Barcelona Supercomputing Center
Centro Nacional de Supercomputación

A Quick guide to apply Clustering and Tracking to your traces

Presentation slides for MIRI-PPTM. C. Gómez

Barcelona, 29 abril 2015

Barcelona Supercomputing Center
Centro Nacional de Supercomputación

CLUSTERING

Outline

《 Clustering

  《 Setting up the environment

  《 Run

  《 Result output files

  《 General tips and common issues

《 Tracking

  《 Set up and run

  《 Tracking GUI

Barcelona
Supercomputing
Center
Centro Nacional de Supercomputación

Clustering

«Characterizes computational bursts that are similar and groups them in clusters

Figure 2: Scatter-plot of CPU burst metrics description

Figure 3: Scatter-plot of Figure 2 colored using the cluster ID
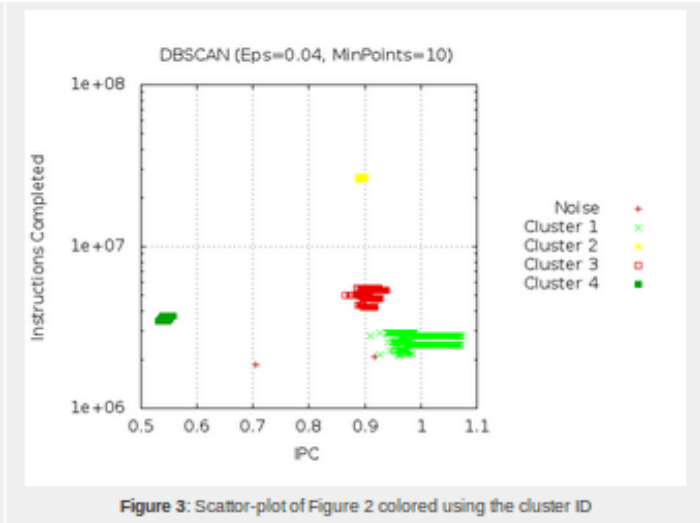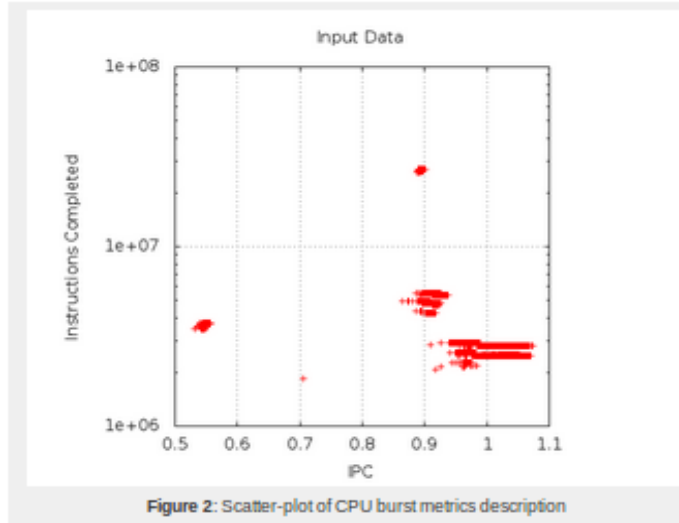
« Allows you to study the behavior of the clusters separately, identify patterns etc.
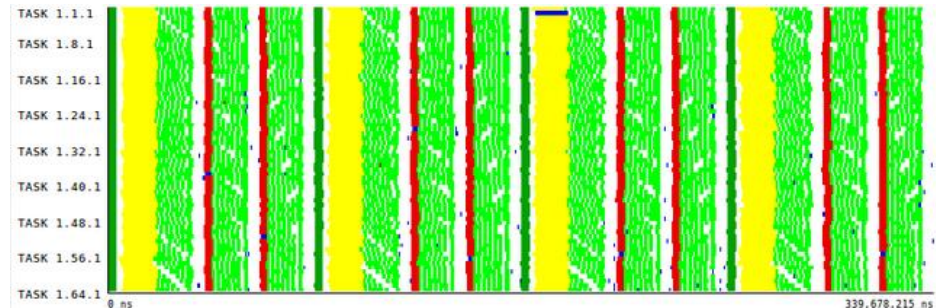
Clustering

《 Manual and more details about the tool

http://www.bsc.es/sites/default/files/public/computer_science/performance_tools/clusteringsuite_manual.pdf

note: If you never heard about or seen any clustering example, you should read the main page info of the tool first.

Clustering – Setting up the enviorment

‹‹ It's recommended to work remotely connected to MN3

    ‹‹ Everything is configured automatically with modules

    ‹‹ Tracking has no distributable package yet

    ‹‹ Log in with: `ssh -X -l <user> mn3.bsc.es`

    ‹‹ Load modules: `module load INTEL BSCTOOLS`

‹‹ Your traces have at least this PAPI counters info

    ‹‹ Configure in extrae.xml: PAPI_TOT_INS , PAPI_TOT_CYC

Clustering – Setting up the environment

❰❰ Locate the cluster.xml configuration file

    ❰❰ `/apps/CEPBATOOLS/ClusteringSuite/latest/share/example/cluster.xml`

    ❰❰ Copy it to your working folder, you ~~may~~ **need** to modify it

❰❰ cluster.xml parameters (try default first!)

    ❰❰ Epsilon – 'radius' in which a burst will be considered similar

    ❰❰ Min points – minimum number of similar points to form a cluster

    ❰❰ Range min/max: Allows to filter very small bursts or focus in a desired area.

Clustering - Run

« Applying clustering to your trace

    « Open Paraver

    « Click on the cog icon

        « Application: clustering

        « Select your trace file...

        « Select your cluster.xml file...

        « Algorithm: XML defined (should be DBScan)

        « Press Run!

Clustering – Output files generated

❰❰ The process will generate several output files

    ❰❰ A New trace `mytrace.clustered.prv`

        ❰❰ In paraver use `clustering/clusterID_window.cfg`

    ❰❰ A Instructions / IPC plot (this is the cool one!)

        ❰❰ Open with `gnuplot mytrace.clustered.IPC.PAPI_TOT_INS.gnuplot`

    ❰❰ Clusters duration information

        ❰❰ `$> less mytrace.clustered.clusters_info.csv`

        ❰❰ % Total duration row, quantifies how 'important' is a cluster.

            ❰❰ Cluster numeration ordered by this metric, being Cluster 1 the highest

Clustering: general tips and issues

« How do I know my clustering 'went well' ?

    « "There's no bad clustering as long as you can extract information."

    « Compare plot against the clustered trace. Are you happy?

        « gnuplot vs trace viewed with clusterID_window cfg.

« Is my Epsilon too high or too small?

    « Lots of noise, or crazy patterns, maybe too small.

    « You have only a couple of big clusters and I think should appear more: too high.

« There's no magic rule

    « Choose some parameters, run clustering and see results…

    « Not good? Refine parameters, repeat until satisfied.

Barcelona
Supercomputing
Center
Centro Nacional de Supercomputación

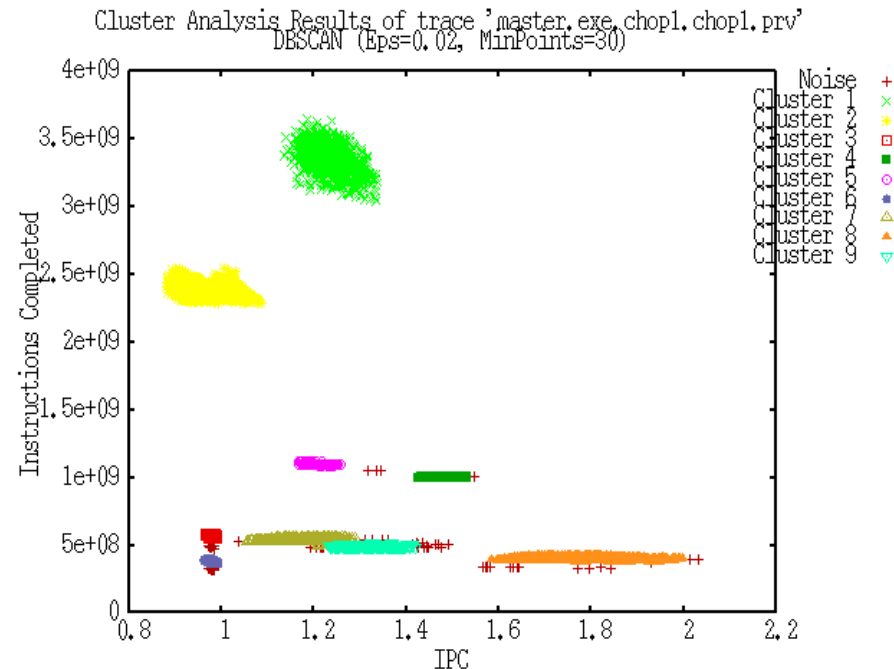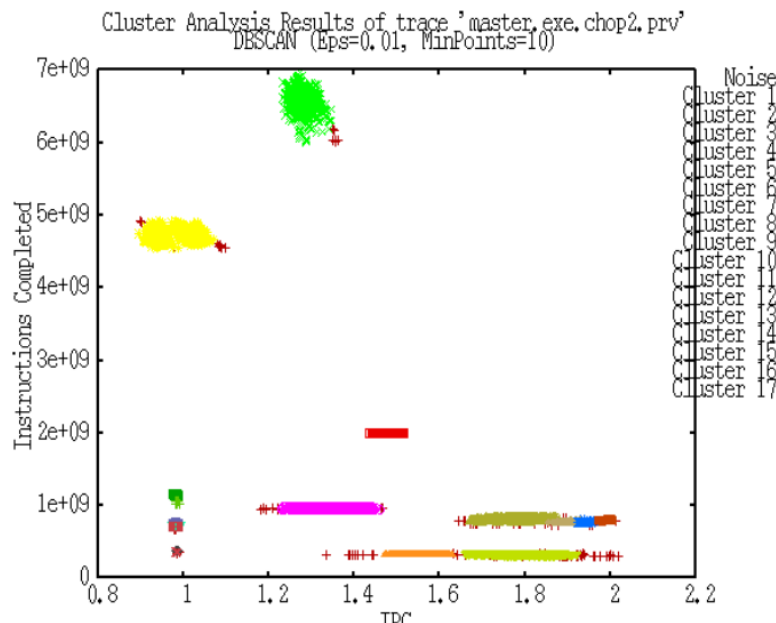# Clustering: general tips and issues

《 Important ! If you have several traces scaling number of cores to do tracking later..

 《 Be careful, the clusters 'move' and maybe they end up out of the min/max ranges.

 《 Use min/max cluster.xml filters to frame the same regions for each trace. Like a cameraman follows the action.

 《 The better adjusted, the easier for the tracking tool.

 《 Look at left image, bottom region, it disappears in the right image, not good!
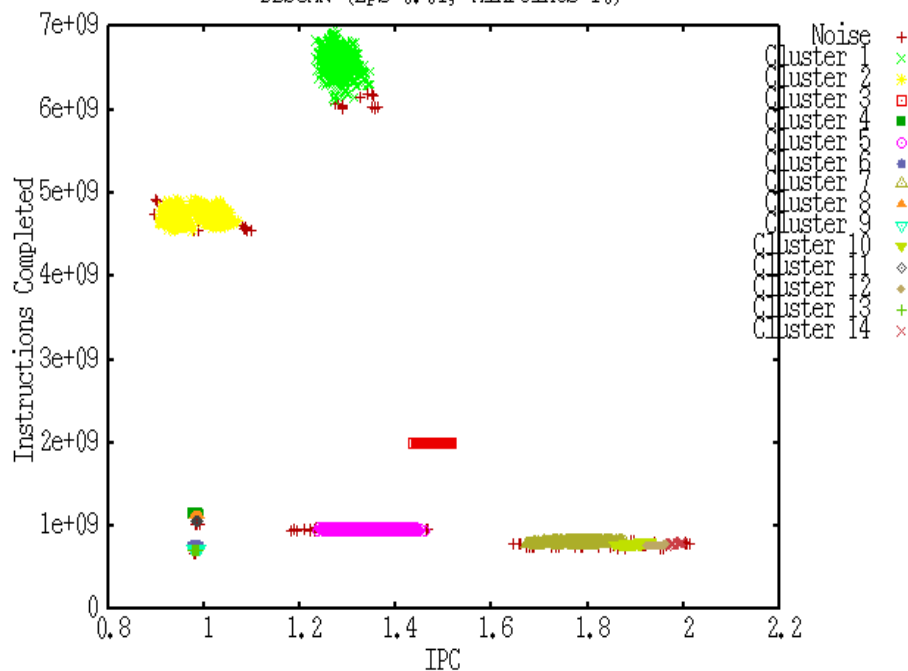

Cluster Analysis Results of trace 'master.exe.chop2.prv' DBSCAN (Eps=0.01, MinPoints=10)

Cluster Analysis Results of trace 'master.exe.chop1.chop1.prv' DBSCAN (Eps=0.02, MinPoints=30)

Clustering: general tips and issues

After adjusting the ranges...
- This is better
- This two clustered traces are ready to be used with the tracking tool

TRACKING

Tracking

« A friendly way to quantify and visualize the evolution of the clusters among several traces.

« Tool has two parts

  « Recognition algorithm 'who is who', based on heuristics.

  « And visualization GUI

« Implemented Heuristics

  « Proximity (default), Callstack (if enabled), density of inst., alignment (experimental)

« Examples analyzing multiple traces

  « Scaling number of cores (64 – 128 - 256… CPU's)

  « Testing different microarchitecture features.

**Barcelona Supercomputing Center**
Centro Nacional de Supercomputación

Tracking – Set up and run

❰❰ We keep assuming you're connected to MN3

❰❰ Your starting point is the folder with al the files generated during clustering.

  ❰❰ You applied clustering to 2 traces or more. i.e (64.prv - 128.prv - 256.prv)

  ❰❰ Remember: module load BSCTOOLS

❰❰ Execute

  ❰❰ `tracking -r 128.clustered.prv 256.clustered.prv [ 512… ]`

  ❰❰ Remember to put the traces in logical order

❰❰ tracking command generates TRACKING.RESULTS.xtrack

  ❰❰ Open with `xtrack TRACKING.RESULTS.xtrack`

  ❰❰ You will also have new clustered traces but with new colors.

« Comments on next slide
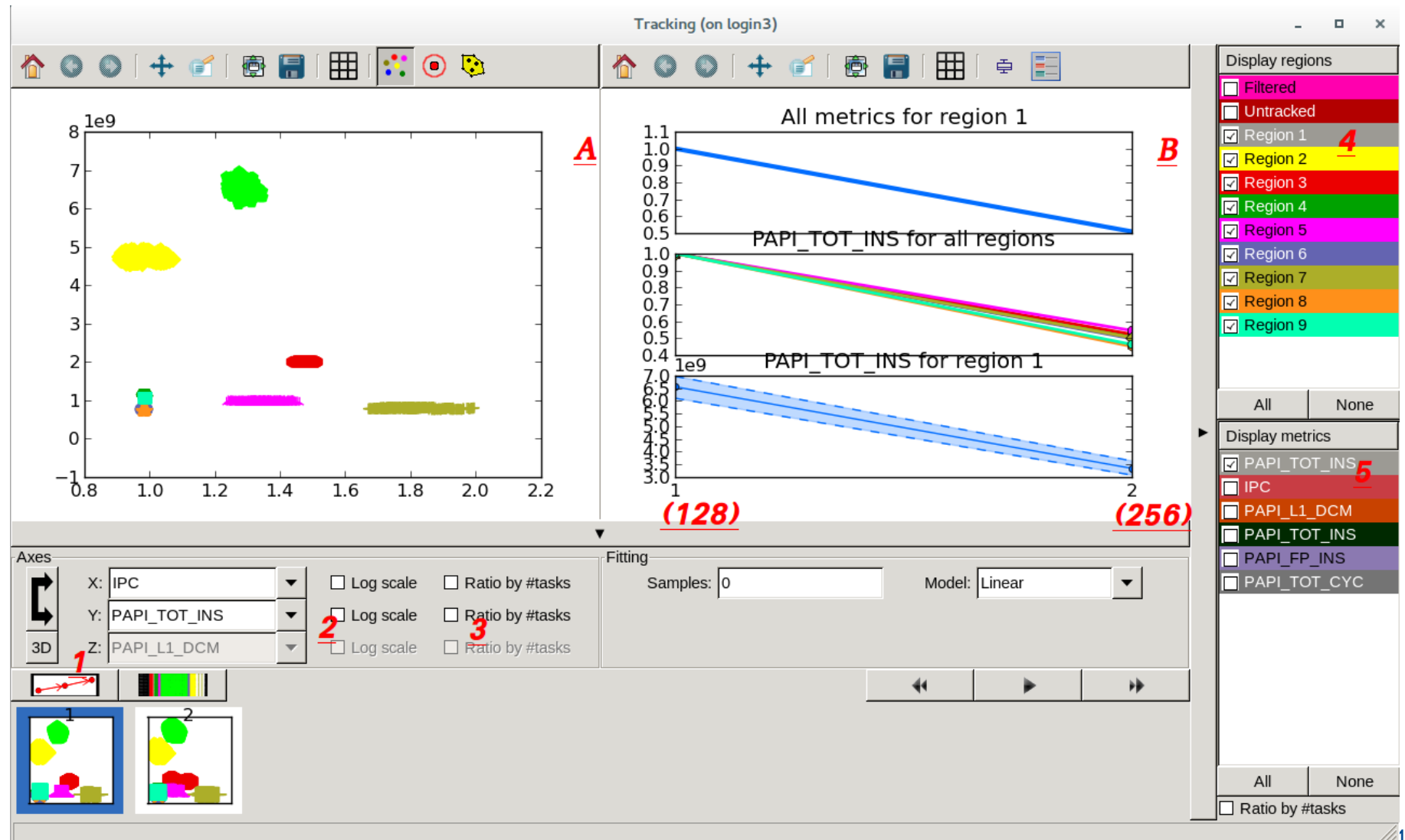
Tracking – GUI

《 Window A shows a plot, by default the Intructions / IPC plot for a single trace.

  《 Push button **1** (dots and arrows). Shows the movement of the clusters along the different traces.

  《 Now push **2**. You can see clearly the movement of the clusters in the lower part of the plot.

  《 **3** Divides the numbers by number of proceses. Useful to see the impact of code replication

《 Window B, has another 3 plots, they can be modified using right controls (**4,5**)

  《 Note that only shows a straight line because we only used two traces (**128,256**).

  《 "All regions" means: all clusters with a check

  《 "For region 1" means: you clicked/selected Cluster 1 label (it becomes grey)

  《 In this example, we can see how the Total Instructions were reduced to 50% for cluster one (top plot).

  《 Hard to explain in slides. Play around with the controls to understand better.

Thanks!

❰ Special thanks to G. Llort @ bsc tools team for teaching me the methodology of use of the tools.

❰ Thanks to everyone that gave me feedback after the presentation.

❰ Feel free to improve / expand this slides :)

Barcelona Supercomputing Center
Centro Nacional de Supercomputación

Thank you!

For further information please contact
constantino.gomez@bsc.es