TSI Manual

The tau index indicates how specific or broadly expressed a gene or transcript is, within studied tissues. The index τ is defined as:

$$\tau = \frac{\sum_{i=1}^{N} (1-x_i)}{N-1}$$

Where, *N* is the number of tissues and *xi* is the expression profile component normalized by the maximal component value (Yanai et al., 2005)

The values of tau vary from 0 to 1: Ubiquitous or broad expr ($\tau \le 0.5$) Intermediate expr ($0.5 < \tau < 0.9$) Tissue-specific or narrow expr ($\tau \ge 0.9$)

TSI calculator allows user to calculate tissue specificity index using normalized expression profile of genes.

Users can follow the following steps to get the TSI table.

1. Input data:

First click on 'choose file' to choose the CSV file of expression value. Browse the file from your system and open it.



You can also use 'example file' to RUN the TSI calculation. Click on 'click here for the example file' to download the example file.

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TSI: Tissue Specificity Index								
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	The tissue specificity index is a measure of the relative used to identify genes that are highly expressed in a sp the roles of the genes involved. The tissue specificity tissue to its expression in all other tissues in a given dat tissue-specific and may be involved in tissue-specific fu have a more universal role. The tissue specificity index functions	$\leftarrow \rightarrow \checkmark \uparrow \blacksquare >$ This PC $\checkmark \eth$ \bigcirc Search This PC						
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Save the file in your system. Then chose this file to run TSI calculation.

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An example .csv file used for calculation of TSI calculation



2. Run the TSI calculation:

After choosing the file Click 'submit' button to submit your file and run the analysis.



3. Get the results

Results will appear on screen after TSI calculation at server.



4. Download the results

Results can be downloaded by clicking on 'click here for the results file' at the bottom.

click here for the result file			
- <u>Home</u> -			
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Results will be downloaded in .txt file format

S.No.	gene_ID_TSI	
1	CB_1nc_0001	0.43777632225315
2	CB_1nc_0006	0.90412517780939
3	CB_1nc_0010	0.74226804123711
4	CB_1nc_0011	0.47204641350211
5	CB_1nc_0012	0.92444963308873
6	CB_1nc_0013	0.98905584300795
7	CB_1nc_0014	0.34943538268507
8	CB_1nc_0015	0.9275515683735
9	CB_1nc_0018	0.97208524128214
10	CB_1nc_0032	0.4422619047619
11	CB_1nc_0038	0.46575342465753
12	CB_1nc_0039	0.12561174551387
13	CB_1nc_0040	0.7057761732852
14	CB_1nc_0043	0.87893291486858
15	CB_1nc_0045	0.43635170603675
16	CB_1nc_0048	0.54134725167183
17	CB_1nc_0054	0.58164414414414
18	CB_1nc_0062	0.52152641878669
19	CB_1nc_0063	0.5010101010101
20	CB_1nc_0065	0.18057663125948
21	CB_1nc_0066	0.69026104417671
22	CB_1nc_0071	0.46449976947902
23	CB_1nc_0072	0.60856864654333
24	CB_1nc_0073	0.44842406876791

5. Going back to home

Click at 'Home' to get back to home page



References:

Yanai, I., Benjamin, H., Shmoish, M., Chalifa-Caspi, V., Shklar, M., Ophir, R. & Shmueli, O. (2005). Genome-wide midrange transcription profiles reveal expression level relationships in human tissue specification. *Bioinformatics*, *21*(5), 650-659.