

methods of computational science

visualization

day ii - bottlenecks/parallel-viz

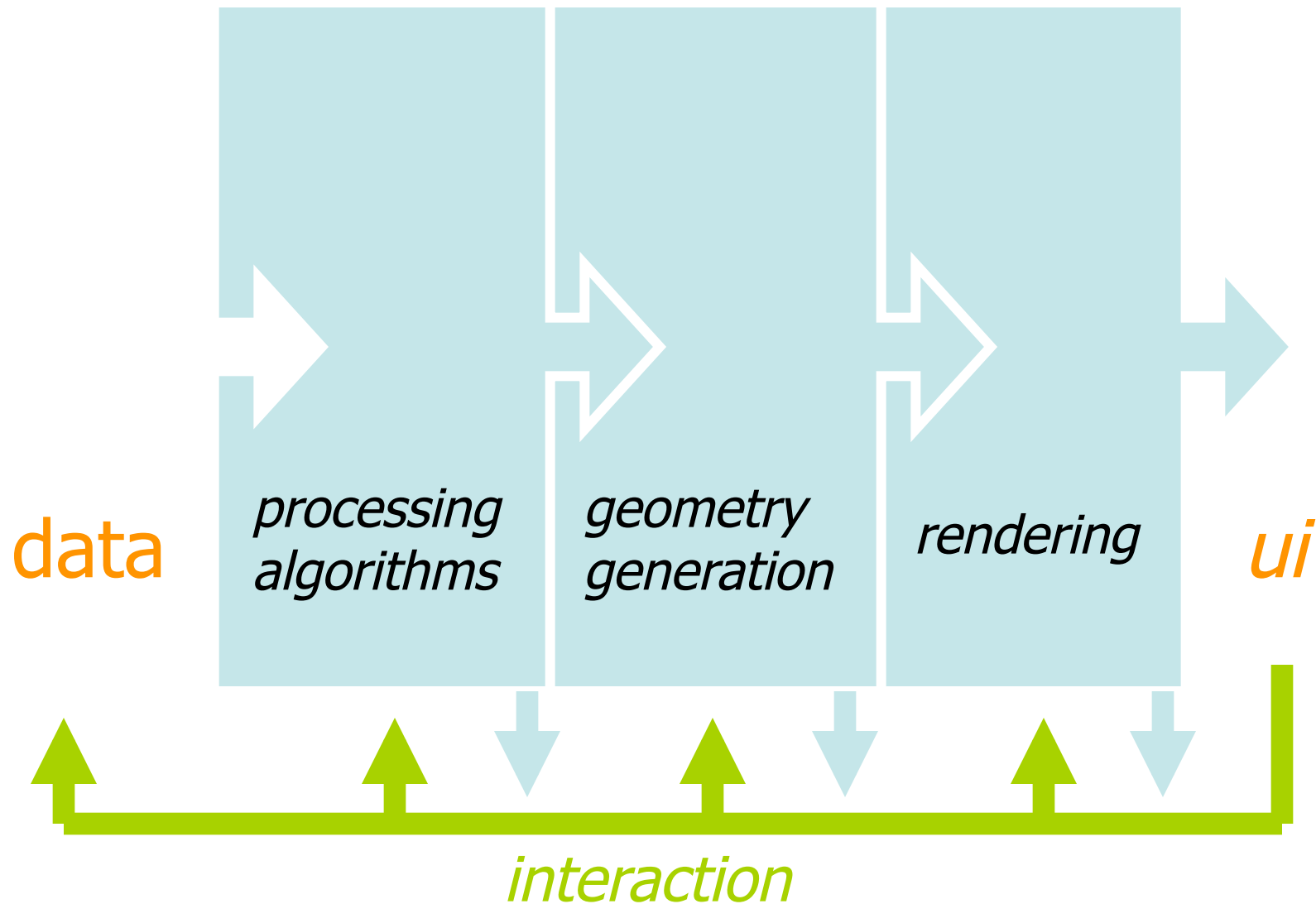
santiago v lombeyda

center for advanced computing research

caltech

quick review:
THE VISUALIZATION PROCESS

usual visualization "engine"



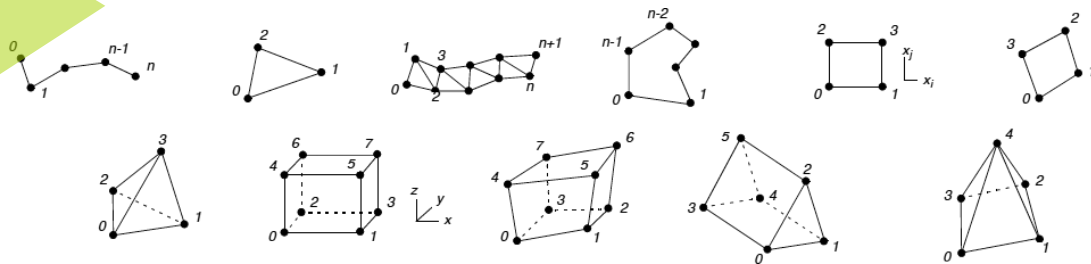
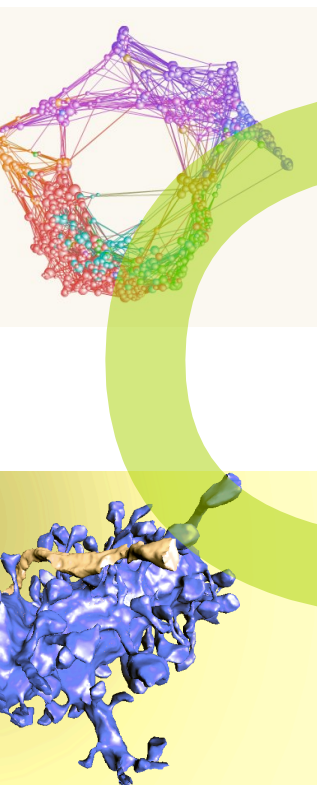
data: geometric structure

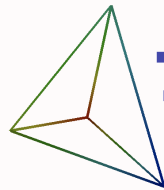
abstract multi-dimensional data records

MPG Cylinders Horsepower Weight Acceleration Year Origin

```
8. 50. 4 2.8 8.2 4 40. 250. 4 1500. 5500. 4 5. 30. 4 69.5 82.5 4 .8 3.2 3  
18.000000 8.000000 130.000000 3504.000000 12.000000 70.000000 1.000000  
15.000000 8.000000 165.000000 3693.000000 11.500000 70.000000 1.000000  
18.000000 8.000000 150.000000 3436.000000 11.000000 70.000000 1.000000  
16.000000 8.000000 150.000000 3433.000000 12.000000 70.000000 1.000000  
17.000000 8.000000 140.000000 3449.000000 10.500000 70.000000 1.000000  
.....
```

2d/3d data + scalar/vector/tensor + time



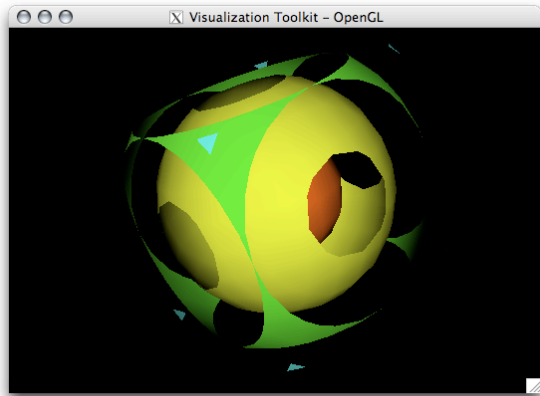


vtk sample: pyramid.vtk

```
# vtk DataFile Version 2.0
My Tet-Pyramid Example
ASCII
DATASET UNSTRUCTURED_GRID
POINTS 4 float
0.0 0.0 0.0
1.0 0.0 0.0
0.5 0.0 0.7
0.5 0.6 0.7
CELLS 1 5
4 0 1 2 3
CELL_TYPES 1
10
POINT_DATA 4
SCALARS vertexData float 1
LOOKUP_TABLE default
0.1
0.2
0.3
0.4
CELL_DATA 1
SCALARS tetData int 1
LOOKUP_TABLE default
1
```

vtk sample: volume.vti

```
<?xml version="1.0"?>
<VTKFile type="ImageData" version="0.1"
  byte_order="LittleEndian">
  <ImageData WholeExtent="0 3 0 3 0 3" Origin="0 0 0"
    Spacing="1 1 1">
  <Piece Extent="0 3 0 3 0 3">
  <PointData Scalars="vertexData">
  <DataArray type="Float32" Name="scalarData"
    format="ascii">
0 1 2 3 1 2 3 4 2 3 4 8 3 6 9 11
2 3 4 5 5 6 7 8 3 4 5 6 4 5 6 7
3 4 5 6 3 4 5 6 4 5 6 7 6 7 8 9
2 3 4 5 2 3 4 5 3 4 5 6 4 5 6 7
  </DataArray>
  </PointData>
  <CellData Scalars="cellData" Normals="cell_normals">
  <DataArray type="Int32" Name="cellData" format="ascii">
1 3 9 2 8 16 3 9 27
2 3 4 6 7 8 6 9 10
0 1 2 0 2 4 1 2 3
  </DataArray>
  </CellData>
  </Piece>
  </ImageData>
</VTKFile>
```



vtkpython: iso.py

```
#!/usr/bin/python
# load VTK extensions
import vtk

# create a rendering window and renderer
renderer = vtk.vtkRenderer()
myWindowRenderer = vtk.vtkRenderWindow()
myWindowRenderer.AddRenderer(renderer)
myWindowRenderer.SetSize(640,480)

myInteractiveWindow = vtk.vtkRenderWindowInteractor()
myInteractiveWindow.SetRenderWindow(myWindowRenderer)

# read mydata from volume.vti file
mydata= vtk.vtkXMLImageDataReader()
mydata.SetFileName("volume.vti")

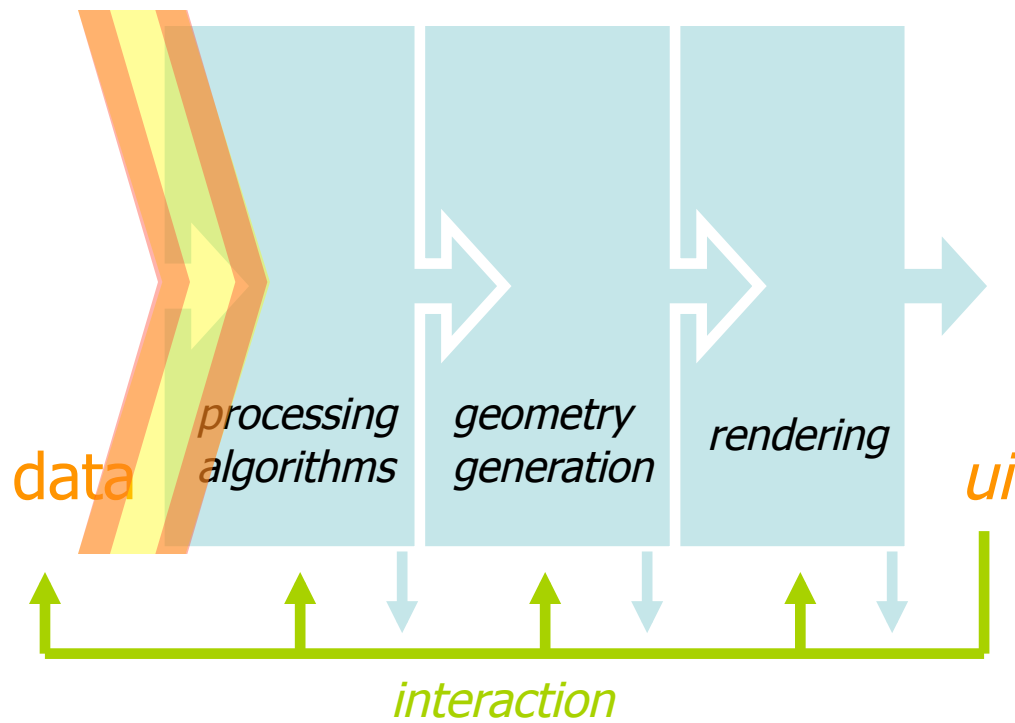
# create filter
mydataIso= vtk.vtkMarchingCubes()
mydataIso.SetInput(mydata.GetOutput())
mydataIso.SetValue(0,0.1)
mydataIso.SetValue(1,0.3)
mydataIso.SetValue(2,0.5)
mydataIso.SetValue(3,0.7)

# pipe results to polymapper, and add actor
mydataMapper= vtk.vtkPolyDataMapper()
mydataMapper.SetInput(mydataIso.GetOutput())
mydataActor = vtk.vtkActor()
mydataActor.SetMapper(mydataMapper)
# assign our actor to the renderer
renderer.AddActor(mydataActor)

# enable user interface interactor
myInteractiveWindow.Initialize()
myInteractiveWindow.Start()
```

closer look:
BOTTLENECKS

visualization bottlenecks

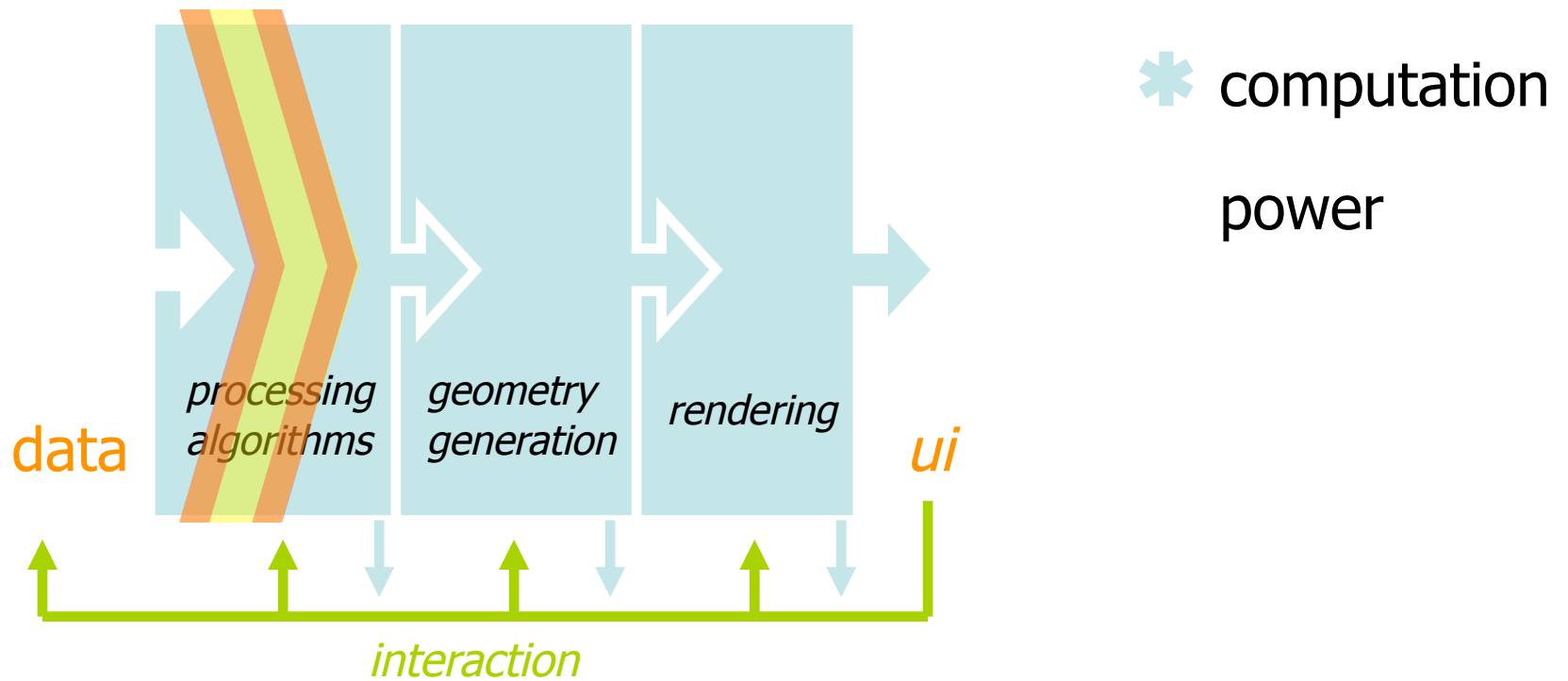


* data size

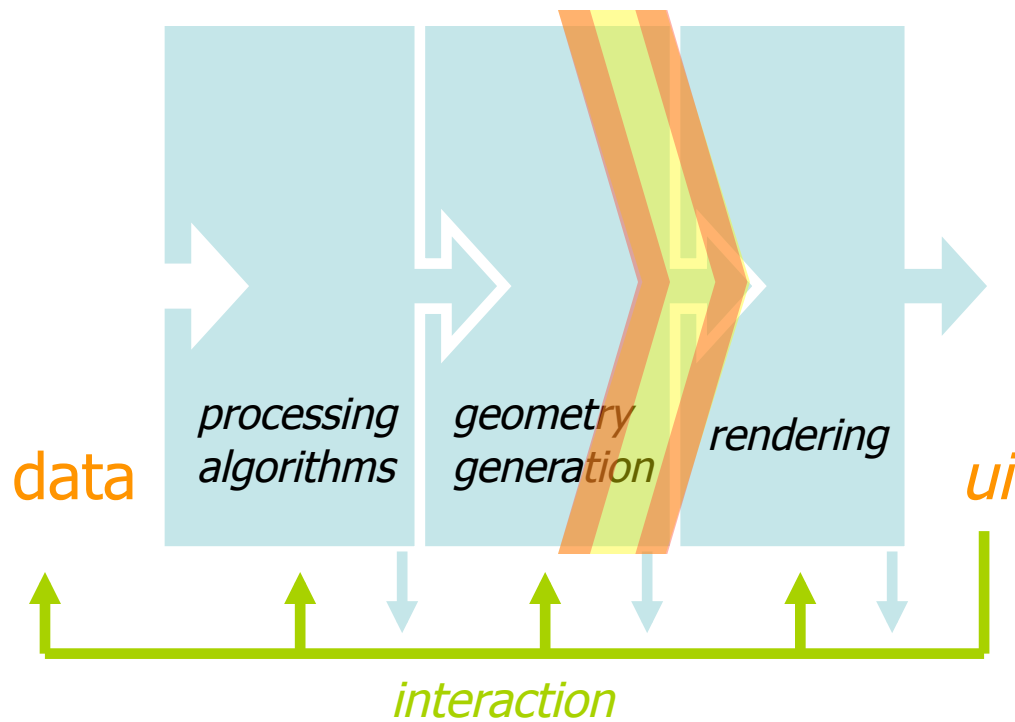
* data format

* xml

visualization bottlenecks

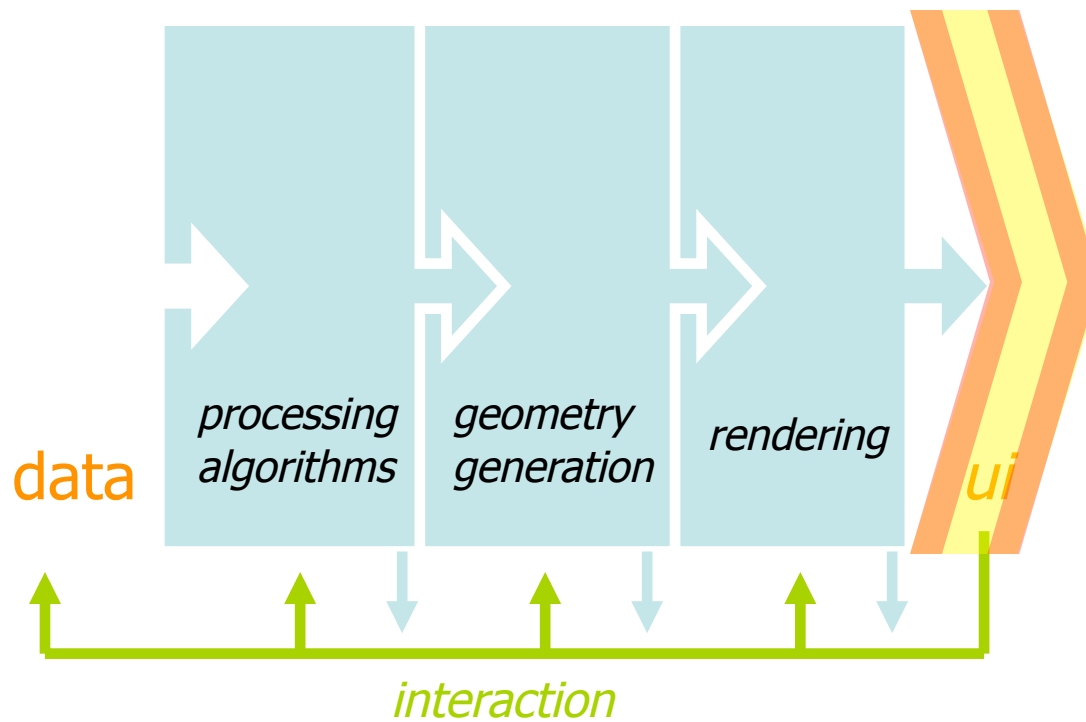


visualization bottlenecks



- * number of triangles
(base rendering units)
- * number voxels

visualization bottlenecks



* knowledge

level of

"end user"

* complexity of

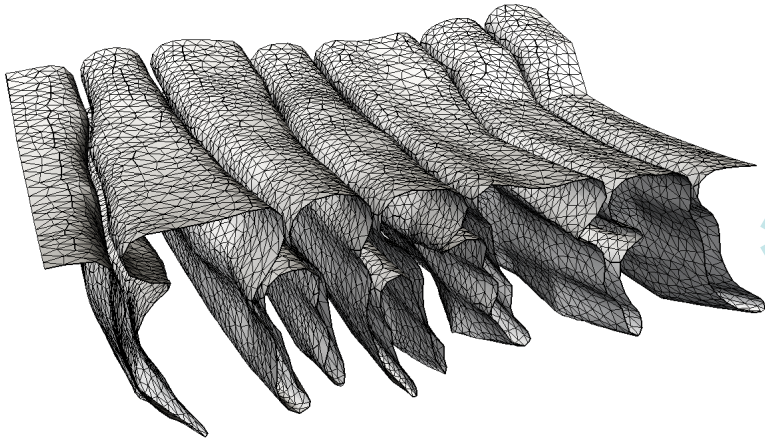
data base

addressing: bottlenecks:
lod vs parallelism

addressing *throughput bottlenecks*

- * level of detail (LOD)
 - * requires preprocessing
 - * requires larger storage (*original+...*)
- * parallel processing/rendering
 - * requires a parallel system
 - * increases sw complexity
 - * less likely to be “portable”

lod: decimation

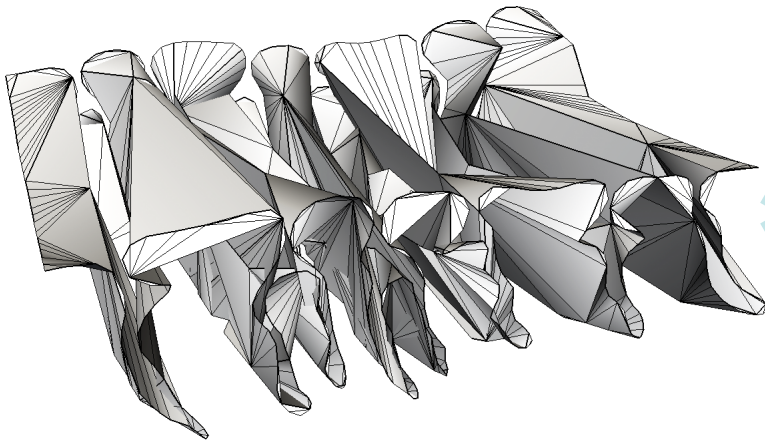


* 25365



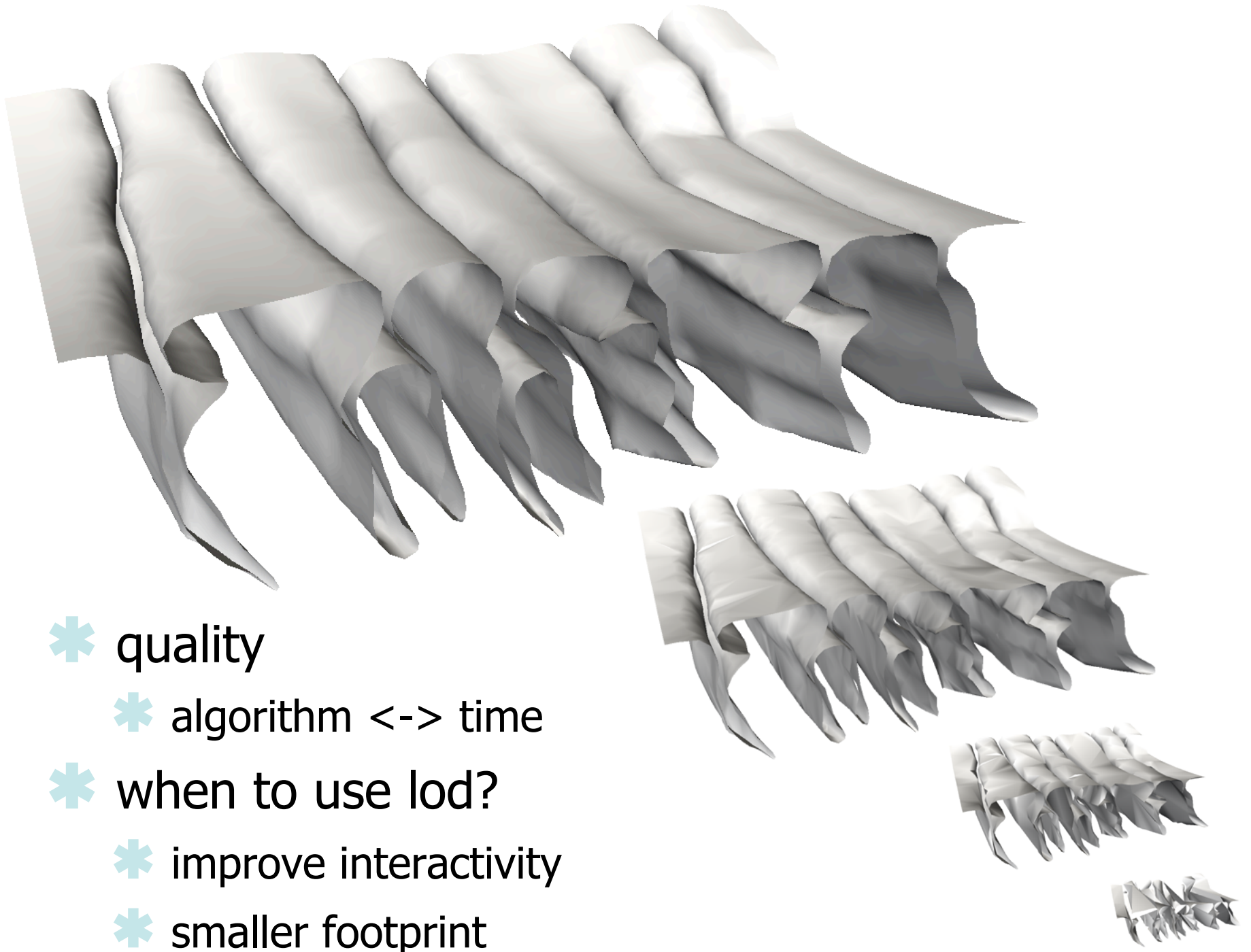
* 12681

* 50%



* 1011

* 4%



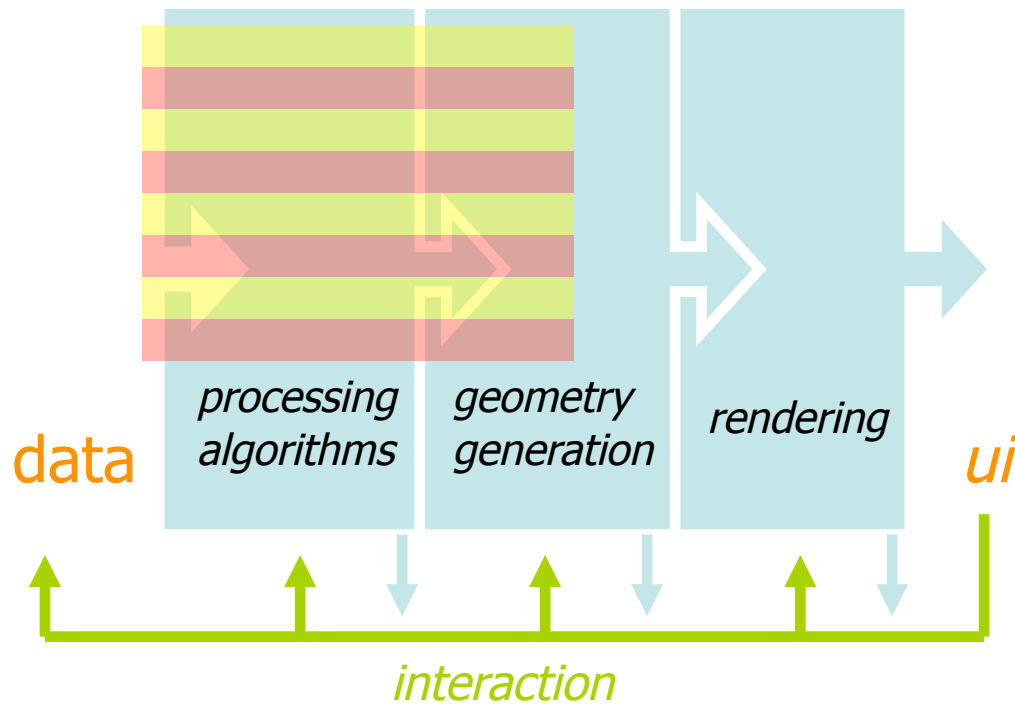
- * quality
- * algorithm \leftrightarrow time
- * when to use lod?
- * improve interactivity
- * smaller footprint

addressing: bottlenecks:
lod vs parallelism

addressing *throughput bottlenecks*

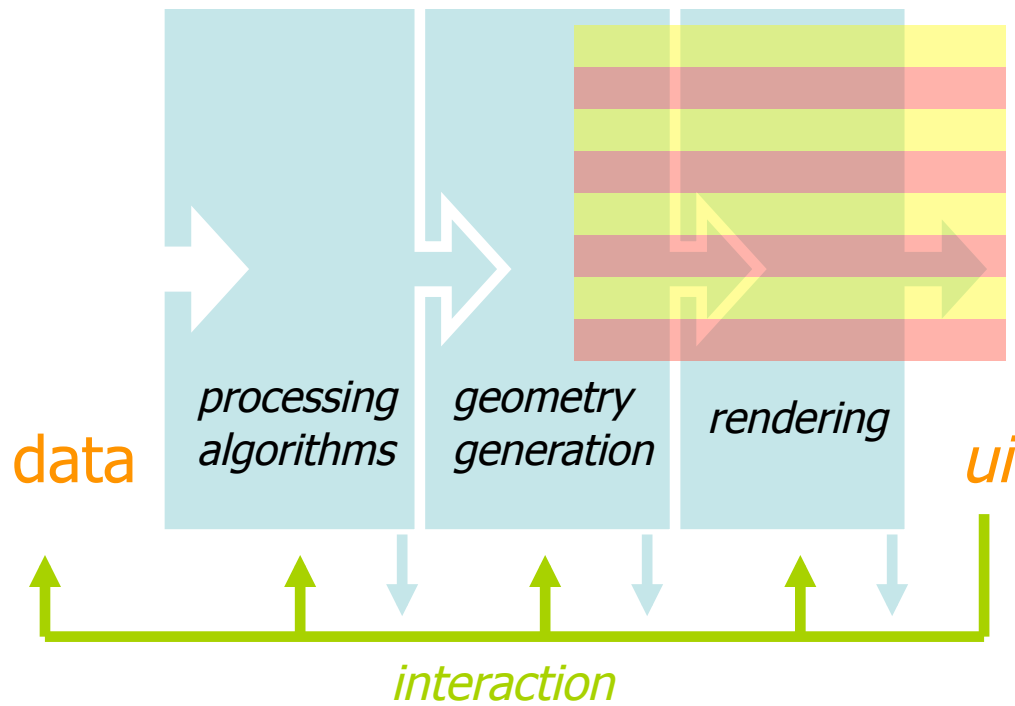
- * level of detail (LOD)
 - * requires preprocessing
 - * requires larger storage (*original+...*)
- * parallel processing/rendering
 - * requires a parallel system
 - * increases sw complexity
 - * less likely to be “portable”

parallel viz...



- * + cpus
- * data?
- * seams?

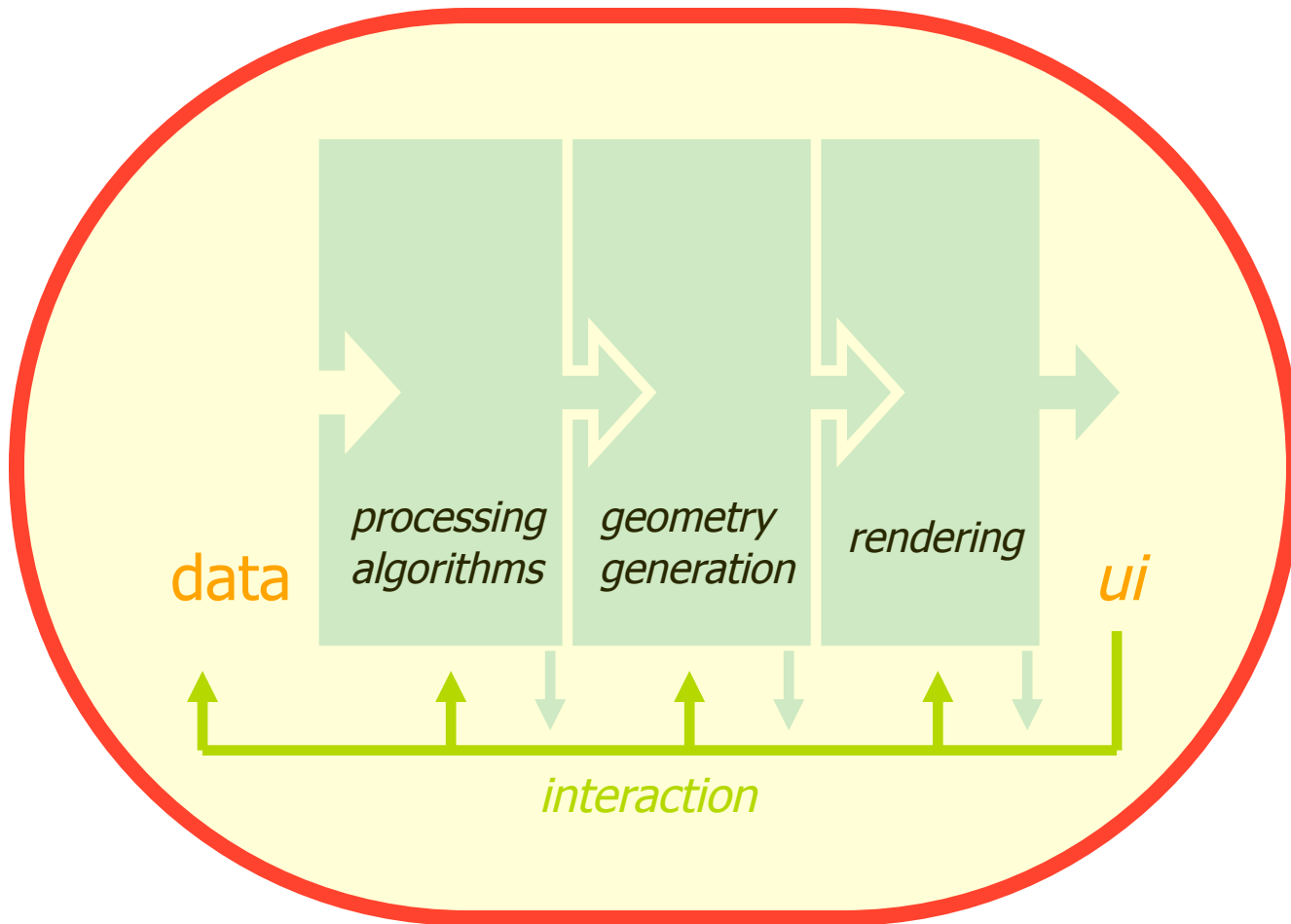
parallel viz...



- * + gpus
- * screen?
- * space?

addressing: bottlenecks:
leverage other peoples work: parallelism

visualization system



- * Paraview^{VTK}
- * LLNL VisIt^{VTK}
- * EnSight^{\$}
- * OpenDX
- * IBM's DataExplorer
- * Mollegro, ...

tools:

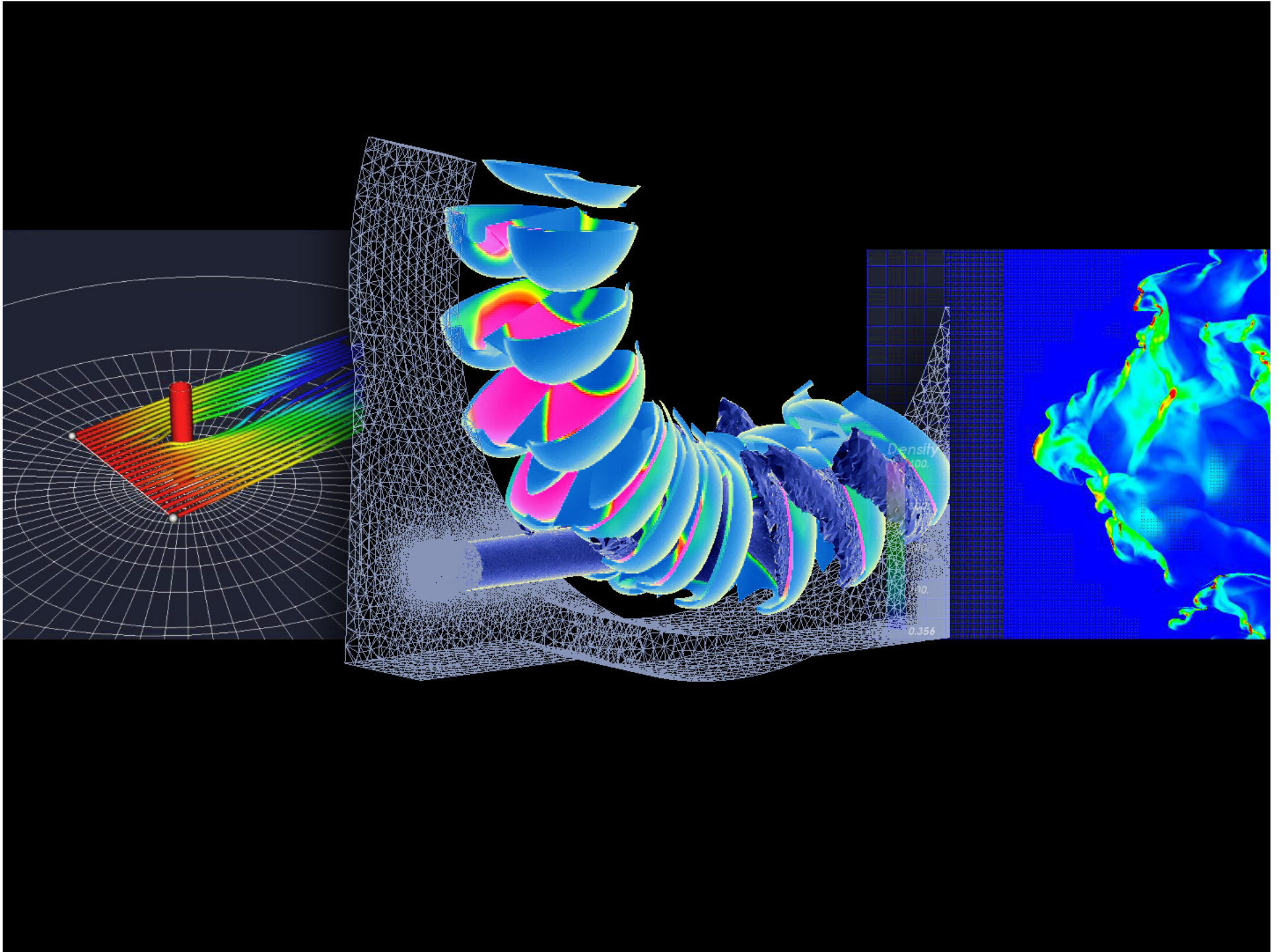
PARAVIEW VTK

paraview

paraview.org

- * vtk based!
- * active community
 - * mailing list + wiki
 - * lead at kitware: *berk geveci*
 - * sandia national lab
 - * los alamos national lab, army research lab
- * parallel!
- * QT based (from version 3.0)
 - * 3.4.0 available in most platforms

quick demo:
PARAVIEW



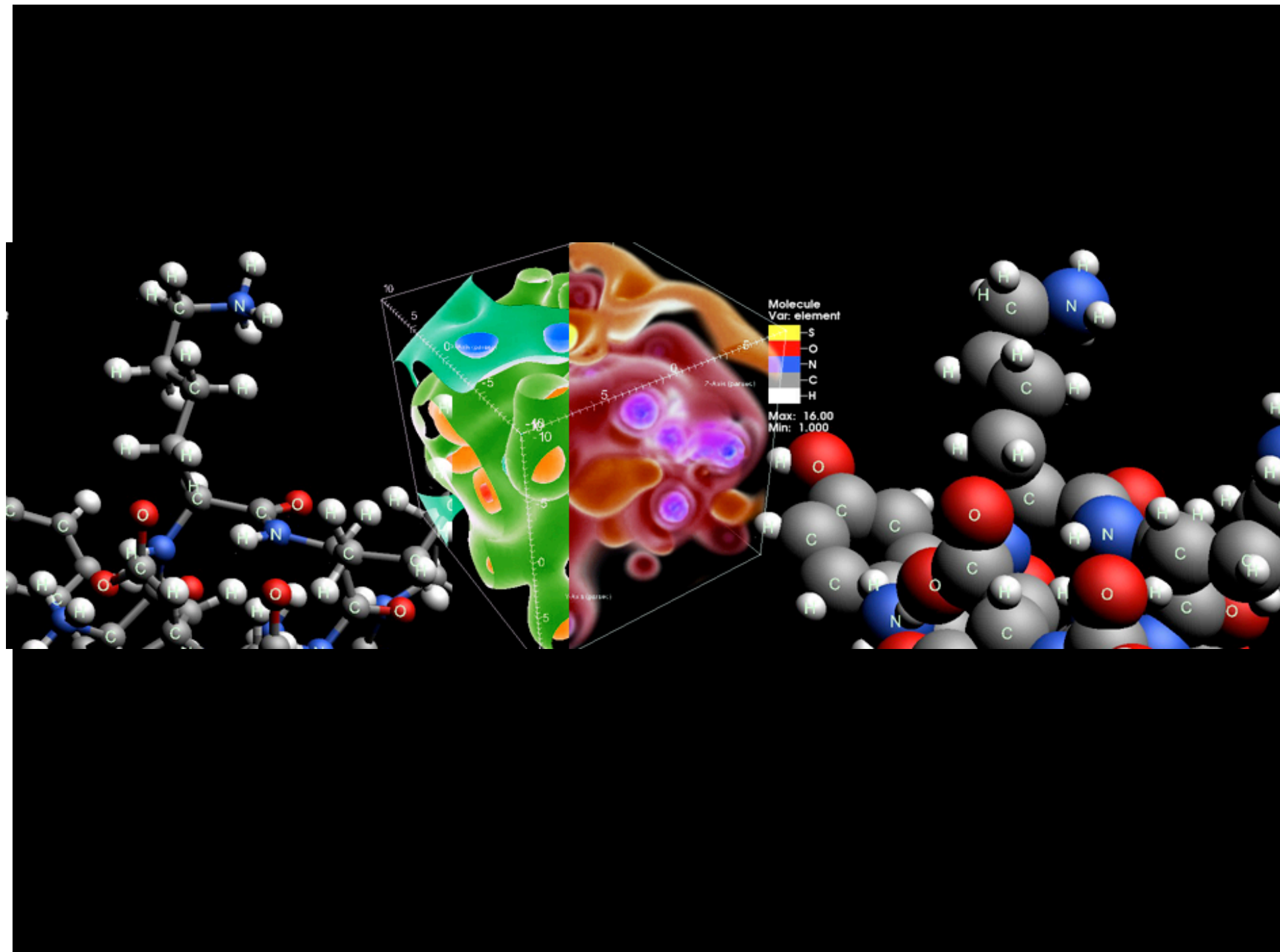
tools:
VISIT VTK

llnl's visit!

- * vtk based!
- * active development
 - * very responsive
 - * lawrence-livermore national lab (asci/doe)
- * designed for large data
- * parallel!
- * presets for large lab machines
- * easily scriptable via python
- * simple docs (minimal pdf)

llnl.gov/visit

demo:
VISIT



why paraview^{PV}? (visit^{V!}?)

* paraview/visit can handle large data!

* parallel

PV: 👍

V!: 👍 👍

* stable

PV: 👍

V!: 👍 👍

* gui

PV: 👍 👍 👍

V!: 👍

* lod

PV: 👍 👍

V!: 👍

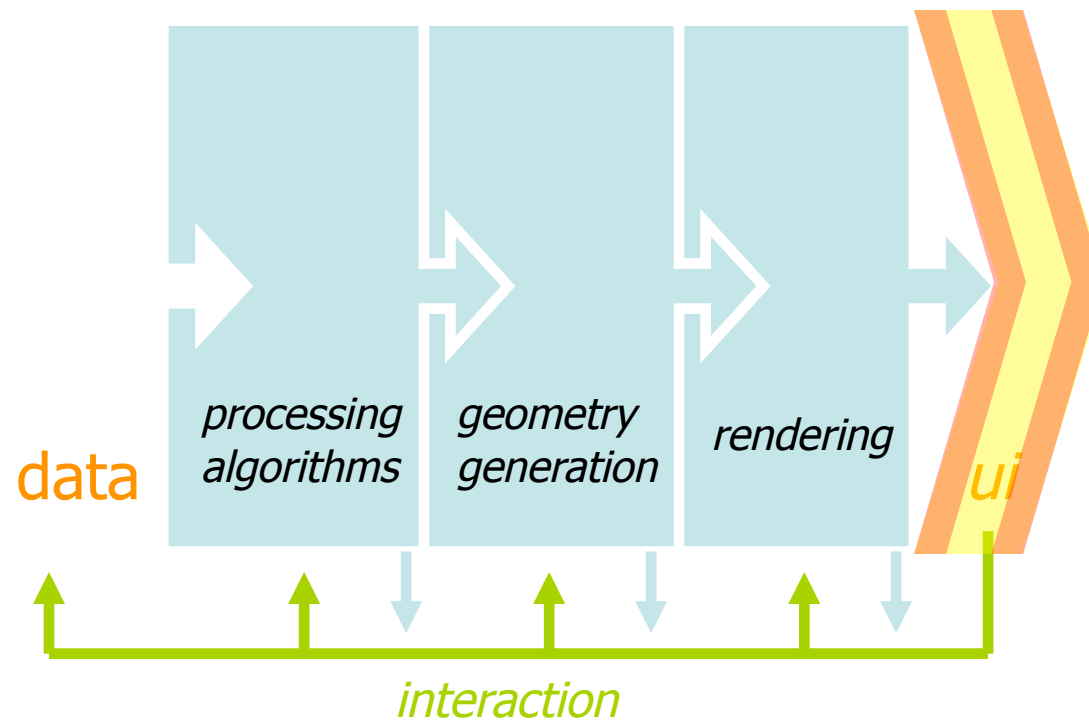
* many filters (all of vtk), open source, binaries for major platforms, 64 bit versions, actively being developed, scriptable (*python!*), ...

* *possible to extend and/or script*

* learning curve

* hard to get everything

visualization bottlenecks



case study: *gui design*
MCELL BIO VIEWER

DREAMM

Table Editing Controls

ENABLE EDITING

Current State Value: 0001

Specify State Value: 1

- Load Current State Value into Edit Fields
- Read Edit Fields Into Current State Value
- Delete Current State Value
- Read Edit Fields Into Specified State Value

Effector Sites, Molecules, Custom Points - Customize

Table Editing Controls

ENABLE EDITING

Current State Value: 0001

Specify State Value: 1

RGB Color Values: 1.00000

Glyph: S02

Height (if applicable):

Visualization Data Files

Output File Names

File Name Iteration Number(s)

Reimport

DReAMM Image Window

File Execute Windows Connection Options Help

Frame Control

Start: 1 | Next: 5 | End: 11

Current: 4

Min: 1 | Increment: 1

Molecules & Custom Points - Default Prop...

Default Rendering Properties for Molecules and Custom Points

Glyph Abbreviations (reference): P01 pixel

RGB Color Values: 1.00000

Opacity: 1.00000

Shade? Yes

Method: Smooth

DReAMM Image Window

File Execute Windows Connection Options Help

Animation Sequence

Frame Settings

	Start	Step	Stop	Current
Keyframe Sequence Indices	1	1	1	1
MCell Iteration Numbers	0	10	100	30
Image Clipping Offsets	0.0	0.0	0.0	0.0
Image File Name Indices	1	1	1	1

Sequence ...

4 ...

Navigation icons: Play, Stop, Previous, Next



intuitive

simple

interactive

effective

* who is the user?

* what is the task?

...inspiration

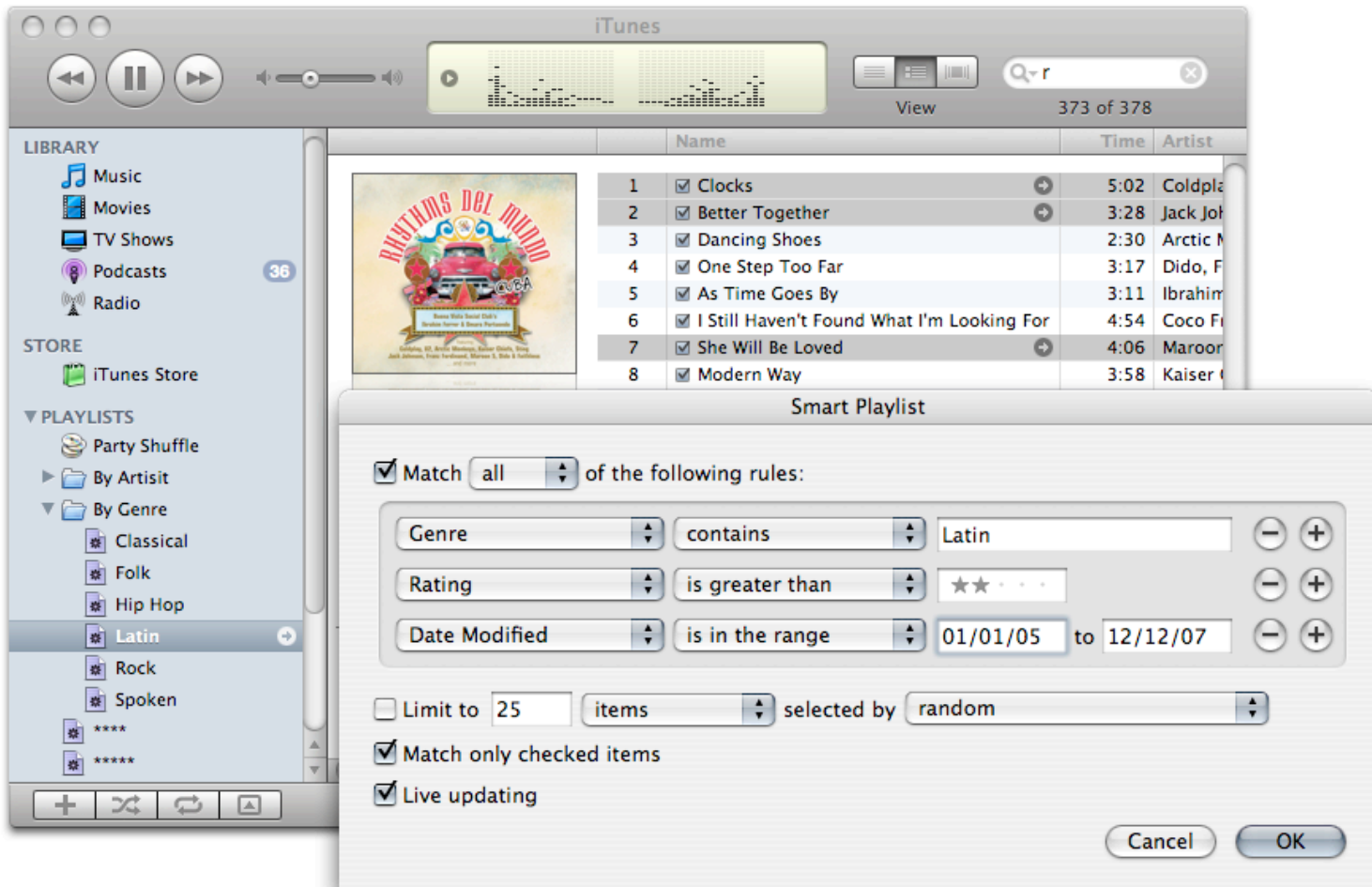
GUI



GUI



GUI



GUI

[bioViewer v.0.1.3]

SEARCH | Interactive | matchcase | A2

SELECT | ALL | INVERSE | NONE | MOVE UP SELECTION |

ACTIONS | | ON selected

on/off	name	type	color	opacity	
<input checked="" type="checkbox"/>	AChR.A2Rc	surface_molecules	#8000ff	0.5	
<input checked="" type="checkbox"/>	AChR.A2Ro	surface_molecules	#8000ff	0.5	
<input checked="" type="checkbox"/>	nmj.basal_lamina1	mesh	#d940ff	0.5	
<input checked="" type="checkbox"/>	nmj.presynaptic1	mesh	#9f40ff	0.5	
<input checked="" type="checkbox"/>	AChE.E	surface_molecules	#ffb340	1	
<input checked="" type="checkbox"/>	AChE.EA	surface_molecules	#ffec40	1	
<input checked="" type="checkbox"/>	AChE.EAs	surface_molecules	#d9ff40	1	
<input checked="" type="checkbox"/>	AChE.Es	surface_molecules	#9fff40	1	
<input checked="" type="checkbox"/>	AChR.ARs	surface_molecules	#40ff8c	1	
<input checked="" type="checkbox"/>	AChR.ART	surface_molecules	#40ffc6	1	
<input checked="" type="checkbox"/>	AChR.R	surface_molecules	#40ffff	1	
<input checked="" type="checkbox"/>	ChR.AR	surface_molecules	#40c6ff	1	
<input checked="" type="checkbox"/>	ChR.ARp	surface_molecules	#408cff	1	
<input checked="" type="checkbox"/>	ChR.R	surface_molecules	#4053ff	1	
<input checked="" type="checkbox"/>	ACh	volume_molecules	#ff4040	1	
<input type="checkbox"/>	nmj.box	box	#6640ff	0	
<input checked="" type="checkbox"/>	nmj.bpjm1	mesh	#ff40ec	0.5	
<input checked="" type="checkbox"/>	nmj.mpjm1	mesh	#ff40b2	0.2	
<input checked="" type="checkbox"/>	nmj.tpjm1	mesh	#ff4079	0.2	
<input checked="" type="checkbox"/>	Ch	volume_molecules	#ff7940	1	

I turn ON ALL | FLIP on/off ALL | turn OFF ALL |

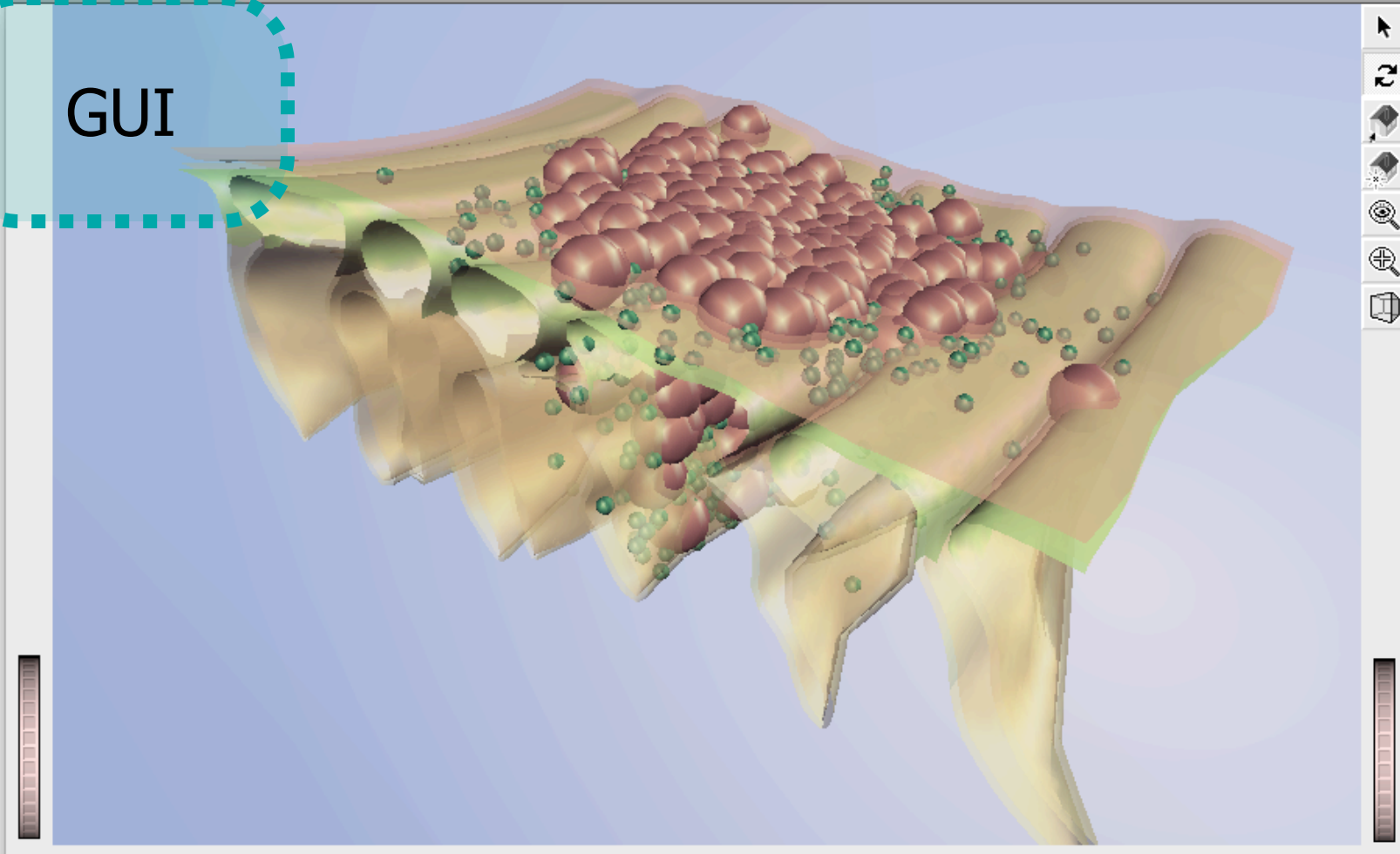
FILE PATH OF "VTK" DIRECTORY:

LAST FRAME NUMBER:

GO!

...a first draft

GUI



Rotx Roty 400 5 / 71 Dolly

- OBJECTS
- | | | | |
|---|---|------------------------------------|-----------------------------------|
| <input type="checkbox"/> nmj.box | <input checked="" type="checkbox"/> nmj.tpjm1 | <input type="checkbox"/> ChR.R | <input type="checkbox"/> AChR.ARt |
| <input checked="" type="checkbox"/> nmj.presynaptic1 | <input checked="" type="checkbox"/> ACh | <input type="checkbox"/> AChR.A2Rc | <input type="checkbox"/> ChR.AR |
| <input checked="" type="checkbox"/> nmj.basal_lamina1 | <input checked="" type="checkbox"/> Ch | <input type="checkbox"/> ChR.ARp | <input type="checkbox"/> AChE.Es |
| <input checked="" type="checkbox"/> nmj.bpjm1 | <input type="checkbox"/> AChE.EAs | <input type="checkbox"/> AChR.A2Ro | <input type="checkbox"/> AChR.R |
| <input checked="" type="checkbox"/> nmj.mpjm1 | <input type="checkbox"/> AChR.ARs | <input type="checkbox"/> AChE.EA | <input type="checkbox"/> AChE.E |

- COLLECTIONS
- ALL
 - MESHES
 - VOLUME_MOLECULES
 - SURFACE_MOLECULES

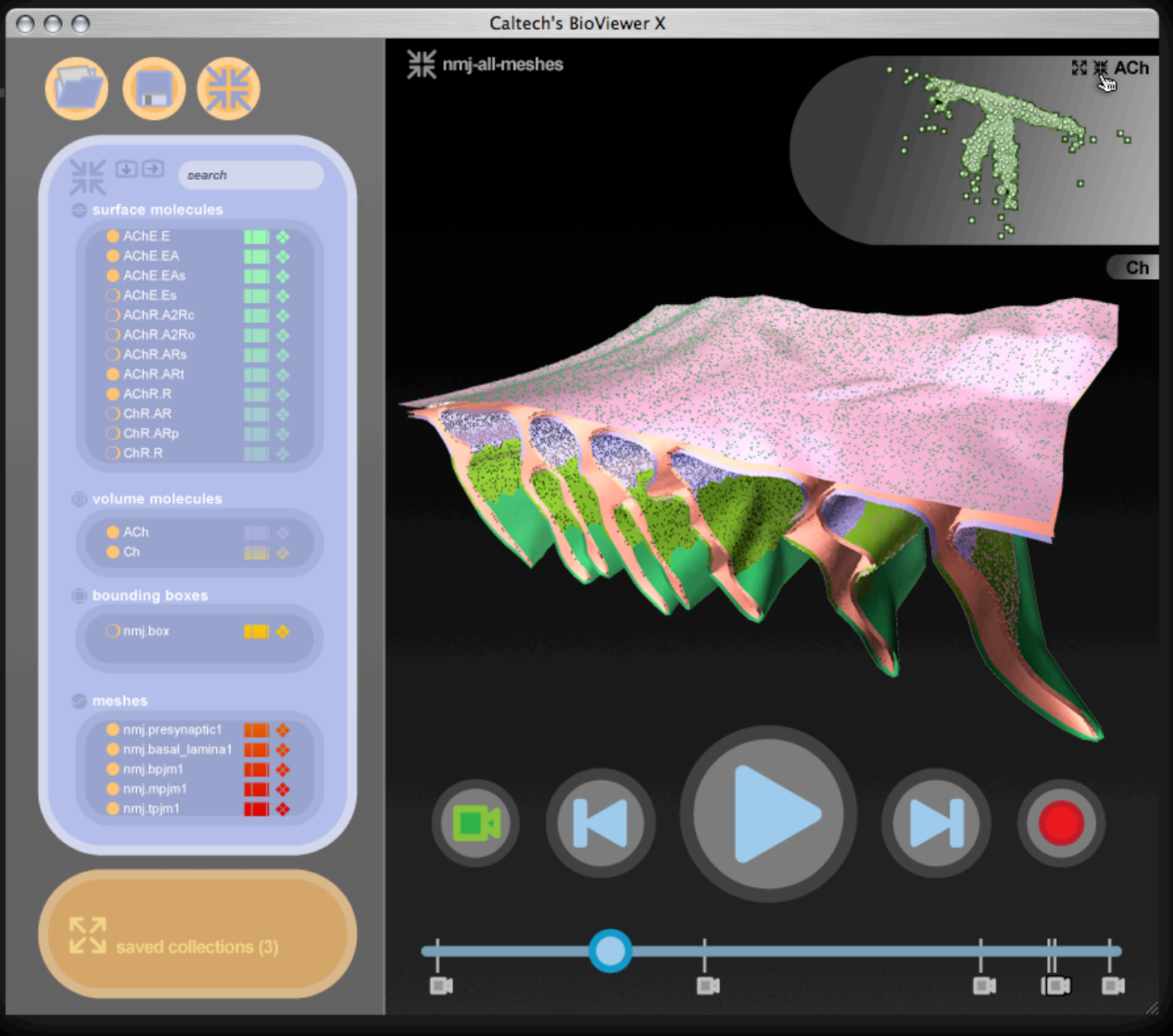
TOOLS

search

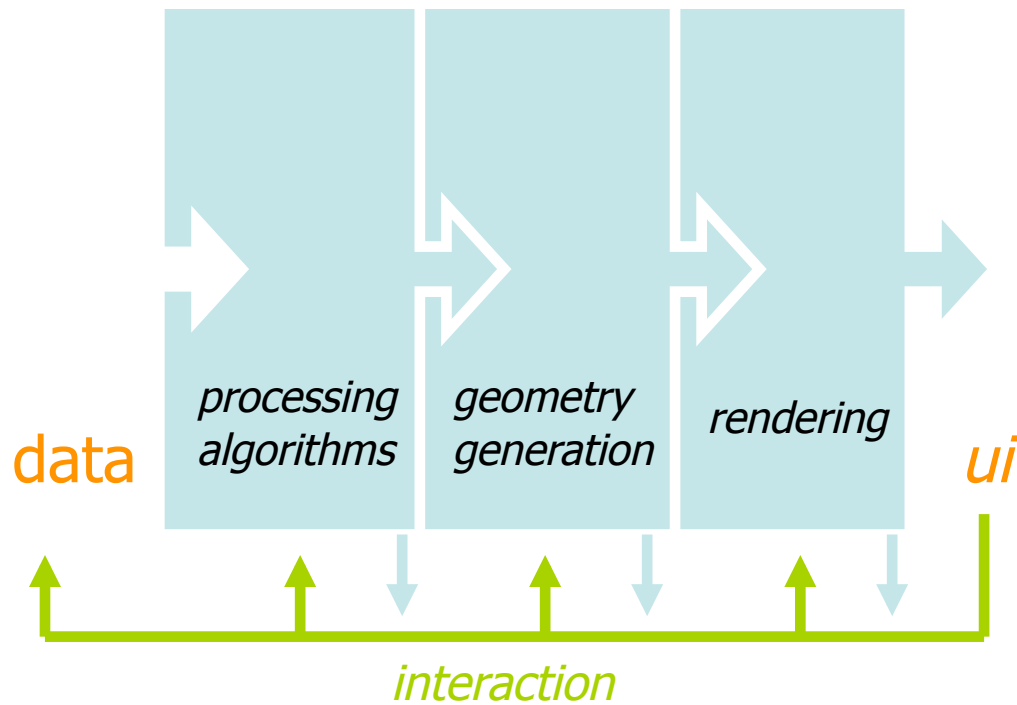
TOGGLE SELECT

TOGGLE VISIBLE

ultimate tool mockup



visualization bottlenecks



*what if
there is
not much
to leverage?*

exercises

- * create your own vtk data file
 - * have at least 100 data points/grid points
 - * if you have some ascii based data already
 - * you can use awk/sed to filter data
 - * then you can manually add the vtk tags
- * create a movie using **paraview!**
(or visit)
- * if you feel ambitious, try **data explorer**, or write a **vtk** program

thanks!

avyakta.caltech.edu:8888/esci101

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