**Manual**

**Introduction:** An application to run TSA-IT

**Installation:** Download and install the executable

**Usage**:

$ tsa-it [-h] [-f] -i Inputfile -o Outputfile [-m mask] [-w window] [-n] [-b] [-t trials\_file] [-x v1, v2, v3...] [--version]  
**Required arguments:**

-i <INPUT> [INPUT ...], --input <INPUT> [INPUT ...]  
   4D input files on which to compute TSA-IT. These can be of the following format type: NIfTI (. nii or.nii.gz), Analyze (.img), DICOM (.dcm), MINC (.mnc). Mask option is not mandatory if the file type is NIfTI, mandatory in all other cases. All the datatypes (int, float) are also supported.

-o <OUTPUT>, --output <OUTPUT>  
Output directory in which the results will be produced. It produces 6 (4D) files:  p-value (log10 and suitable signs), q-value (log10 and suitable signs), t-value (the t-value for the corresponding statistical test of change from the onset of the trial), z-values (t-values converted to z-values), mean difference from the baseline (percent signal change) and the standard deviation of the differences of the percent signal change from baseline.

-t or -x option (see below for their functionality)  
  
**Optional arguments:**

  -h, --help       Show this help message and exit

  -f, --file         Whether input is to be given as a file or not. If this option is given, then the -i <INPUT> is a file containing the names of input files and -t <trials.txt> is a file containing the list of EV files corresponding to the input files (-x option cannot be used in this case). These files contain multiple runs for the same subject and the trials in these need to be combined to produce the final inter-trial TSA output.

  -m <MASK>, --mask <MASK> NIfTI mask file (3D) for masking input data. If <MASK> is a number then input files are thresholded by that number to produce the mask. If no mask is provided then the entire brain is used for further computations.

  -w begin end, --window begin end  
The arguments begin and end can be integers or floating-point numbers. They are basically the time window (in seconds) from begin to end, relative to the start trials (begin can also be negative, which means that the window starts before the trial; end can also be negative or positive) for which to compute the ITS. The default window size is set to 25 seconds after the end of the task condition, which is the maximum duration for which hemodynamic response function can influence the BOLD signal)

  -n, --normal       Consider a null hypothesis of that the percentage signal change from the baseline is normally distributed with a mean of zero to calculate ITS probabilities (default).  
  -b, --binomial   Consider a null hypothesis of that the percentage signal change from the baseline is binomially distributed with a parameter p=0.5 (i.e., equal chance of the signal change random variable assuming a positive or negative value) to calculate ITS probabilities (default).

  -t <trials.txt>       Path to the location of the trials file (EV file). The file may be in a single column format (consisting of only the onset of the trial blocks) or three column formats (consisting of the onset, duration, and trial amplitude of the trial blocks) of FSL.

  -x v1, v2, ...          A list of volume numbers indicating the beginning of trials. Cannot be used with -t option.

  --version             Show program's version number and exit

**Error Messages:**

* Error and warning messages will be shown to the screen if the input doesn’t conform to the requirements of the tool. Please read them carefully and give the input in the specified format.
* If the trials file (EV file) is neither in 1 column or 3 column formats then an error message will be printed telling you which file is faulty. If the trial file is not at the specified path, then an error message will be shown.
* Please give the input path of only a single file, if more files are specified after the first file, then an error will be shown.
* Specify exactly 2 arguments to provide the window size (if not specified, the default window size of 25 after the end of the trial is used), if more than 2 or less than 2 are specified, an error will be shown.
* All the mandatory input parameters must be specified (the input functional file and the output directory), and one of -t or -x option must be specified, all with their correct paths, otherwise an appropriate error message will be shown.
* The -f option can only be used along with -t option. If -x option is used instead of -t then an error message is shown.
* If -t option is used along with -x option then an error message will be shown.
* If using the -f option, providing a mask is mandatory otherwise an error is shown. If an integer threshold is provided, it is neglected as the thresholded number of voxels will be different for each 4D file, so in this case the entire brain data is used for all the files.
* If the mask is not a 3D file, or the specified path to the mask file is incorrect, then an appropriate error message is shown.
* When -f option is used, if one of the files is not a 4D functional file, and error message will be shown along with the name of the faulty file.
* For the -w option if the start time is greater than the end time then an error message will be shown.
* When using the -f option make sure that the affine of all the 4D images are the same otherwise an error will be shown.
* If -f option is used make sure that you correctly the number of 4D files specified in the input text file is the same as the number of EV files specified in its text file. Otherwise, an error will be shown.

**Output:** The 4D images of statistical test results (t-test, p values, z-values, FDR corrected p-values (q-values), mean, standard deviation.) are generated in the output folder specified in the argument. The results can be viewed using any 4D image viewer e.g., FSL.