

I have extracted graphlets for all 23 chromosomes from the contact maps, using ice normalization and I have thresholded it (test.py). I then separated individual orbitals from each cell category and put them together. That is, I have put orbital 0 from MIT, ALL, RL and CALL4 together and put them in a file. Then I did the same for orbital 1 and put them in a separate file and so forth. I then ran MINE.jar for each file and captured pairwise MIC values for each orbital. By doing so, the result would have a dataset of the following shape:

Cell 1	Cell 2	Orbital	MIC value
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My plan was to find a significance of pair-wise MIC values for example, using a null hypothesis of $H_0 : MIC_{MIT-ALL} = 0$. This would mean That MIT-ALL are totally independent of each other. However, What we are trying to prove is that they are not the same, which is different. Actually I have to test this null hypothesis:

$$H_0 : MIC_{MIT-ALL} = 1$$

which if cannot be rejected, means that the two sets of MIT and ALL are similar to each other.

In order to validate my method, I have to be able to compare the two normal cell data that I have, namely, MIT and the one from Rao et. al. I have to be able to get a high value between the two.