How to do Pre-ranked GSEA Analysis:

1. Generate a gene list file (Groupx.rnk) with two columns: Gene\_name & Rankdata. Rank was calculated as -log10(pvalue) \* sign(log2FC). You don’t have to sort the genelist.
2. Gene expression file (Groupx.gct) as the following format:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| #1.2 |  |  |  |  |
| 23378 | 3 |  |  |  |
| NAME | DESCRIPTION | S01 | S02 | S03 |
| TSPAN6 | NA | 304.6014 | 731.5352 | 139.2234 |
| DPM1 | NA | 2308.612 | 1857.138 | 521.1297 |
| SCYL3 | NA | 1873.76 | 698.4292 | 1287.497 |

1. Class file (Groupx.cls) as the following format (ensure the first name in row 3 match the first word in row2):

11 2 1

# OSHIGH OSLOW

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Attached cicpt4213prerank.pl could generate both gct and rnk file.