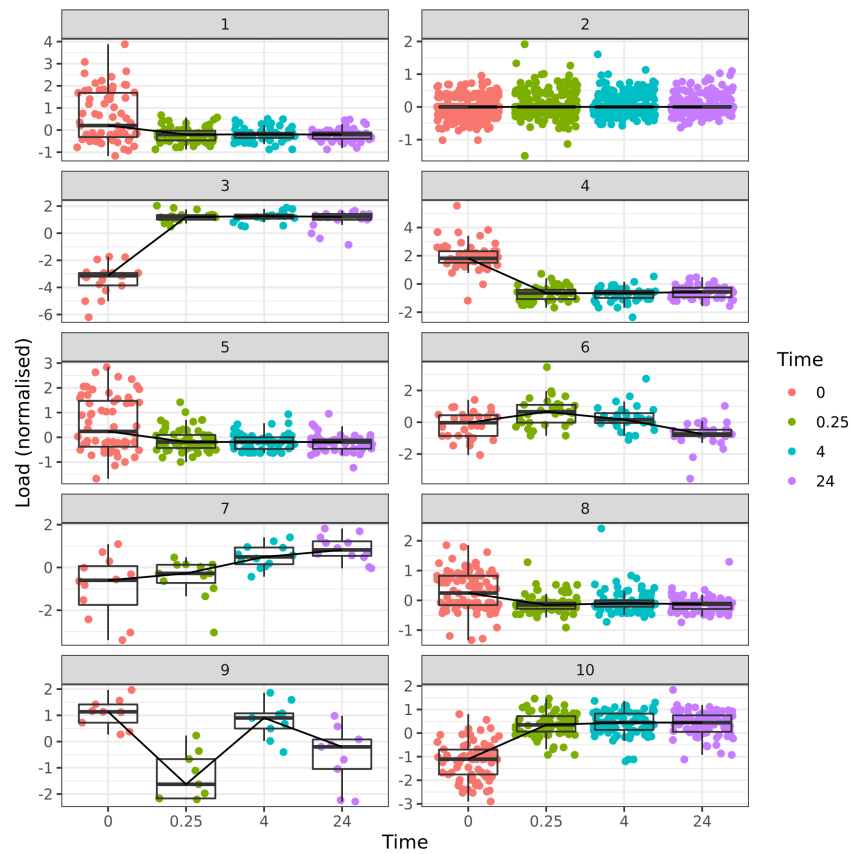
4.7 Figure 7: WGCNA

4.8 Figure 8: Overlap Between the response, body and leg

Don't think we need it now.

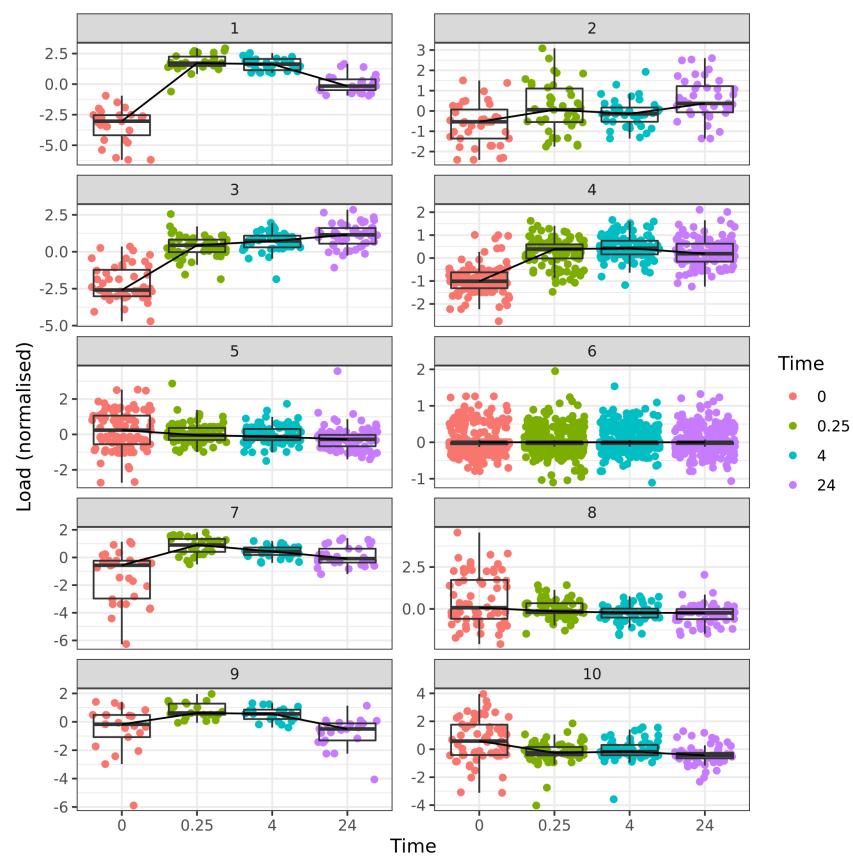
4.9 Figure 9: Time Course Legs

4.9.1 DEET



1. Supplemental Tables figure9/DEET/Legbox

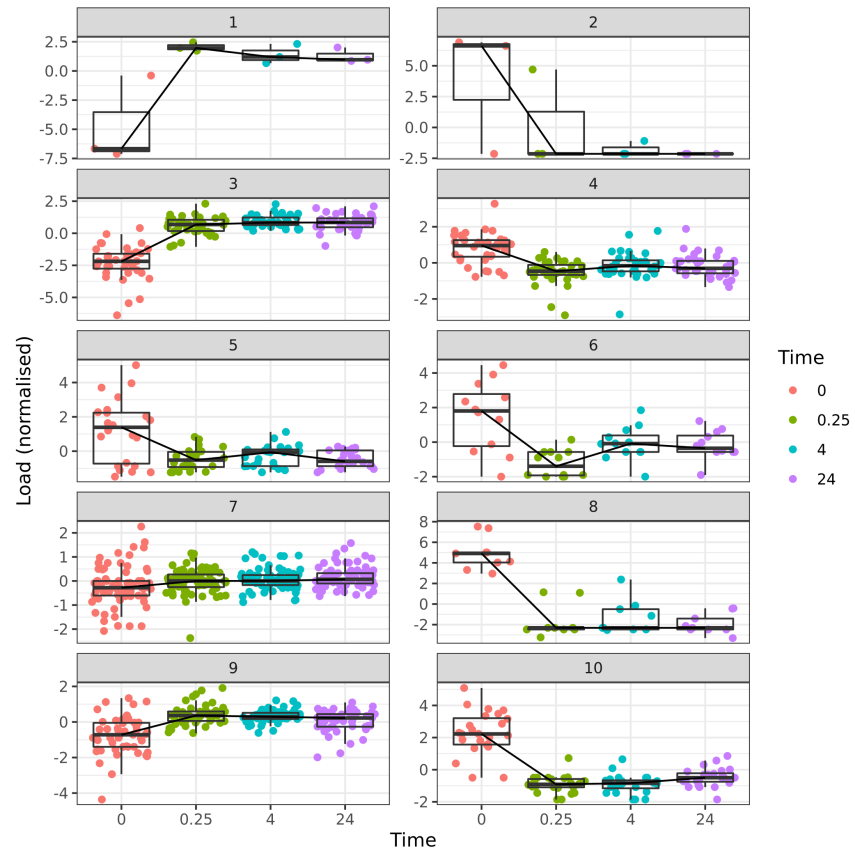
4.9.2 PERM



1. Supplemental Tables figure9/PERM/Legbox

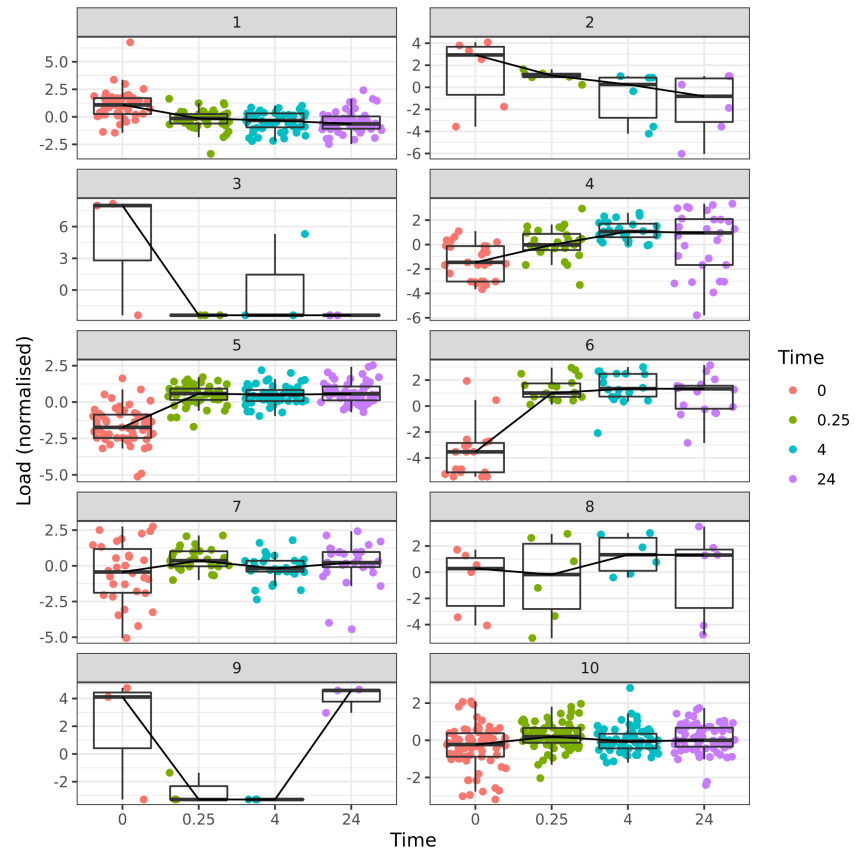
4.10 Figure 10: Time Course Body

4.10.1 DEET



1. Supplemental Tables [figure10/DEET/Bodybox/](#)

4.10.2 PERM



1. Supplemental Tables [figure10/PERM/Bodybox/](#)

5 Discussion