McNemar's Analysis of Bovine HD770K SNP Chip Data - test on chromosome 28 SNP only

Case control study of bovine congestive heart failure (BCHF) as described in

Publication: Association of *ARRDC3* and *NFIA* variants with bovine congestive heart failure in feedlot cattle

DOI : XXXXXXXX

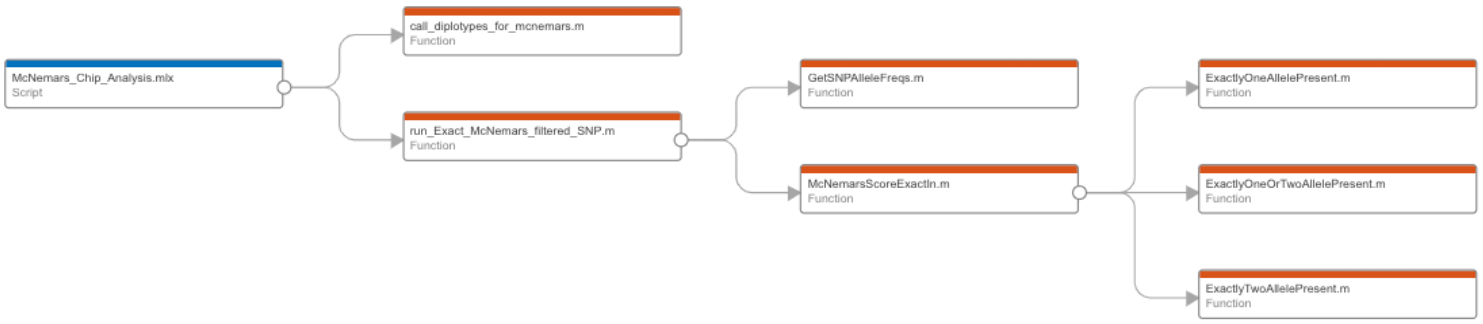
Wrapper script to fire off McNemar's analysis. Assume PLINK files in current directory. Make sure scripts are in the command path.

- This is an example script using SNP for chr28 only, PED and MAP files supplied at GitHub.
- User must supply their own file PED and MAP files for their data.
- For computational efficiency, the PED files must be sorted by animal pair, then by control and case with control preceding the case in each pair in the PED. See GitHub Readme for sed and awk commands to do this.
- Columns 1 - 6 in the PED are coded according to the following data Pair ID, Anim ID, PID, MID, SEX, PHENO. The control was coded with PHENO = 1 and case being coded with PHENO = 2 in column 6 of the PED. The control was and is expected to precede the case animal in every pair.
- The functions use the Parallel Computing and Statistics & Machine Learning Toolboxes.
- **Please add files in functions directory into your Matlab path**

Inputs: PED and MAP files

Outputs: McNemar's analysis in CSV file for each SNP in PED file as well as a binary MATLAB MAT output file.

This script calls multiple custom functions according to the dependency graph below




```
% start the timer
tStartGenome = tic;

plinkMAP = 'BCHF102pairsHD770FFFSortFiltered_extract_chr28.map';
plinkPED = 'BCHF102pairsHD770FFFSortFiltered_extract_chr28.ped';
basename = 'BCHF102pairsHD770FFFSortFiltered_extract_chr28';

% create result file names and workspaces
McNemarsResultsFileName = strcat(basename,'.McNemarsResults.csv');
ChromoWorkSpace = strcat(basename,'.mat');
```

```
% call diplotypes, this is the time consuming step and has been
% parallelized using the Parallel Computing Toolbox within call_diplotypes_for_mcnemars
DiploType = call_diplotypes_for_mcnemars(plinkPED);
```

```
Elapsed time is 35.577431 seconds.
```

```
% run McNemar's
McNemarsResult = run_Exact_McNemars_filtered_SNP(DiploType,plinkMAP,...
    McNemarsResultsFileName);
```

```
Elapsed time is 9.286196 seconds.
```

```
% save workspace to binary file
save(ChromoWorkSpace);

% stop timer
tStopGenome = toc(tStartGenome);
```