



# Profiling Tutorial #3



Using ProfVis - GUI Features



# Outline:

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ProfVis GUI reference:

- All the features of the GUI and a reference for future.
- Examples of things to look out for.

# ProfVis GUI Features

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# Looking at your results:

There are a few ways to alter your view of the data:

[Ctrl+Level #] to switch levels,  
[Ctrl-D] to open the data.

- Scale (1x, 2x, 3x)

(Found at: View... Scale)

Zoom. Especially useful when you are working with a small number of processors or a large number of quick regions over a long simulation time. “Long, skinny data set.”

- Levels - Used in Profiling PlotFiles

(Found at: View... Level. )

Profiling data has levels, same as AMRVis plotfiles.  
Can zoom into deeper levels to obtain finer results / the data set.

For most profiling data, levels are visualized using `stride`.

# ProfVis Window

Region Type



Time

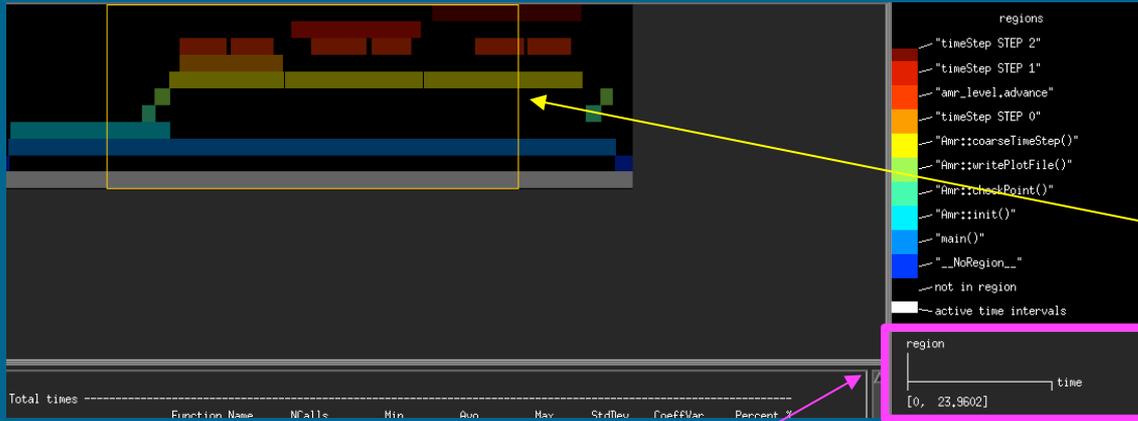
Each color corresponds to a different region.

Each region can appear multiple times, but will appear the same number of times on each rank.

Regions are identified by type and the instance of that type. (e.g. 3rd call of the 5th unique region called.)

Currently based on computational rank 0. (Will be variable in the future.)

# Subregions Example: [Ctrl-S]



Used in Profvis to filter your analysis time to a absolute minimum and maximum across all MPI ranks.

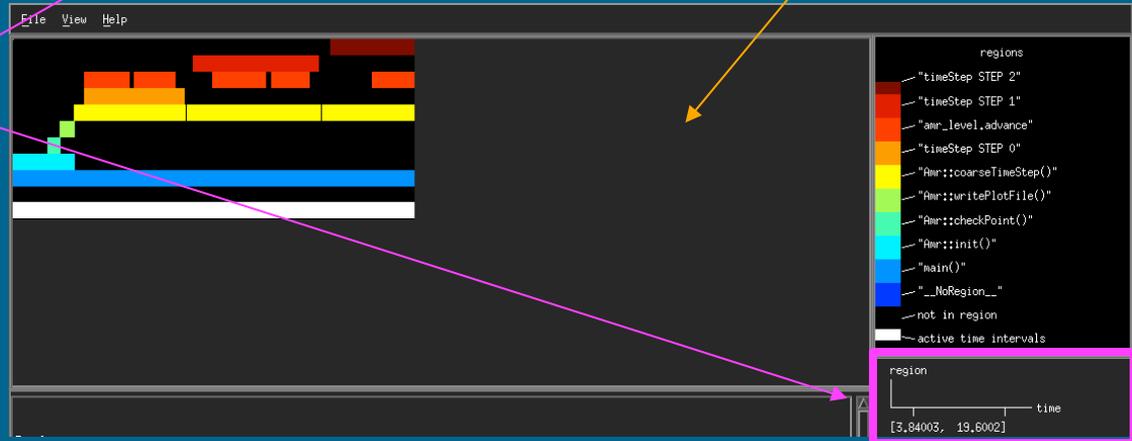
If you select this region (left click & drag), then subregion...

...you will end up with this new ProfVis window.

Note the 'legend' times are different.

Analyses will now be limited to within this new time window for all MPI ranks.

(This is the 'highest' level parse. Think of it as the "first" filter step.)



# ProfVis Window:

# Select your regions

Right Click:  
Add region

Middle Button:  
Remove region

Left click and drag:  
Select a time range.  
(Slicing).

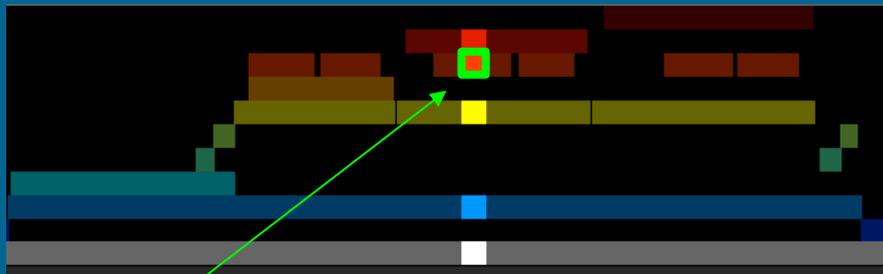
Left click:  
Get info about the  
selected region in the  
amrvis command window.



```
amrvis2dpp  
File  
[[[]]: fileType is amrex::Amrvis::PROFDATA.  
click at 231 76 !  
dpX dpY = 231 98  
ivLowOffset = (0,0)  
calcTimeRange calcTime clickTime = [0, 23,9602] 23,9602 9,24007  
dataValueIndex regName rtri timerange = 5 "Amr::coarseTimeStep()" 0 [6,26003, 10,6004]
```

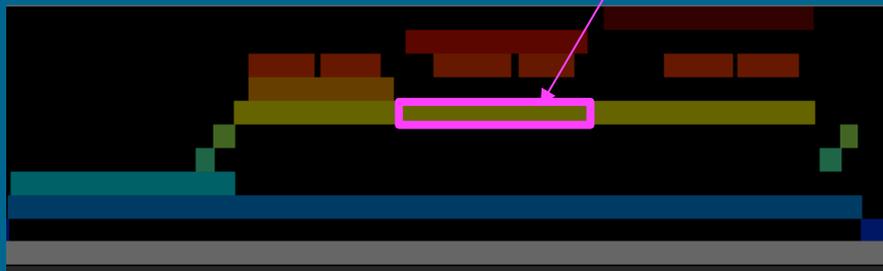
# Regions:

Turning regions on and off turns them off relative to the time of the selected region, (Entire matching vertical block).



Turn this region on ....

...followed by turning this off.



Turn these regions on ....

...followed by turning these off.



Although not displayed, the selected time region for each MPI rank will be based on the local time of the matching region. Can be seen in stdout when “Generate Func List” is clicked if interested. Look for:

“filterTimeRanges[rank][time block] = [##, ##]”.

The exact time for each rank **should not match**. It will include the time for the selected regions on all ranks.

# Function List: Breakdown of timers

```
Total times -----
```

Function Name	NCalls	Min	Avg	Max	StdDev	CoeffVar	Percent %
FabArray::ParallelCopy()	161	4,4049	4,7660	5,3654	0,2796	5,8670	20,53 %
TagBoxArray::collate()	9	3,9997	4,2713	4,5952	0,1499	3,5085	18,40 %
LevelAdvance::LevelAdvance_RRM()	21	1,5561	2,1552	2,8214	0,3182	14,7629	9,28 %
FabArrayCopyDescriptor::CollectData()	14	1,1914	1,3896	1,6235	0,1053	7,5799	5,99 %
HyperCLaw::testTimeStep()	10	0,9011	0,9848	1,0660	0,0417	4,2382	4,24 %
DistributionMapping::LeastUsedCPUs()	8	0,2591	0,8659	1,1745	0,2145	24,7706	3,73 %
Amr::writePlotFile()	2	0,7411	0,8527	0,9092	0,0342	4,0136	3,67 %
Amr::checkPoint()	2	0,7316	0,8281	0,9027	0,0432	5,2157	3,57 %
CollectData_Alltoall()	14	0,3830	0,7439	0,9792	0,1539	20,6860	3,20 %

Function Name

Number of calls  
on MPI rank 0.

Minimum, average, and  
maximum time spent in  
region across all MPI ranks.

Standard deviation and  
coefficient of variation  
across all MPI ranks.

Percent of total  
selected time.

3 Lists, in order:

- Alphabetical, exclusive.
- Total times & percent selected.
- Percent time, exclusive.
- Total time, inclusive.

- Prior to clicking on “Generate Function List”, it provides a simple overview similar to that provided by TINYPROFILER.
  - (Does not require parsing through the profiling database. VERY quick, even for large databases.)
- After clicking on “Generate Function List”, it is more exact data from the full database information.
- ★ The function list results will filter based on both the **subregion** and the **selected regions**.

# Function List: What to Look Out For

```
Total times -----
```

Function Name	NCalls	Min	Avg	Max	StdDev	CoeffVar	Percent %
ProfParserBatchFunctions()	1	13,6311	13,6380	13,6412	0,0016	0,0114	92,55 %
RegionsProfStats::OpenAllStreams	1	0,6279	0,6286	0,6288	0,0002	0,0371	4,27 %
RegionsProfStats::ReadBlockNoOpen()	16	0,1723	0,2273	0,2905	0,0313	13,7676	1,54 %
RegionsProfStats::ReadBlock()	512	0,0000	0,1182	3,7834	0,6583	556,7764	0,80 %
RegionsProfStats::InitRegionTimeRanges_Parallel()	1	0,0301	0,0933	0,1489	0,0313	33,4995	0,63 %
RegionsProfStats::WriteSummary()	1	0,0000	0,0112	0,3596	0,0626	556,6244	0,08 %
BLProfStats::CloseAllStreams	1	0,0037	0,0088	0,1548	0,0262	298,2775	0,06 %
OpenStream	512	0,0000	0,0080	0,2558	0,0445	556,7764	0,05 %
VisMF::Initialize	1	0,0014	0,0014	0,0014	0,0000	0,3117	0,01 %
RegionsProfStats::InitRegionTimeRanges()	1	0,0005	0,0009	0,0012	0,0002	20,7453	0,01 %
BLProfStats::InitFilterTimeRanges()	1	0,0001	0,0002	0,0003	0,0001	36,2476	0,00 %
FABio_binary::write_header	1	0,0000	0,0000	0,0004	0,0001	556,7764	0,00 %
PD_convert	1	0,0000	0,0000	0,0004	0,0001	556,7764	0,00 %
RD:convertFromNativeFormat_os	1	0,0000	0,0000	0,0004	0,0001	556,7764	0,00 %
DataServices::WriteSummary()	1	0,0000	0,0000	0,0000	0,0000	9,0504	0,00 %
FABio_binary::write	1	0,0000	0,0000	0,0002	0,0000	556,7764	0,00 %
FArrayBox::writeOn	1	0,0000	0,0000	0,0000	0,0000	556,7764	0,00 %
FABio::write_header	1	0,0000	0,0000	0,0000	0,0000	556,7764	0,00 %

```
=====
```

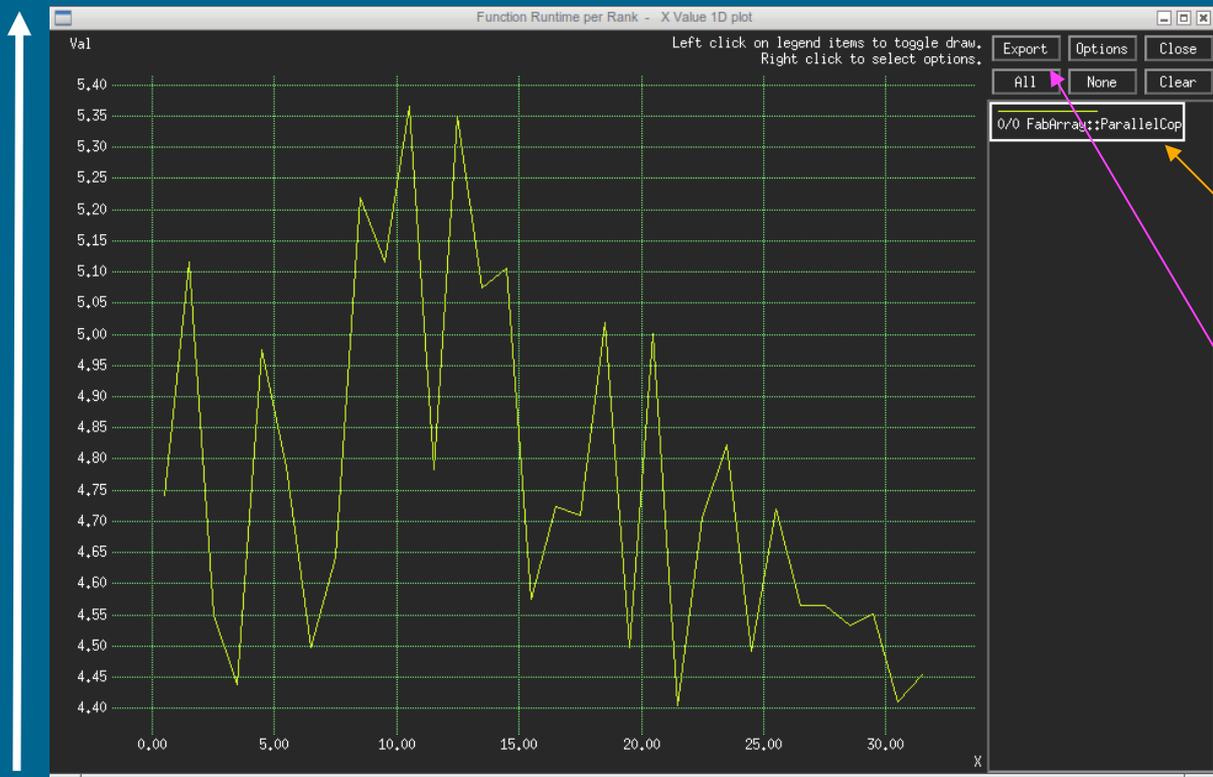
MaxCallStackDepth = 6

- ❖ Top time consuming functions and total percent spent in them.
- ❖ Functions that you wouldn't expect to be called.
- ❖ Very high number of calls.
- ❖ Very high standard deviation or coefficient of variation.

# Function Plot:

Click on a function in the function list to get a plot of the amount of time each MPI rank spent in that function.

Function time (sec)



Left click to recenter plot.  
Left click & drag to zoom to box.  
Right click to reset the view.

Can plot multiple functions on a single plot. Turn on and off by left clicking on the function.

In the future, will be able to export the time/rank data for your own processing. (No output formatting options setup yet for Profvis.)

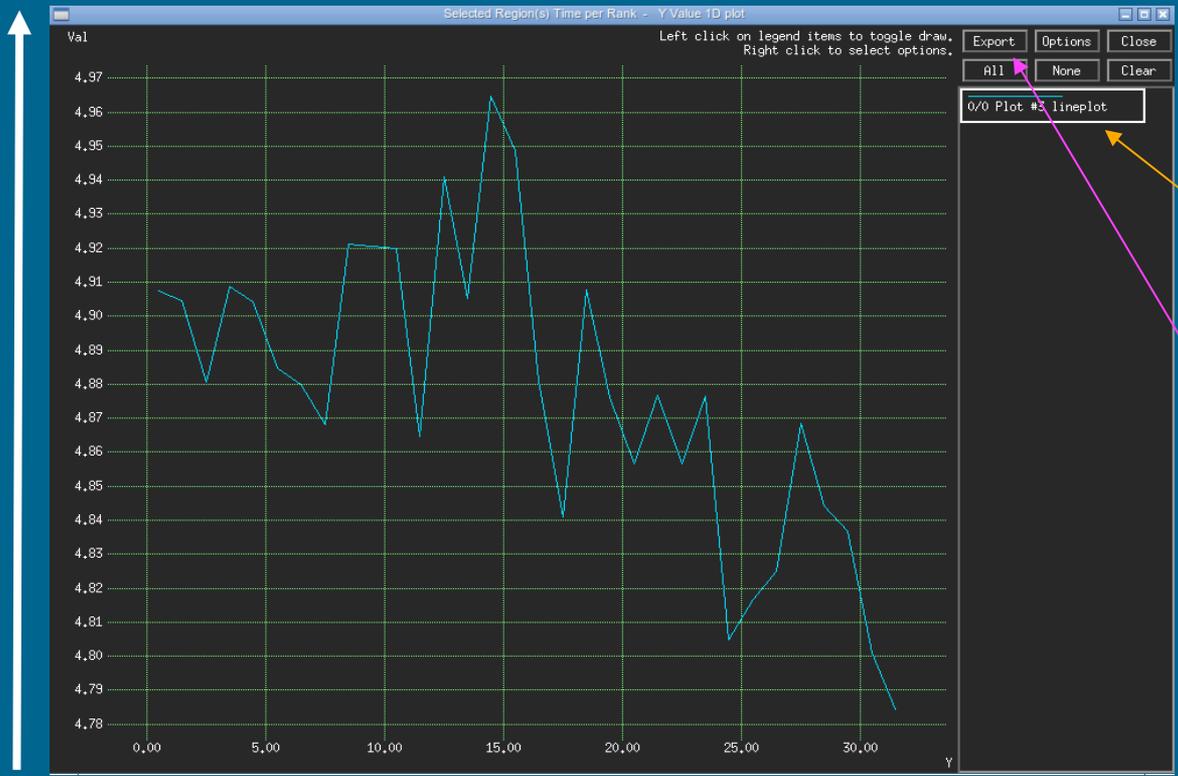
BEWARE the time axes!!! Will scale based on the min/max time of the selected functions, so can be misleading.

MPI rank #

# Region Time Plot:

Select regions of interest and click on “Generate Region Time Plot” to make a plot of total time in the selected regions for each MPI.

Total Region Time (sec)



Left click to recenter plot.  
Left click & drag to zoom to box.  
Right click to reset the view.

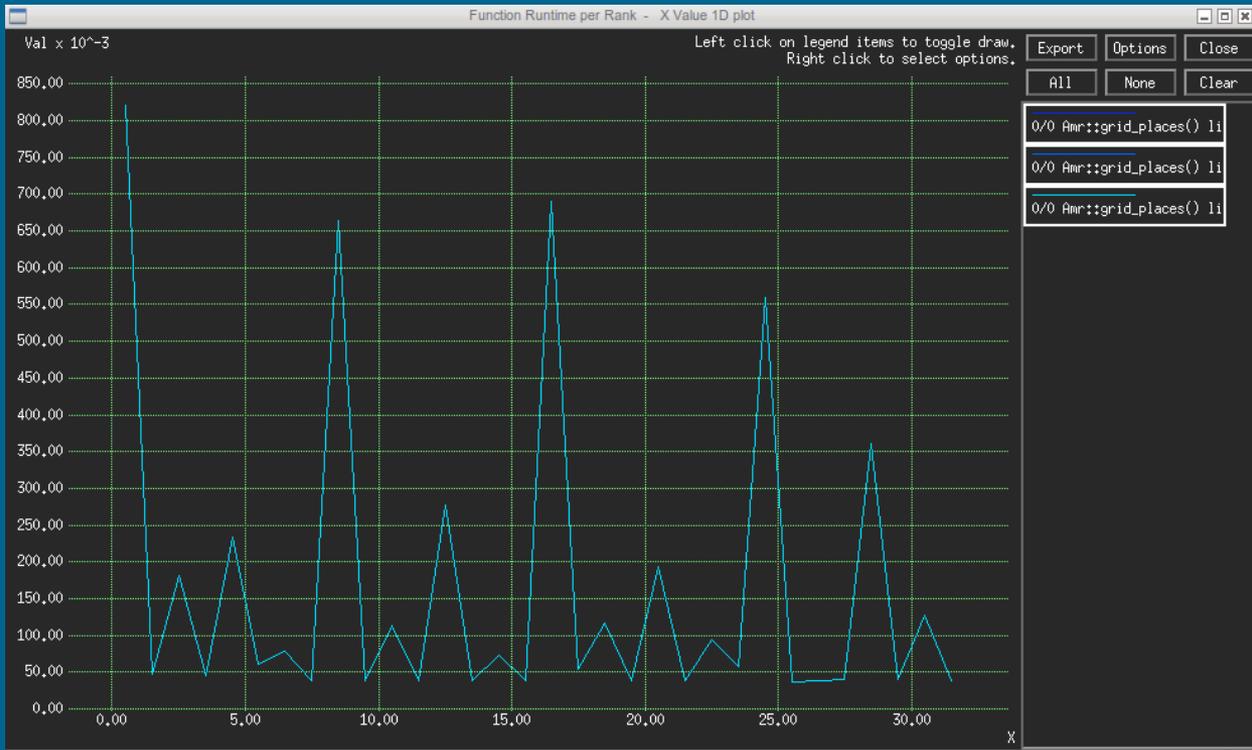
Can plot multiple functions on a single plot. Turn on and off by left clicking on the function.

In the future, will be able to export the time/rank data for your own processing. (No output formatting options setup yet for Profvis.)

BEWARE the time axes!!! Will scale based on the min/max time of the selected functions, so can be misleading.

MPI rank #

# Function Plot & Region Time Plot: What to look out for

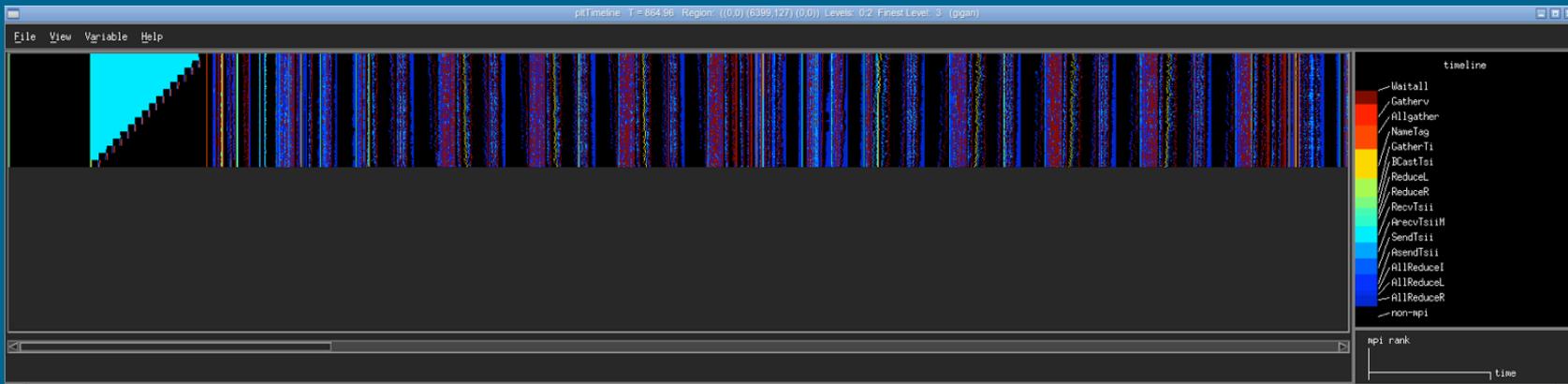


- ★ Very large range of runtimes.
- ★ Single / small number of MPI ranks that are doing all the work.
- ★ Unexpected patterns of work.

# Timeline Plotfile:

“Generate Timeline” creates a plot of MPI calls for each process over time, giving a picture of the communications across your application.

MPI rank #



Time

- Extremely useful to visualize your communication and find bottlenecks.
- Parses based on slicing but not regions (would leave giant blank areas between regions.)
- Currently, the time is incorrect in sliced timelines, but the chart is still accurate.

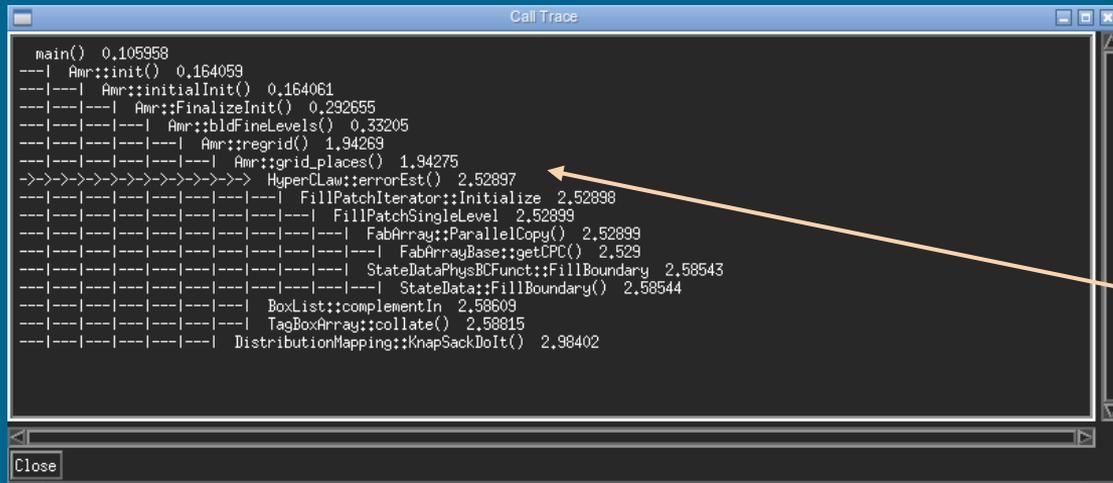
# Timeline Plotfile: Call trace



Open with "View...Call Trace".

Click and drag to select a region.

Ctrl - Left Click and drag to select a box that covers all processors (vertical box).

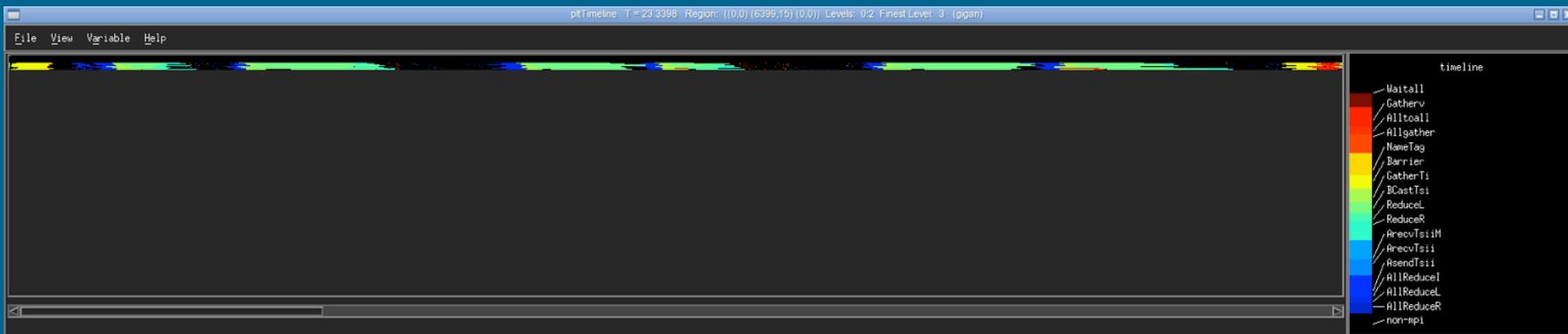


Useless for a call trace, but: Shift - Left Click and drag to select all time (horizontal box).

Displays entire call trace history in the box and start time of that call.

Arrows denote location at the end of the box. (Everything below was ran and exited.)

# Timeline Plotfile: What to Look Out For



- Large barriers or MPI calls waiting for results.
- Blocks of MPI calls (suggesting processors are waiting.)
- Non-structured communication patterns that can be improved.

Colors / legend can be confusing.

Be sure to double check what's what by looking at the data set.

# Send/Recv List:

Detailed list of all point-to-point MPI calls, sorted chronologically.

Time	Type	From	To	Size	Tag	Regions
0.2880845063885254	ArecvTsiim	1	29	48	1000	"main()" "Amr::init()"
0.2880885601043701	ArecvTsiim	3	29	768	1000	"main()" "Amr::init()"
0.2880911827087402	ArecvTsiim	5	29	12288	1000	"main()" "Amr::init()"
0.2880928516387939	ArecvTsiim	7	29	768	1000	"main()" "Amr::init()"
0.2880940437316895	ArecvTsiim	10	29	768	1000	"main()" "Amr::init()"
0.2880949974060059	ArecvTsiim	13	29	48	1000	"main()" "Amr::init()"
0.2880964279174805	ArecvTsiim	19	29	6144	1000	"main()" "Amr::init()"
0.2880976200103760	ArecvTsiim	25	29	384	1000	"main()" "Amr::init()"
0.2884385585784912	ArecvTsiim	26	29	6144	1000	"main()" "Amr::init()"
0.2884438037872314	ArecvTsiim	27	29	6144	1000	"main()" "Amr::init()"
0.2884449958801270	ArecvTsiim	28	29	384	1000	"main()" "Amr::init()"
0.2885591383795166	AsendTsiim	29	1	48	1000	"main()" "Amr::init()"
0.2885644435882568	AsendTsiim	29	3	768	1000	"main()" "Amr::init()"
0.2885661125183105	AsendTsiim	29	5	12288	1000	"main()" "Amr::init()"
0.2885935306549072	AsendTsiim	29	7	768	1000	"main()" "Amr::init()"
0.2885949611665818	AsendTsiim	29	10	768	1000	"main()" "Amr::init()"
0.2885961532592773	AsendTsiim	29	13	48	1000	"main()" "Amr::init()"
0.2885971069335938	AsendTsiim	29	19	6144	1000	"main()" "Amr::init()"
0.2886037828538086	AsendTsiim	29	25	384	1000	"main()" "Amr::init()"
0.2886049747487041	AsendTsiim	29	26	6144	1000	"main()" "Amr::init()"
0.2886130809783936	AsendTsiim	29	27	6144	1000	"main()" "Amr::init()"
0.2886223793029785	AsendTsiim	29	28	384	1000	"main()" "Amr::init()"
0.2959861755371094	ArecvTsiim	1	28	12288	1000	"main()" "Amr::init()"
0.29599004670715332	ArecvTsiim	5	28	48	1000	"main()" "Amr::init()"
0.2959914207458496	ArecvTsiim	7	28	768	1000	"main()" "Amr::init()"
0.2959923744201660	ArecvTsiim	10	28	768	1000	"main()" "Amr::init()"
0.2959933280944824	ArecvTsiim	19	28	6144	1000	"main()" "Amr::init()"
0.2959945201873779	ArecvTsiim	27	28	6144	1000	"main()" "Amr::init()"
0.2959954738616943	ArecvTsiim	29	28	384	1000	"main()" "Amr::init()"
0.2960212230682373	AsendTsiim	28	1	12288	1000	"main()" "Amr::init()"
0.2960393428802490	ArecvTsiim	0	15	12288	1000	"main()" "Amr::init()"
0.2960627079010010	ArecvTsiim	0	12	768	1000	"main()" "Amr::init()"
0.2960636615753174	ArecvTsiim	4	15	1536	1000	"main()" "Amr::init()"
0.2960653305053711	ArecvTsiim	5	15	768	1000	"main()" "Amr::init()"
0.2960655689239502	AsendTsiim	28	5	48	1000	"main()" "Amr::init()"
0.2960665225982666	ArecvTsiim	1	12	768	1000	"main()" "Amr::init()"
0.2960665225982666	ArecvTsiim	6	15	48	1000	"main()" "Amr::init()"
0.2960674762725830	ArecvTsiim	7	15	48	1000	"main()" "Amr::init()"
0.2960679531097412	ArecvTsiim	2	12	6144	1000	"main()" "Amr::init()"
0.29606868683654785	ArecvTsiim	12	15	6144	1000	"main()" "Amr::init()"
0.2960691452026367	ArecvTsiim	3	12	48	1000	"main()" "Amr::init()"

Lists in chronological order:

- Time of function call
- Type of MPI function call
- From rank
- To rank
- Size of the message
- Message tag
- Regions that the call occurred within.

Filtered by both **subregions** and **region** selection.

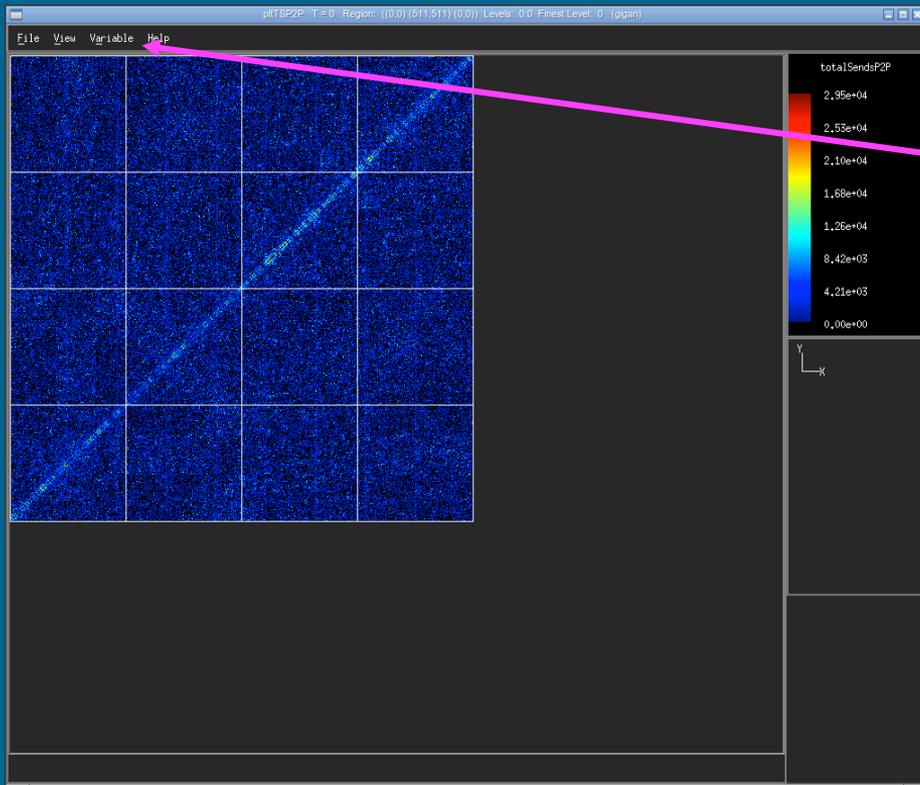
Specially made for MPI analysis for Cy Chan's research group.

If you can parse the data yourself, feel free to use it in your own studies. If you need a different version of something similar, let me know.

# Sends Plotfile:

Creates plot file describing the total number of MPI point-to-point sends and the total size of messages between each pair or MPI ranks.

To MPI rank #



Use the “**Variable**” drop-down menu to switch between:

number of calls

(totalSendsP2P)

total message size in bytes

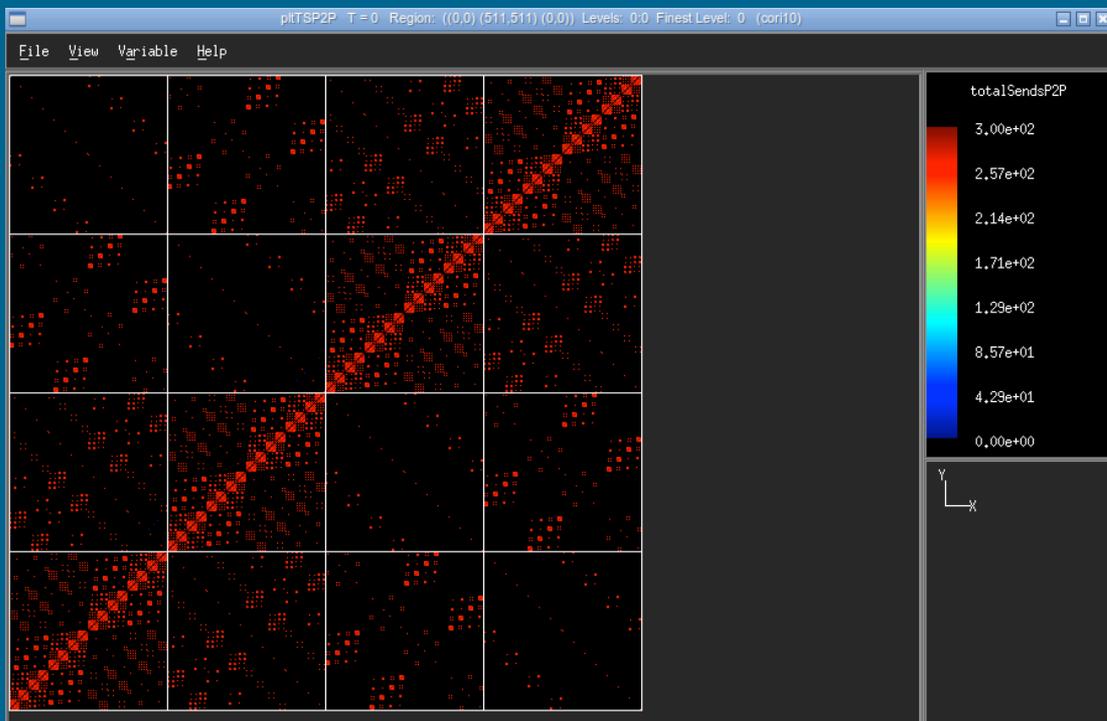
(totalSentDataP2P)

Currently, building a Sends plotfile in the GUI **only works in a serial build** of AMRVIS.

However, the serial version will properly filter over subregions and regions.

From MPI rank #

# Sends Plotfile: What to look out for



- Hotspots in data sent or number of calls.
- Extremely asymmetric plots; all the data is going one-way.
- Procs with no communication at all; black columns or rows.
- More 'far away' communication than 'nearby' communication; biggest contributions are away from the diagonal.

# For Profiling Help Contact:

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