

```

(*****Use the Benjamini-Hochberg procedure to generate p-
values that are corrected for multiple comparisons. In this example,
these are 3 groups being compared and this 3 different comparisons
(A vs. B, A vs. C, and B vs. C). Follow the file structure conventions
outlined in ExportDataForSemiWeightedStats1.nb*****)

mainDir = "";

(***Group A vs. Group B vs. Group C***)

pAvsB =
  Import[StringJoin[mainDir, "/SemiweightedStats/GroupAvsGroupB/SemiweightedStruct/",
    "groupAvsGroupB_pValSW.txt"], "List"][[1]];

pAvsC =
  Import[StringJoin[mainDir, "/SemiweightedStats/GroupAvsGroupC/SemiweightedStruct/",
    "groupAvsGroupC_pValSW.txt"], "List"][[1]];

pBvsC =
  Import[StringJoin[mainDir, "/SemiweightedStats/GroupBvsGroupC/SemiweightedStruct/",
    "groupBvsGroupC_pValSW.txt"], "List"][[1]];

(***First sort p-values from smallest to largest***)

sortedLabelsAndPs =
  Sort[{{"pAvsB", pAvsB}, {"pAvsC", pAvsC}, {"pBvsC", pBvsC}}, #1[[2]] < #2[[2]] &];

(***Next, multiply each p-
value by the total number of comparisons and divide the result by its rank order***)

In[ ]:= bhCorrectedLabelsAndPs = Table[{sortedLabelsAndPs[[n, 1]],
  (sortedLabelsAndPs[[n, 2]] * Length[sortedLabelsAndPs]) / n},
  {n, 1, Length[sortedLabelsAndPs]}];

(***Next, make sure that the resulting sequence of p-
values is monotonically increasing. If the sequence is decreasing at any point,
make the preceding p-value equal to the subsequent p-
value. The result is final list of multiple-comparisons-corrected p-values.***)

In[ ]:= nondecbhCorrectedLabelsAndPs =
  Table[{bhCorrectedLabelsAndPs[[n, 1]], Which[n < Length[bhCorrectedLabelsAndPs] &&
    bhCorrectedLabelsAndPs[[n, 2]] ≤ bhCorrectedLabelsAndPs[[n + 1, 2]],
    bhCorrectedLabelsAndPs[[n, 2]], n < Length[sortedLabelsAndPs] &&
    bhCorrectedLabelsAndPs[[n, 2]] > bhCorrectedLabelsAndPs[[n + 1, 2]],
    bhCorrectedLabelsAndPs[[n + 1, 2]], n == Length[bhCorrectedLabelsAndPs],
    bhCorrectedLabelsAndPs[[n, 2]]}], {n, 1, Length[bhCorrectedLabelsAndPs]}]

```