**Decosus Summary**

**Title:** Decosus consolidates the results of 7 independently published deconvolution softwares to generate a robust estimation of cell composition in heterogenous tissue from bulk expression data.

**Description:**

* The inability to identify the phenotype and abundance of cells is a major limitation of bulk expression data sets. Deconvolution methods use gene signatures from purified cell populations to estimate the presence of different cells.
* Decosus combines the results from 7 independent deconvolution methods in order to more accurately estimate the abundance of key immune cells than by using one method alone.
* A unique advantage of Decosus is the ability to adapt the tool to facilitate the type of downstream analyses required, thus two versions of Decosus are possible:
  + **Sample**: includes data from all 7 methods to give the most comprehensive overview of cell composition, and allows across-sample comparison for each cell type.
  + **Cell:** only uses methods which enable estimation of cell proportion, in order to compare the abundance of one cell type to another, as well as across-sample comparison.

**To use:**

* Run array or bulk RNAseq data as a data frame through the tool to generate 3 outputs:
  + Main\_samples for across-sample comparison version of the tool
  + Main\_cells for the within-sample comparison version of the tool
  + Raw\_results for the results of each individual method in one table
* Each of the contributing methods utilises a different combination of cells; when a particular cell type appears in 2 or more of the contributing methods, a consensus for that cell type is generated and this cell is labelled cellname\_consensus in the output tables.
* When a cell type is unique to one of the contributing methods, it is labelled cellname\_methodname.
* All consensus cells and all unique cells for each version are included in the results table, but if needed, irrelevant or non-consensus cells can be removed from the results once generated.
* As the Cells version of the tool uses fewer contributing methods, the main\_cells output table contains fewer cell types than main\_samples.