**01/22/18 Botrydial**

**Dan:**

Do GWAS on the Botrydial cluster and the Arabidopsis genes that show co-expression with these transcripts? This would give us a network view on GWAS but also have a defined potential for cause/effect relationships. i.e. Botrrydial may cause the Arabidopsis transcript?

What do you think?

If you like it, do you have a list of Arabidopsis transcripts that show co-expression with two or more genes in the Bot cluster?

**Wei:**

 I went though the At-Bc networks across three plant genotypes and did found some Arabidopsis transcripts that highly correlated with the botrydial transcripts.

However, we have two sets of At-Bc interaction networks, one is with "0" expressed Botrytis transcripts and one is without "0" expressed Botrytis genes. The At-Bc net that without the "0" expression were shrunk with less Arabidopsis genes that correlated botrydial transcripts. The question is which sets of genes you would like to use for GWAS?

**Dan:**

Without 0 was taking Botrytis transcripts that had 0 in any isolate or in X number of isolates?

**Wei:**

Please see the attached file for the Arabidopsis gene lists. I showed you both the correlation results that one is after the removal of the low expressed Botrytis transcripts and one is before removal of the low expressed Botrytis transcripts.

In NES PC C:\Users\nesoltis\Documents\Projects\BcAt\_RNAGWAS\data\Vivian\_Bc\botryNets\ BotrydialCorrelatedAtGeneList.xlsx

**01/23/18**

**Wei:**

Please see the attached files for the z-scores of the top Botrytis networks in Col-0 background.

In NES PC folder C:\Users\nesoltis\Documents\Projects\BcAt\_RNAGWAS\data\Vivian\_Bc\topNets\regwa.zip

I first pull the Botrytis transcripts condensed in each network from the Least Square Mean table. Here I used the least square mean table including all Bc transcripts but fixed the negative expressed values with "0". Then, I used the function "scale(x, center = TRUE, scale = TRUE)" from the R {base}. If any questions about the z-scaled method please let me know.

Further, if you guys need more details about these top networks and the nodes, just tell me. I am currently working on the manuscript for this part and will update A.S.A.P.

**Dan:**

So you z-scaled each transcript first and then averaged across the transcripts?

What happens if you use these pathway Z-scores to try and find co-expressed Arabidopsis genes?

**Wei:**

I am a little confused about your two questions.

I would like to clear that I used the LSmean of each Botrytis transcript derived from the nbGLM model rto conduct the spearman correlation analysis. Then the correlations were used to construct the Bc network.

For Z-scaled expressions of those networks, do you mean I should use raw gene counts data for those genes condensed in the network to run a z-scale? I am sorry I am lost.