

International Allegro CL Free Express Edition
 8.0 [Windows] (Jun 6, 2006 15:50)
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 Lisp in a box User

CG version 1.81.2.23 / IDE version 1.80.2.21
 Loaded options from C:\Documents and Settings\NRM\My Documents\allegro-prefs.cl.

;; Optimization settings: safety 1, space 1, speed 1, debug 2.
 ;; For a complete description of all compiler switches given the current optimization settings

[changing package from "COMMON-LISP-USER" to "COMMON-GRAPHICS-USER"]

CG-USER(1):

"HPS_COMPILE_AND_LOAD_IS_ON"

"HPS_APPLICATION_STARTED"

Invoking the HPS 'DNA APPLICATION OF THE HPS TRANSFORM : [a sublinear time D

HPS_STARTED

The HPS Transform application files expected to be installed here ... ["F:/HPS_DATA/"]
 Input files to the HPS Transform are expected to be placed be here .. ["F:/HPS_DATA/HPS_INPUT"]
 The output of the HPS Transform will be placed be here ["F:/HPS_DATA/HPS_OUTPUT"]
 Verifying path to input directory for the HPS transform to be ["F:/HPS_DATA/HPS_INPUT"]
 Verifying path to output directory for the HPS transform to be ["F:/HPS_DATA/HPS_OUTPUT"]
 "Invoking the HPS Transform as (HPS_TRANSFORM atimeseries)"
 PARAMETERS VALUES ARE[]: [](HPS_FULL_OUTPUT_MODE ==> NIL)[]
 PARAMETERS VALUES ARE[]: [](HPS_TRANSIENT_FILLER ==> T)[]
 PARAMETERS VALUES ARE[]: [](CONDITIONING_TYPE ==> NIL)[]
 PARAMETERS VALUES ARE[]: [](PRINTDUR ==> 3)[]
 PARAMETERS VALUES ARE[]: [](MSEDELAY ==> 1)[]
 PARAMETERS VALUES ARE[]: [](MSERELAX ==> 0.70710677)[]
 PARAMETERS VALUES ARE[]: [](SEGTRIVIAL ==> 1)[]
 PARAMETERS VALUES ARE[]: [](FORECAST_WINSIZE ==> 60)[]
 PARAMETERS VALUES ARE[]: [](K ==> 3)[]
 PARAMETERS VALUES ARE[]: [](ALPHALEVEL ==> 0.01)[]
 PARAMETERS VALUES ARE[]: [](SEGLIMIT ==> 90)[]
 PARAMETERS VALUES ARE[]: [](TIMESHIFT ==> 30)[]
 PARAMETERS VALUES ARE[]: [](MP ==> 30)[]
 PARAMETERS VALUES ARE[]: [](M ==> 60)[]
 PARAMETERS VALUES ARE[]: [](DATASETFILE ==> HPS_FULldata.DAT)[]
 PARAMETERS VALUES ARE[]: [](REPORTFILE ==> RESULTANT_HPS_APPROXIMATION.HTM)[]
 PARAMETERS VALUES ARE[]: [](OUTPUTDIR ==> F:/HPS_DATA/HPS_OUTPUTS/)[]
 PARAMETERS VALUES ARE[]: [](OUTPUTFILE ==> HPS_3DNA_APPROXIMATION_SERIES.DNA)[]
 PARAMETERS VALUES ARE[]: [](BASEDIR ==> F:/HPS_DATA/)[]
 PARAMETERS VALUES ARE[]: [](INPUTFILE ==> HPS_3DNA_INPUT_SERIES_ENCODED.DNA)[]

HPS Transform being executed from directory : ["F:/HPS_DATA/"]
 Verifying path to input directory for the HPS transform to be ["F:/HPS_DATA/HPS_INPUT"]
 Resultant HPS Transform data files being written to directory : ["F:/HPS_DATA/HPS_OUTPUT"]
 HPS Transform being applied to input time series in file : ["F:/HPS_DATA/HPS_INPUT"]
 Computed dataset (approx. size (500 * N) B) will be written to file: ["F:/HPS_DATA/HPS_OUTPUT"]
 Resultant HPS Approximation time series will be placed in file : ["F:/HPS_DATA/HPS_OUTPUT"]
 Analysis of the resultant HPS Approximation will be placed in file : ["F:/HPS_DATA/RESULTANT"]
 HPS output mode for the resultant HPS Approximation is set to : [LEAN_OUTPUT_FAST_PERF
 HPS Transform being applied with m=[60] m'=[30] at alpha=[0.01]

-----HPS_TRANSFORM_START-----

HPS Transform loading t-table from file: ["F:/HPS_DATA/HPS_INPUTS/HPS_T_TABLE_GENERATOR.DAT"]
 L0: i-th: [1000]

L0: i-th:[2000]
 L0: i-th:[3000]
 L0: i-th:[4000]
 L0: i-th:[5000]
 L0: i-th:[6000]
 L0: i-th:[7000]
 L0: i-th:[8000]
 L0: i-th:[9000]
 L0: i-th:[10000]
 L0: i-th:[11000]
 L0: i-th:[12000]
 L0: i-th:[13000]
 L0: i-th:[14000]
 L0: i-th:[15000]
 L0: i-th:[16000]
 L0: i-th:[17000]
 L0: i-th:[18000]
 L0: i-th:[19000]
 L0: i-th:[20000]
 L0: i-th:[21000]
 L0: i-th:[22000]
 L0: i-th:[23000]
 L0: i-th:[24000]
 L0: i-th:[25000]
 L0: i-th:[26000]
 L0: i-th:[27000]
 L0: i-th:[28000]
 L0: i-th:[29000]
 L0: i-th:[30000]
 L0: i-th:[31000]

-----HPS_TRANSFORM_DONE-----

"Invocation of the HPS transform completed successfully."

HPS_STENO_START

CONSTRUCTING HPS SEGMENT TABLE FOR : F:/HPS_DATA/HPS_OUTPUTS/HPS_3DNA_APPROXIMATION_SERIES
 DNA SEGMENT TABLE WILL BE PLACED IN : F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_SEGMENT_TABLE.DNA

AVE SEG DURATION THRESHL: 30

MIN SEG DURATION THRESHL: 7

READING INPUTSERIES FROM: "F:/HPS_DATA/HPS_OUTPUTS/HPS_3DNA_APPROXIMATION_SERIES.DNA"

WRITING SEGMENT TABLE TO: "F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_SEGMENT_TABLE.DNA"

AVE SEG DURATION THRESHL: 30

MIN SEG DURATION THRESHL: 6

READING INPUTSERIES FROM: "F:/HPS_DATA/HPS_OUTPUTS/HPS_3DNA_APPROXIMATION_SERIES.DNA"

WRITING SEGMENT TABLE TO: "F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_SEGMENT_TABLE.DNA"

AVE SEG DURATION THRESHL: 30

MIN SEG DURATION THRESHL: 5

READING INPUTSERIES FROM: "F:/HPS_DATA/HPS_OUTPUTS/HPS_3DNA_APPROXIMATION_SERIES.DNA"

WRITING SEGMENT TABLE TO: "F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_SEGMENT_TABLE.DNA"

AVE SEG DURATION THRESHL: 30

MIN SEG DURATION THRESHL: 4

READING INPUTSERIES FROM: "F:/HPS_DATA/HPS_OUTPUTS/HPS_3DNA_APPROXIMATION_SERIES.DNA"

WRITING SEGMENT TABLE TO: "F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_SEGMENT_TABLE.DNA"

HPS_STENO_DONE

Marking lingered memory state for clean-up

Invoking the allegro common lisp's garbage collector

HPS_DNA_START

_____ :
 PATTERN MINING FOR MATCHES AT COARSEGRAIN PATTERN MATCH GOAL OF .. : [0.4]

PATTERN MINER RESULTS AT THIS LEVEL ARE LOCATED WITHIN THE : [----- - SEARCH OPERAT
ANALYSIS PATTERN MATCH GOAL OF : 0.4
ANALYSIS RUN FROM DIRECTORY FOUND ON: "F:/HPS_DATA/"
ANALYSIS DATA FILES WILL BE FOUND ON: "F:/HPS_DATA/HPS_OUTPUTS/"
STENO ANALYSIS WILL BE PLACED ON : "F:/HPS_DATA/HPS_REPORT_STENO.HTM"
DNA ANALYSIS WILL BE PLACED ON : "F:/HPS_DATA/HPS_DNA.HTM"
CONSTRUCTING HPS SEGMENT TABLE FOR : "HPS_3DNA_APPROXIMATION_SERIES.DNA"
DNA SEGMENT TABLE WILL BE PLACED IN : "F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_SEGMENT_TABLE.DNA"
VERIFYING PATH TO OUTPUT DIRECTORY : "F:/HPS_DATA/HPS_OUTPUTS/"
FINDING ALL POSSIBLE PATTERN MATCHES: THRESHOLD IS 165.15001

(0 0 141)

GENERATING ALIGNMENT DATA MAPS :
SELECTING BEST PATTERN MATCHES :
(OPTIONAL) WRITING ALL HPS SEGMENT TABLES: [HPS_*_SEGTABLE.DNA] type files
GENERATING LAMBDA, TVAL HISTOGRAMS : [HPS_DNA_*_HISTOGRAM*.DNA] type files
GENERATING MATCH BEHAVIOR ANALYSIS DATA : [HPS_DNA_MATCHBEHAVIOR_HISTOGRAM.DNA]
GENERATING MATCH BEHAVIOR ANALYSIS DATA : F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_MATCHING_PATTERNS
GENERATING REPORT FOR HPS PATTERN MINING : [F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_BESTMATCHING_PA
GENERATING DETAILED REPORT FOR P-MATCHES : [F:/HPS_DATA/HPS_OUTPUTS/HPS_DNA_BESTMATCHING_PA

BEST HPS DNA SHAPE APPROXIMATE PATTERN MATCHES BETWEEN SIGNATURE AND TEST SEQUENCE					
MATCH_STARTS	AND_ENDS_AT	MATCH_RATING	MATCH_SPANS	MATCH_WEIGHT	COS
23384	24440	0.98214287	1057	877.0	0
MATCH_STARTS	AND_ENDS_AT	MATCH_RATING	MATCH_SPANS	MATCH_WEIGHT	COS
23355	24404	0.86885244	1050	1019.0	0
MATCH_STARTS	AND_ENDS_AT	MATCH_RATING	MATCH_SPANS	MATCH_WEIGHT	COS
10095	11095	0.47058824	1001	1883.0	0

GENERATING DATA FILES FOR PLOTTING ANALYSIS:
GENERATING GNUPLOT COMMANDS TO BE INVOKED: F:/HPS_DATA/PNG-HPS-DNA-PLOTS.PLT
GNUPLOT_STARTED
Verifying path to output directory for the GNU plot interfaces: ["F:/HPS_DATA/HPS_OUTPU
PATH to GNUPLOT for win32 binaries has been setup to be: ["C:/Program Files/gnu
Running GNUPLOT interface: ["F:/HPS_DATA/HPS_DNA_V
GNUPLOT_DONE
HPS_DNA_DONE
Marking lingered memory state for clean-up :
Invoking the allegro common lisp's garbage collector :

HPS_DONE

"HPS_APPLICATION_DONE"