***Install the package –****RECLV2*

***Package Dependencies***- install RCurl and XML package before running below codes.

***Host setting-***Change the host settings in ‘hostsetting.txt’ file in R library path.

***Begin.Hpcc***('y')– begin the R code part which needs to be executed in HPCC.

***Execute.Hpcc***('y') – to execute the R code part written after Begin.Hpcc('y').

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Example 1- Fetch the record structure of logical files from HPCC and then do the sorting and other statistical operation (min, max, standard deviation, Mean).

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

##Fetch the layout of logical file from HPCC (need to run in the R)

***hpccData.layout***(*logicalfilename*='tutorial::om::randdata',*out.struct*='randata')

##Part of code need to run in HPCC/ECL

***Begin.Hpcc***('y')

## Read data from logical file using above layout (e.g.; out.struct)

***hpccRead.Data***(*logicalfilename*='tutorial::om::randdata', *layoutname*='newdata',

*in.struct*=randata, *filetype*='THOR', *out.dataframe*='ranout')

## Sort the above data

***hpccSort***(*dataframe*="ranout", *fields* ="height", *out.dataframe*="sortfile")

## Calculate Minimum of different fields

***hpccMin***(*dataframe*='sortfile', *fields*='height,weight', *out.dataframe*='minhw')

## Calculate the Max

***hpccMax***(*dataframe*='sortfile', *fields*='height,weight', *out.dataframe*='maxhw')

## Calculate the Average

***hpccMean***(*dataframe*='sortfile', *fields*='height,weight', *out.dataframe*='meanhw')

## Calculate the Standard Deviation

***hpccSd***(*dataframe*='sortfile', *fields*='height,weight', *out.dataframe*='sdhw')

##Execute the above piece of code in HPCC

***Execute.Hpcc***('y')

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Example 2-

Sort an inline data in HPCC through R editor/command line-

*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*start\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\**

*## Begin HPCC environment*

***Begin.Hpcc***('y')

*## Input inline dataset*

***hpccRead.InlineData*** (*layoutname*='myrec',*linedata*="

{'M','M',8},

{'C','C',2},

{'A','X',3},

{'B','G',4},

{'A','B',5}",

*fieldtype*="STRING1 Value1;STRING1 Value2;UNSIGNED1 Value3;",

*out.dataframe*="somefile")

*##Sort the data*

***hpccSort***(*dataframe*="somefile",*variable*="value1",*out.dataframe*="sortfile")

*##Execute the above written code*

***Execute.Hpcc***('y')

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*end\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

Example3-

Rollup an inline data in HPCC through R editor/command line-

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*start\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

*## Begin HPCC environment*

***Begin.Hpcc***('y')

*## Input inline dataset*

***hpccRead.InlineData*** (*layoutname*='myrec',*linedata*="

{'M','M',8},

{'C','C',2},

{'A','X',3},

{'B','G',4},

{'A','B',5}",

*fieldtype* ="STRING1 Value1;STRING1 Value2;UNSIGNED1 Value3;",

*out.dataframe*="somefile")

*##Sort the data*

***hpccSort***(*dataframe*="somefile",*variable*="value1",*out.dataframe*="sortfile")

*## transform condition while removing the duplicates*

***hpccTransform***(*funcname*="Rollthem",

*parameterlist*="somefile L,MyRec R",

*condition*="SELF.Value3 := IF(L.Value3 < R.Value3,L.Value3,R.Value3);

SELF.Value2 := IF(L.Value2 < R.Value2,L.Value2,R.Value2);

SELF := L;")

*## roll up function to remove the duplicates with transform condition* ***hpccRollup***(*dataframe*="sortfile",

*condition*="LEFT.Value1 = RIGHT.Value1",

*calltransfunc*='Rollthem',

*out.dataframe*='rollout')

*## Execute the code in HPCC*

***Execute.Hpcc***('y')

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*end\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*