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| **Function Name** | **Function group** | **Task** | **Arguments** | **Analysis step/**  **Position in pipeline** |
| tl\_Shan\_div | tl | Calculate Shannon diversity score for specified cell groups | data, sub\_l, group\_com, per\_categ, rep, sub\_column, normalize=True | Position: 1 |
| pl\_Shan\_div | pl | Plot the output of the Shannon diversity calculation | tt, test\_results, res, group\_com, coloring, sub\_l, output\_dir, save=False, ordering=None, fig\_size=1.5 | Position: 1 |
| pl\_stacked\_bar\_plot | pl | Plot a stacked bar plot of percentage of column variables per group (example: percentage of cell types grouped by sample) | data, per\_cat, grouping, cell\_list, output\_dir,norm=True, save\_name=None, col\_order=None, sub\_col=None, name\_cat = 'Cell Type',fig\_sizing=(8,4), h\_order=None, pal\_color=None,remove\_leg=False | Position: 1 |
| pl\_swarm\_box | pl | Plots a swarm-box plot of column variables per group | data, grouping, replicate, sub\_col, sub\_list, per\_cat, output\_dir, norm=True, figure\_sizing=(10,5), save\_name=None, h\_order=None, col\_in=None, pal\_color=None, flip=False | Position: 1 |
| pl\_cell\_type\_composition\_vis | pl | Plots three different visualizations of cell type composition per sample:   1. Stacked bar plot of absolute counts 2. Absolute counts as side-by-side bar plots 3. Stacked bar plots of percentage | data, sample\_column = "sample", cell\_type\_column = "Cell Type", output\_dir = None | Position: 1 |
| tl\_neighborhood\_analysis\_2 | tl | Calculates neighborhoods and adds a column called neighborhoods\_k to the original data frame. The added column indicates for each cell the respective neighborhood by a number between 0 and n\_neighborhoods | data, values, sum\_cols, X = 'x', Y = 'y', reg = 'unique\_region', cluster\_col = 'Cell Type', k = 35, n\_neighborhoods = 30, calc\_silhouette\_score = False | Position: 1 |
| pl\_neighborhood\_analysis\_2 | pl | Plots spatial plots of newly assigned neighborhoods for every region. Additionally, a heatmap is generated that shows which cell types are enriched in which neighborhood | data, k\_centroids, values, sum\_cols, X = 'x', Y = 'y', reg = 'unique\_region', output\_dir = None, k = 35, plot\_specific\_neighborhoods = None | Position: 2 |
| tl\_cell\_types\_de | tl | Generate matrix (neighborhood x cell type) of enrichment values as well as a matrix (same shape) with p- values for every result. | ct\_freq, all\_freqs, neighborhood\_num, nbs, patients, group, cells, cells1 | Position: 2 |
| pl\_cell\_types\_de | pl | Visualizes DE results as heatmap | dat, pvals, neigh\_num, output\_dir | Position: 2 |
| tl\_community\_analysis\_2 | tl | Calculates Communities and adds a column called communities\_k to the original data frame. The added column indicates for each cell the respective neighborhood by a number between 0 and n\_communities | data, values, sum\_cols, X = 'x', Y = 'y', reg = 'unique\_region', cluster\_col = 'neigh\_name', k = 100, n\_neighborhoods = 30 | Position: 2 |
| pl\_community\_analysis\_2 | pl | Plots spatial plots of newly assigned communities for every region. Additionally, a heatmap is generated that shows which neighborhoods are enriched in which community | data = cells\_df2, values = values, sum\_cols = sum\_cols, output\_dir = output\_dir, X = X, Y = Y, reg = reg, save\_path = None, k = k\_commun, neighborhood\_name = neighborhood\_name, k\_centroids = k\_centroids, plot\_specific\_community = None | Position: 3 |
| tl\_Perform\_CCA | tl |  | cca, n\_perms, nsctf, cns, subsets, group | Position: 2 |
| pl\_Visulize\_CCA\_results | pl |  | CCA\_results, save\_path, save\_fig = False, p\_thresh = 0.1, save\_name = "CCA\_vis.png", colors = None | Position: 2 |
| tl\_build\_tensors | tl |  | df, group, cns, cts, counts | Position: 2 |
| pl\_plot\_modules\_heatmap | pl |  | dat, cns, cts, figsize = (20,5), num\_tissue\_modules = 2, num\_cn\_modules = 5 | Position: 2 |
| pl\_plot\_modules\_graphical | pl |  | dat, cts, cns, num\_tissue\_modules = 2, num\_cn\_modules = 4, scale = 0.4, figsize = (1.5, 0.8), pal=None,save\_name=None, save\_path = None | Position: 2 |
| pl\_evaluate\_ranks | pl |  | dat, num\_tissue\_modules = 2 |  |

Legend:

* Position: 1; Unmodified df | 2; Neighborhoods calculated | 3; Communities calculated