

# PyMOLViz

Despite its age, PyMOL is still a popular tool to display (and manipulate) molecular files. Unfortunately its great graphical capabilities are often hidden by incomplete documentation and obscure syntax. This python module is an attempt to comprehensively consolidate my understanding of these capabilities.

## Setup

### Requirements

- `numpy`
- `scipy`
- `matplotlib`
- `gemmi` if you want to load .mtz files

Surprisingly PyMOL is not necessarily required to run PyMOLViz, only to display the generated files.

## Installation

In order to install the module you should navigate to the `module` folder and type:

```
pip install -e .
```

```
~/PyMolViz$ cd module/  
~/PyMolViz/module$ pip install -e .
```

This should install the module in your current environment and automatically load any updates to the module.

## Introduction

The way that PyMOLViz is currently set up, it does not interact with PyMOL directly (although this is planned to be a possibility for a future update) but rather to generate python scripts that can then be loaded into PyMOL. This has the benefit that PyMOLViz does not have to run in the same environment (nor under the same operating system or even on the same computer) as PyMOL.

## Simple Example

In a simple example we will create a set of points and display them in PyMOL.

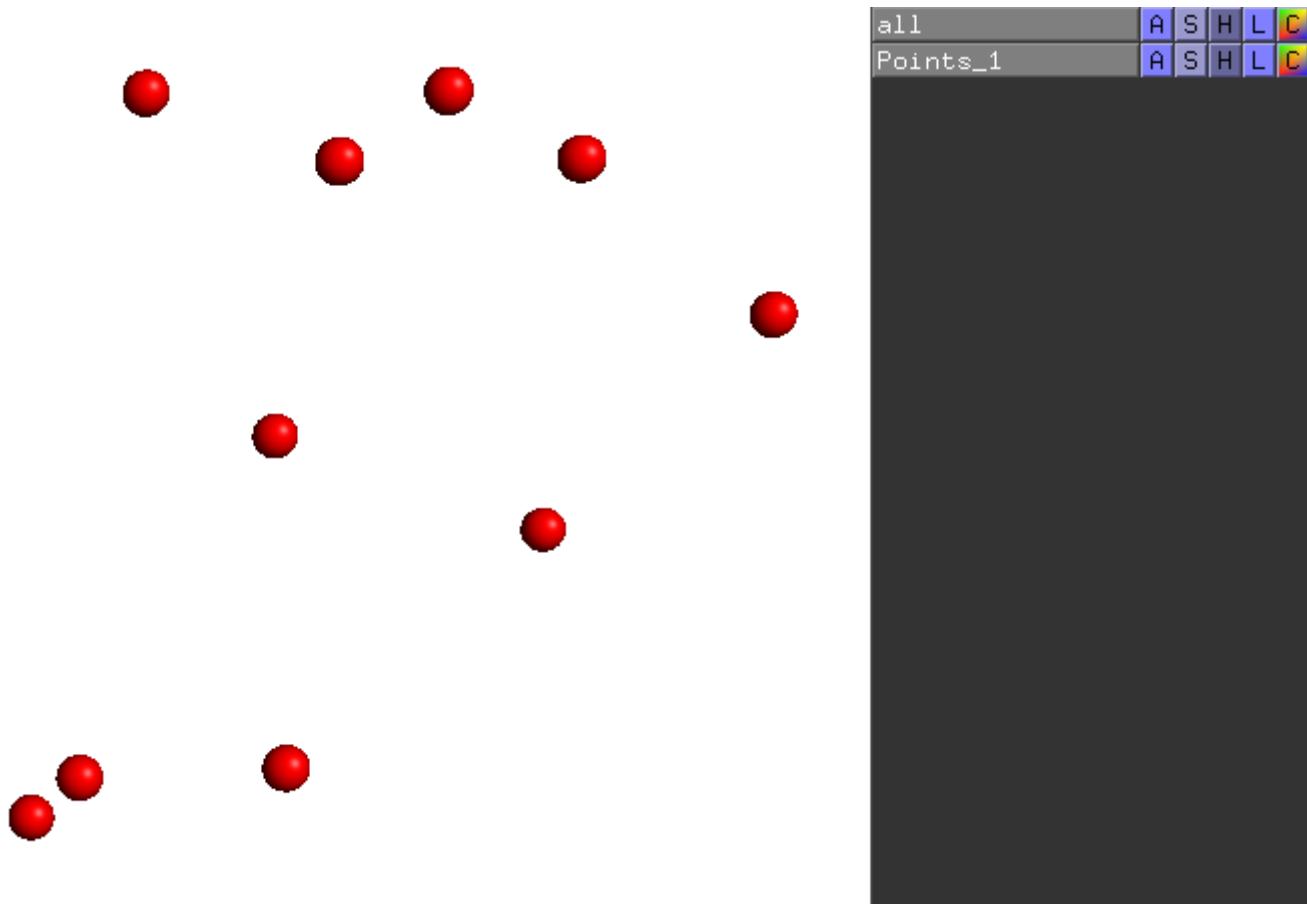
```
import numpy as np
import pymolviz as pmv

points = np.random.rand(10, 3) * 10
pmv.Points(points).write("out/points.py")
```

This generates a python script in out:

```
(base) highgarden@DESKTOP-5B09I4T:~/PyMolViz/test/00-Introduction/out$ ls
points.py
```

When we load this into PyMOL we can see 10 points:



## Displayables

There are a couple of things of note here. PyMOLViz is based on so called *Displayables*. A *Displayable* is everything that gets a separate entry in the objects side bar in PyMOL in this example case *Points\_1*.

all	A	S	H	L	C
Points_1	A	S	H	L	C

Displayables can always be written to a script via the `write` method and they always have a name. From the example we can see, that a dummy name will be generated if none is provided by the user.

## Points, Lines and Arrows

Some of the easiest to create and useful objects are points, lines and arrows (especially during debugging). These objects have the advantage over pseudo atoms or measurements that they are significantly less computationally intensive, allowing to display larger datasets.

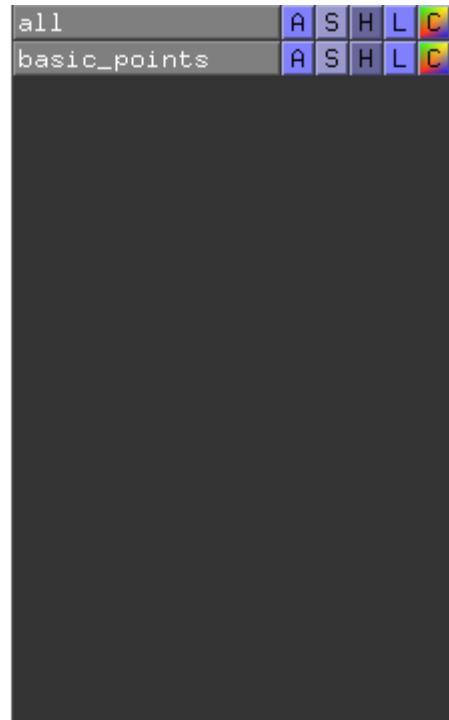
### Points

*Points* are defined by a set of *vertices* (positions) and *color*. As they are inheriting from *Displayables*, they also have a name and can be written to a script via `write`.

```
import numpy as np
import pymolviz as pmv

vertices = np.random.rand(10,3) * 10
p = pmv.Points(vertices, color = "red", name = "basic_points")

p.write("basic_points.py")
```



## Render Types

By default, points are rendered as Spheres. Even more performant is rendering them as "Dots" (pixels):

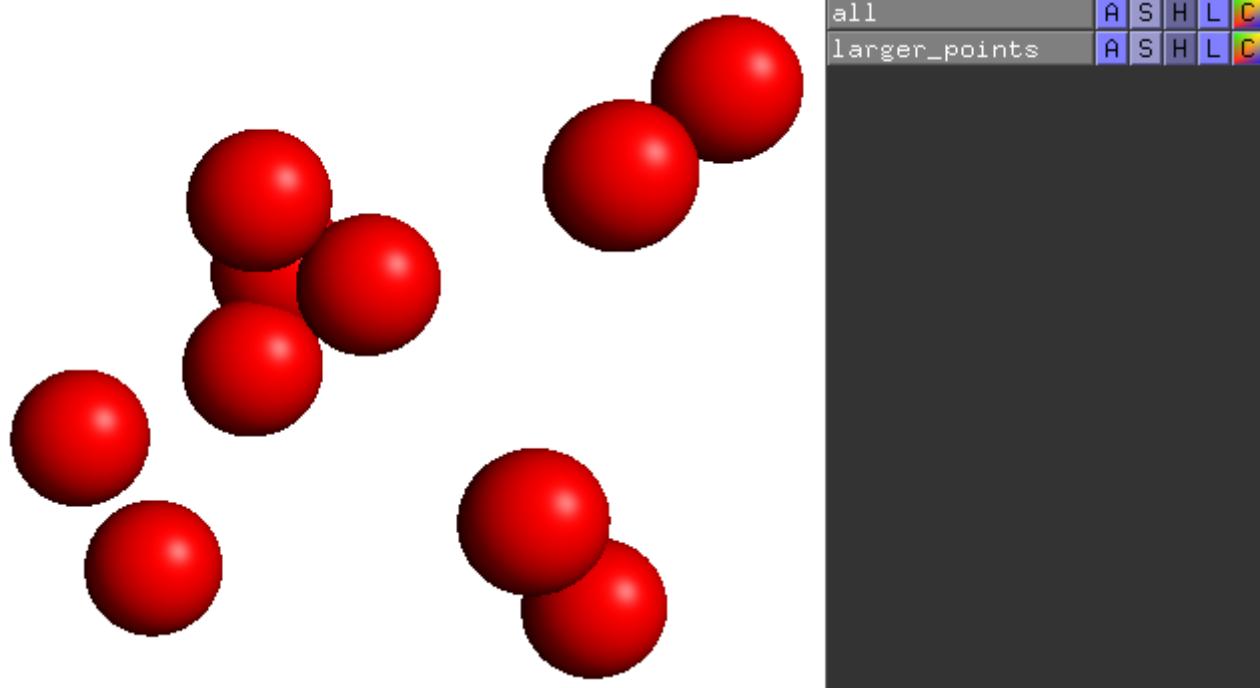
```
p2 = pmv.Points(vertices, render_as="Dots", name = "dot_points")
p2.write("out/dot_points.py")
```



When rendering as spheres you can pass the additional keyword *radius* which is 0.3 by default.

```
p3 = pmv.Points(vertices, radius = 1, name = "larger_points")
```

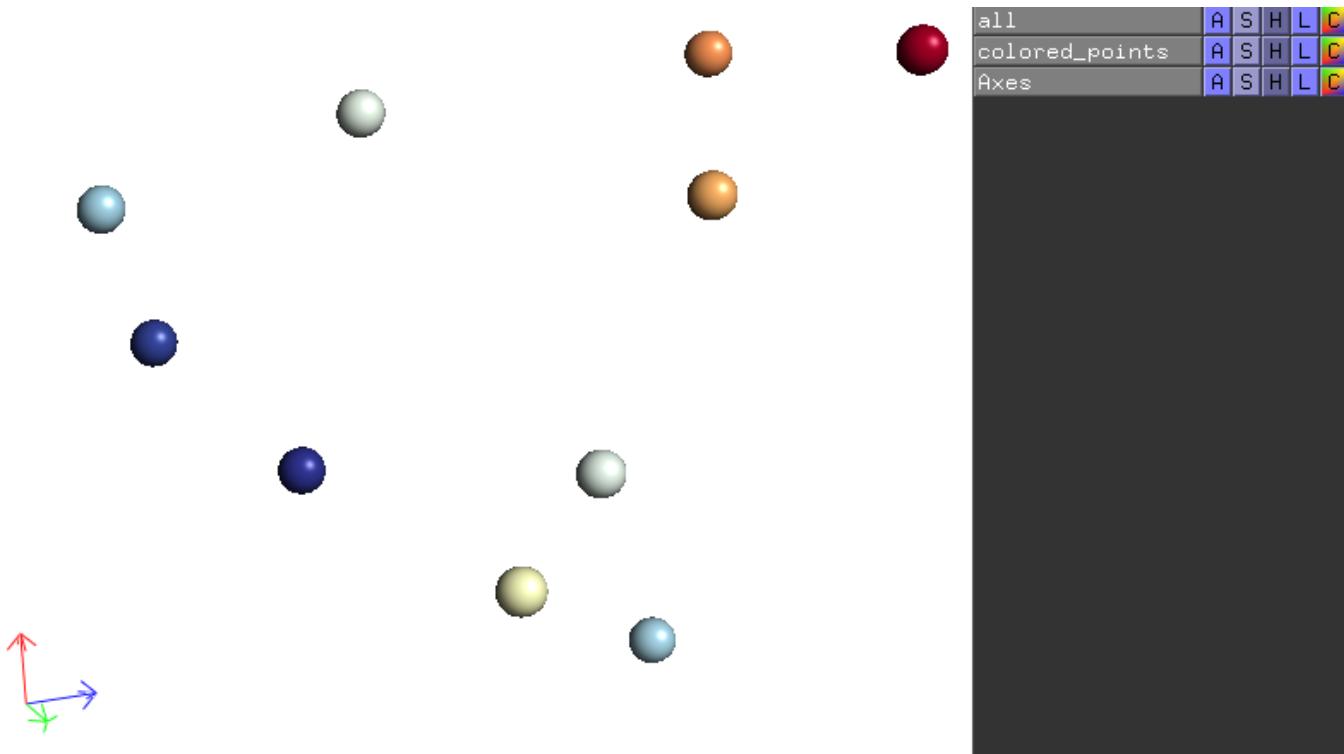
```
p3.write("out/larger_points.py")
```



## Automatic color inference

Instead of passing a color as a string we can pass any value that is accepted by the *ColorMap* class explained below. Specifically we can just pass a set of values and they will be automatically colored. For an example, we will color the points based on their distance to the origin:

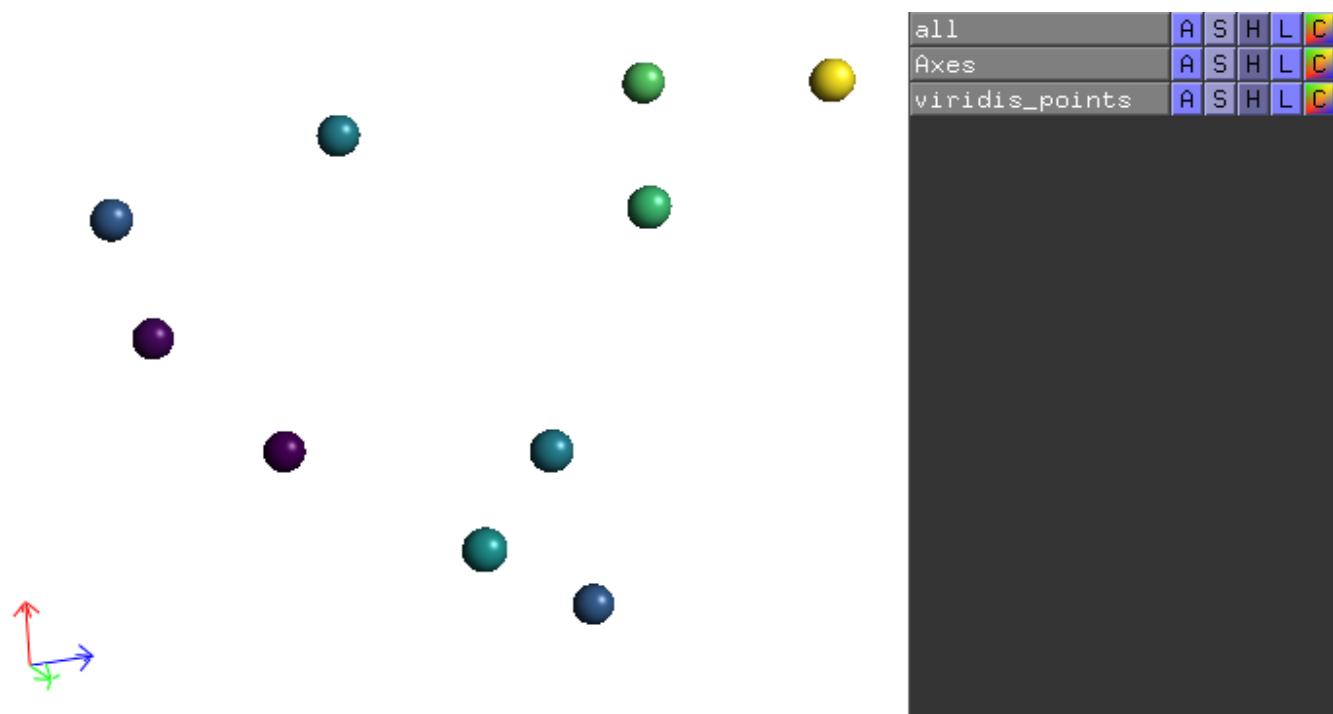
```
values = np.linalg.norm(vertices, axis = 1)
p2 = pmv.Points(vertices, color = values, name = "colored_points")
p2.write("out/colored_points.py")
```



For reference axes were added at the origin, see below in the Arrows chapter.

We can change the colormap being used by passing a different argument to `colormap`:

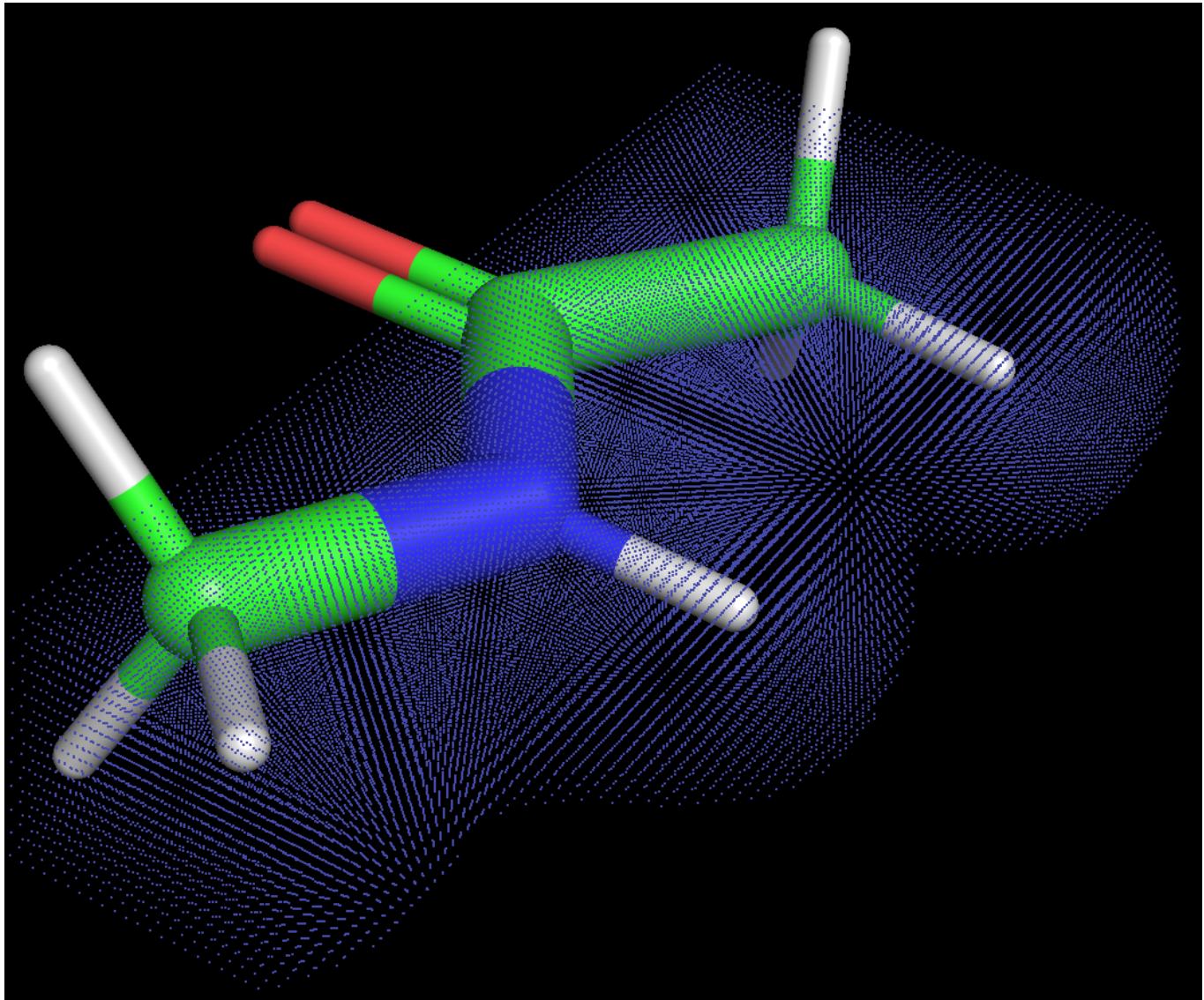
```
p3 = pmv.Points(vertices, color = values, name = "viridis_points",
colormap="viridis")
p3.write("out/viridis_points.py")
```



`colormap` can be a string describing a [matplotlib colormap](#), a matplotlib colormap itself or a PyMOLViz.ColorMap. The latter is particularly useful if you want to customize your colormaps easily.

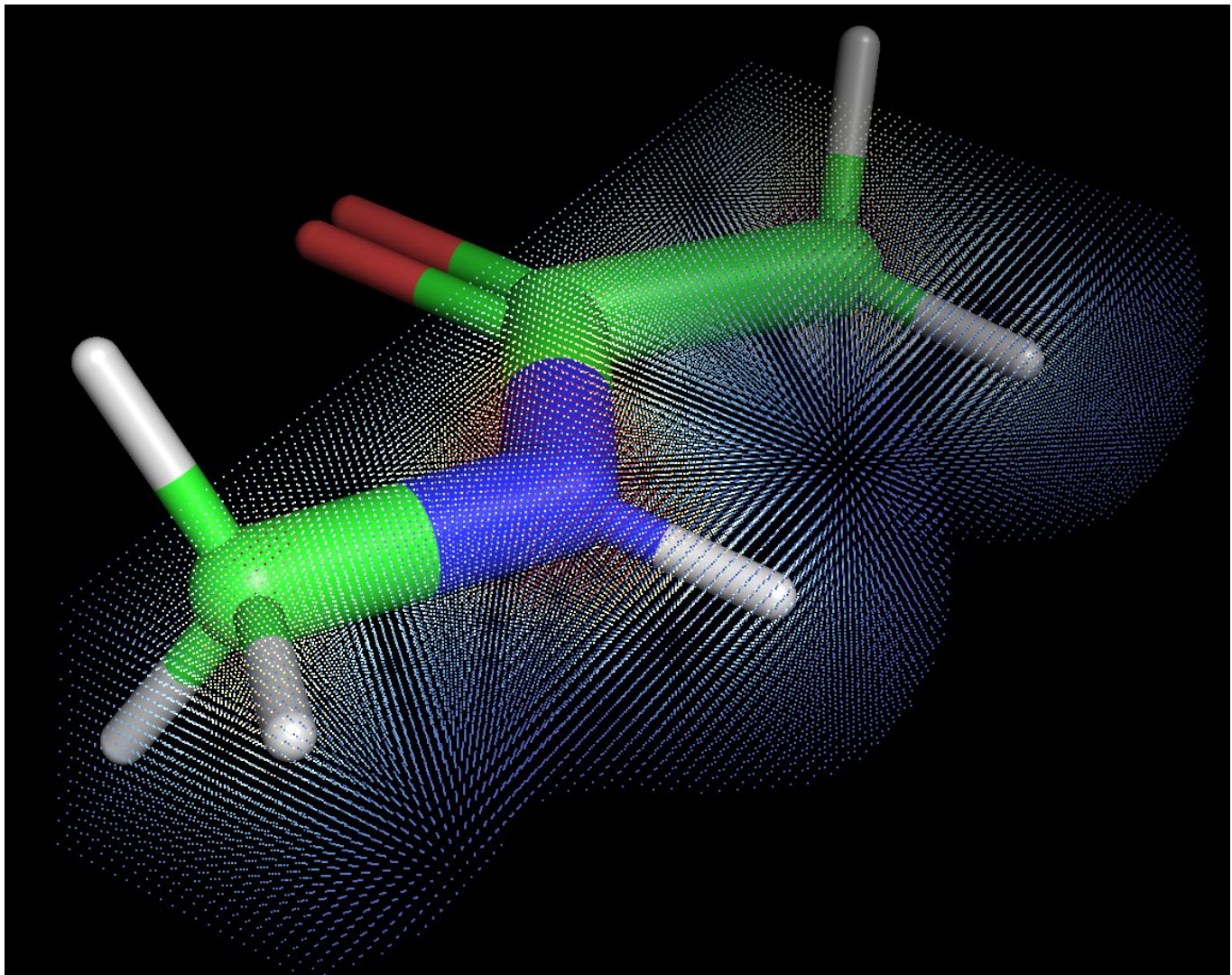
As an example we will plot results of a electron density calculation for N-methyl acetamide as points (**you should almost never actually do this! Instead you should use a volumetric display as explained below.**). To easily read in the data we make use of the PyMOLViz GridData class which will be explained below.

```
data = pmv.GridData.from_xyz("../data/td.xyz")
vertices = data.get_positions()
values = data.values
vertices = vertices[values > 1e-2]; values = values[values > 1e-2]
p4 = pmv.Points(vertices, color = values, render_as= "Dots", name =
"td_points")
p4.write("out/td_points.py")
```



Almost all points get assigned a blue color. This is because the colors are normalized against the minimum and maximum values. The density exactly around the atoms is very large! In order to change the coloring into a more useful range, we pass a custom PyMOLViz colormap.

```
p6 = pmv.Points(vertices, color = values, render_as= "Dots", name =
"td_points", colormap = pmv.ColorMap([0, 0.5]))
p6.write("out/td_points.py")
```



## Lines

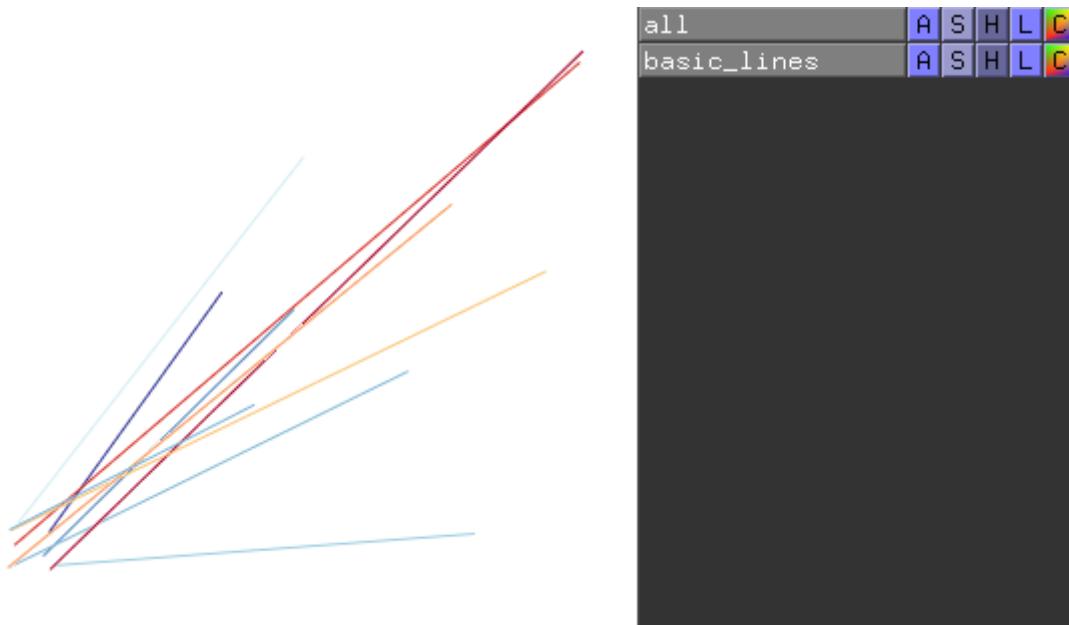
Instead of points lines can also be generated. For this the *Lines* constructor can be used. Lines inherits from Points and also accepts a set of vertices as its first argument. Lines are then drawn between each 2 consecutive points. If the color argument is an array-like, it can either specify a color for each single line or each point.

```

starts = np.random.rand(10,3) * 1
ends = np.random.rand(10,3) * 10
values = np.linalg.norm(ends, axis = 1)

l = pmv.Lines(np.hstack([starts, ends]), name = "basic_lines", color = values)
l.write("out/basic_lines.py")

```

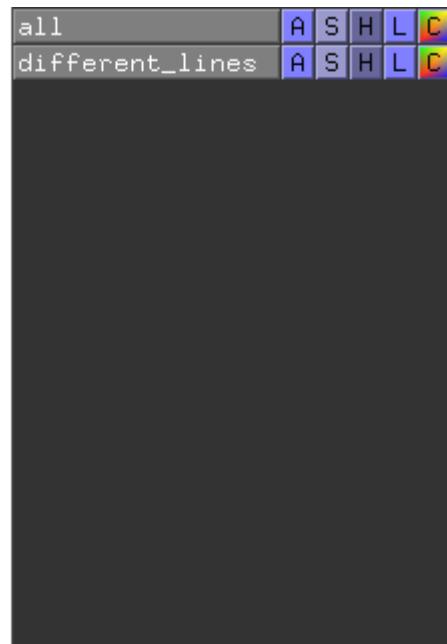
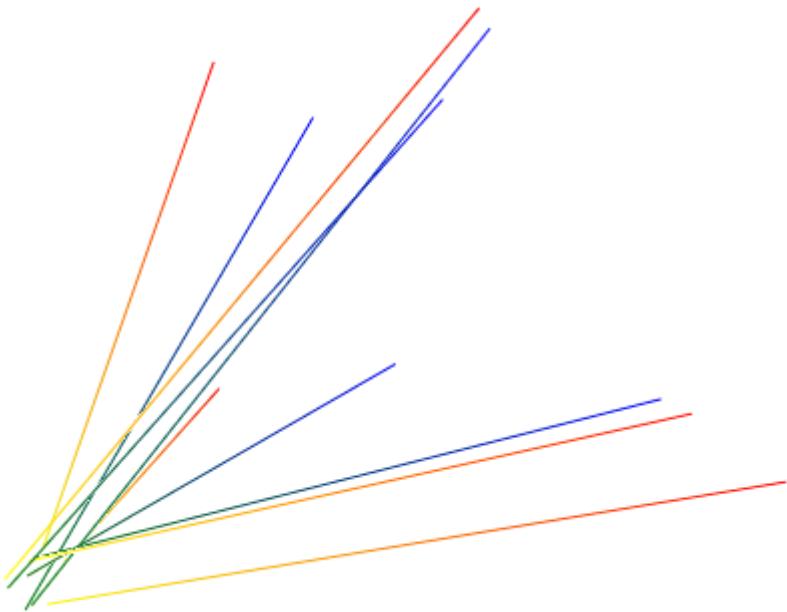


With a color value for each point:

```

values = np.full((5,4), ["yellow", "red", "green", "blue"]).flatten()
l2 = pmv.Lines(np.hstack([starts, ends]), name = "different_lines", color =
values)
l2.write("out/different_lines.py")

```



## Arrows

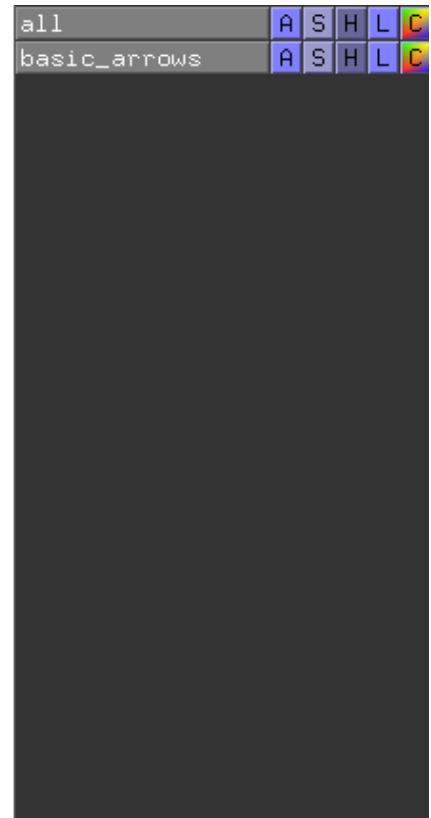
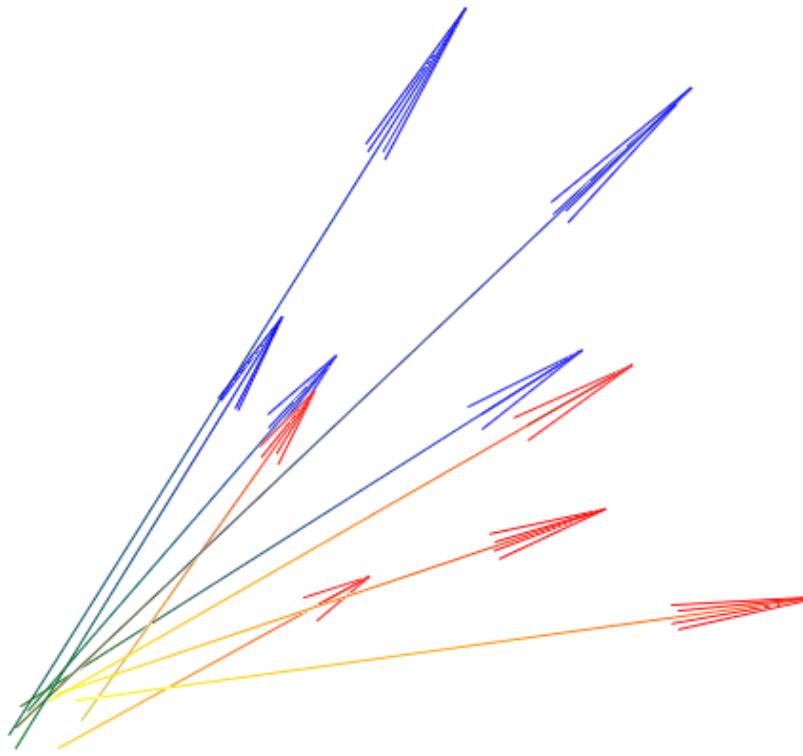
Instead of just creating lines, the direction can be indicated via Arrows. Arrows inherit from lines.

Arrows get 2 additional keywords, indicating how their head should be shaped:

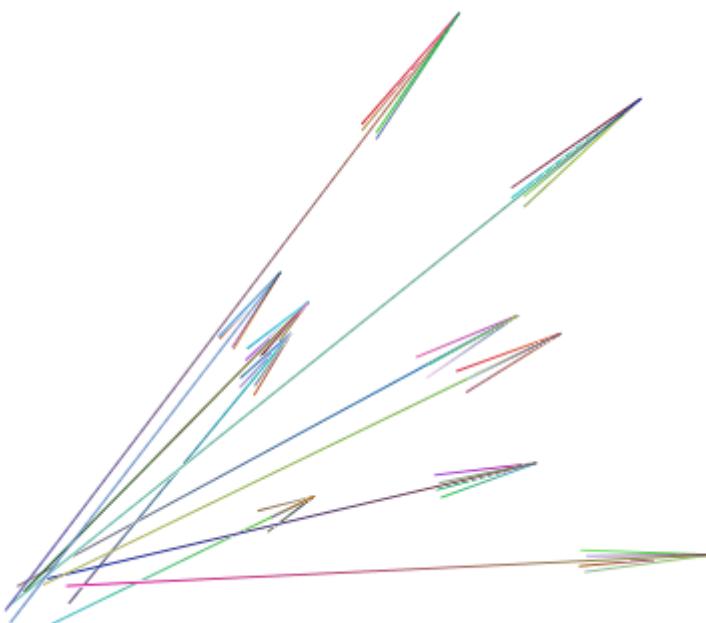
*head\_length* and *head\_width* both are relative values w.r.t. their length and default to .2.

If color is an array, it can either be passed as with lines, i.e. each line, or each end, or for each point of the arrow (first two for the line, next 8 for each line constituting the head).

```
a1 = pmv.Arrows(np.hstack([starts, ends]), name = "basic_arrows", color = values)
a1.write("out/basic_arrows.py")
```



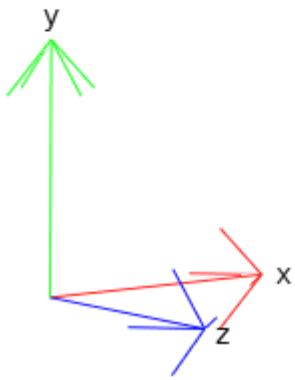
```
values = np.random.rand(10,10, 3).reshape(-1, 3)
a2 = pmv.Arrows(np.hstack([starts, ends]), name = "random_arrows", color =
values)
a2.write("out/random_arrows.py")
```



## Coordinate Axes

Using the *Arrows* and the *Labels* classes we can create coordinate axes:

```
start = np.zeros((3,3))
end = np.eye(3)
a3 = pmv.Arrows(np.hstack([start, end]), name = "coordinate_axes_arrows",
color = end)
labels = pmv.Labels(end * 1.1, name = "coordinate_axes_labels", labels = ["x",
"y", "z"])
pmv.Group([a3, labels], "coordinate_axes").write("out/coordinate_axes.py")
```



all	A	S	H	L	C
- coordinate_axes	A	S	H	L	C
coordinate_axes_arrows	A	S	H	L	C
coordinate_axes_labels 1	A	S	H	L	C

## Colors

Colors in PyMOLViz are exclusively determined via the *ColorMap* class.

## ColorMap

One of the most reoccurring tasks is to apply a colormap to a set of values. In order to simplify this as much as possible, PyMolViz has implemented an auxiliary *ColorMap* class which automatically tries to gracefully interpret different types of input.

## Display

The colormap class implements two functions to display them. One to show them as a matplotlib figure:

```
cmap.get_figure(orientation = "horizontal", figsize=(10, 1))
```

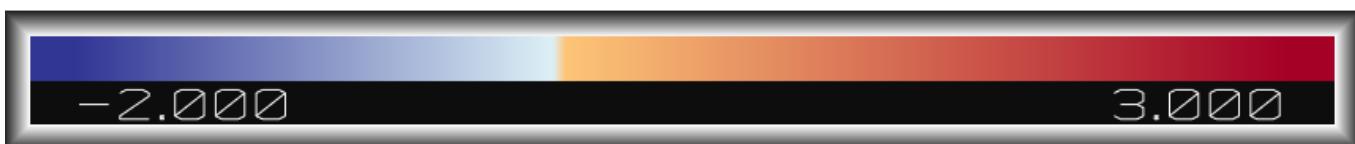
As in:

```
def plot_colors(cmap, x):
    # plotting given points
    test_colors = cmap.get_color(x)
    print("\n\nColored points:")
    plt.scatter(x, np.full_like(x, 0.5), color = test_colors)
    plt.show()

    #plotting the colorbar
    print("Colorbar:")
    cmap.get_figure(orientation = "horizontal", figsize=(10, 1))
```

The other way is to show them as a ColorRamp in PyMOL:

```
values = [-2, 0, 0, 3]
color_values = [0, 0.4, 0.65, 1]
cmap = pmv.ColorMap(list(zip(values, color_values)), name ="colormap")
cmap.write("colormap.py")
```



## Inputs

In the following every possible *color* input to the ColorMap class is discussed.

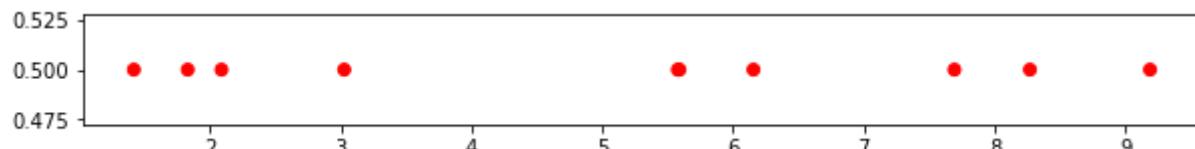
### Single Color Input

Sometimes instead of a color for every point / line / mesh, you just want a single color (this is in fact the default if no color is passed). For this the colormap can be passed only a single color and will assign this color to any value that is passed to it.

Single Color Inputs can be:

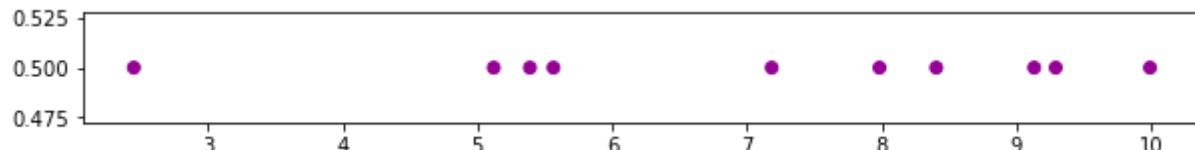
- A colors name

```
cmap = pmv.ColorMap("red")
plot_colors(cmap, np.random.rand(10) * 10)
```



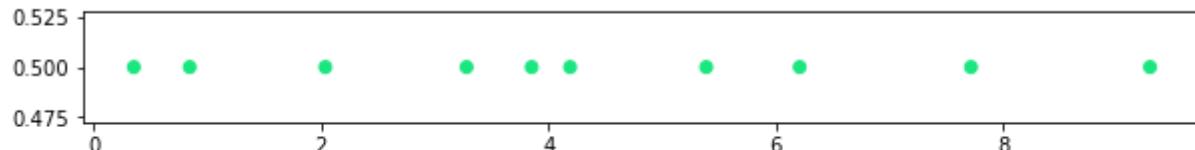
- An elements name (which then gets converted based on pymols element colors)

```
cmap = pmv.ColorMap("I")
plot_colors(cmap, np.random.rand(10) * 10)
```



- An array-like with 3 or 4 entries as rgb (a), either indicating values as float between 0 and 1 or as integer between 0 and 255.

```
cmap = pmv.ColorMap([0.1, 0.9, 0.5])
plot_colors(cmap, np.random.rand(10) * 10)
```



## Multiple Color Input

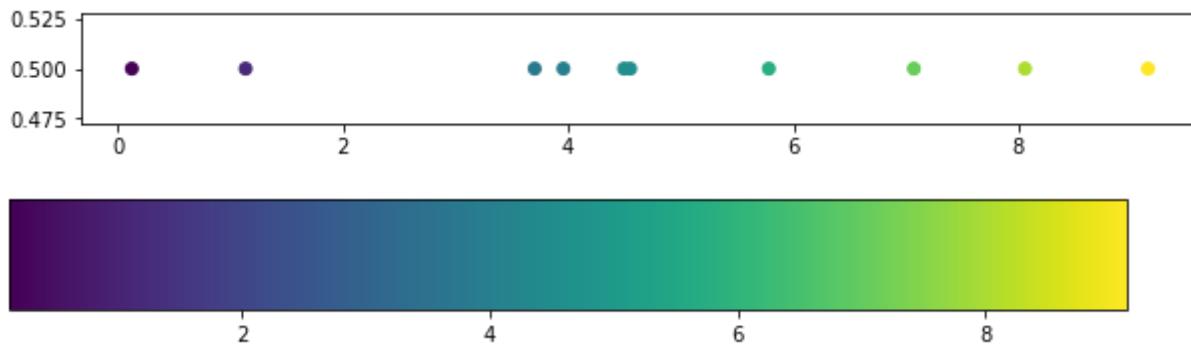
The more interesting case is if you want to assign different colors to different values. For

this the ColorMap class can infer the colormap scaling from a set of values passed to it. In this case the passed `colormap` keyword is used to infer the colormaps colors. Alternatively if a list of single colors (see above) is passed to it, it will map each index to the corresponding color.

Multiple Color Inputs can be:

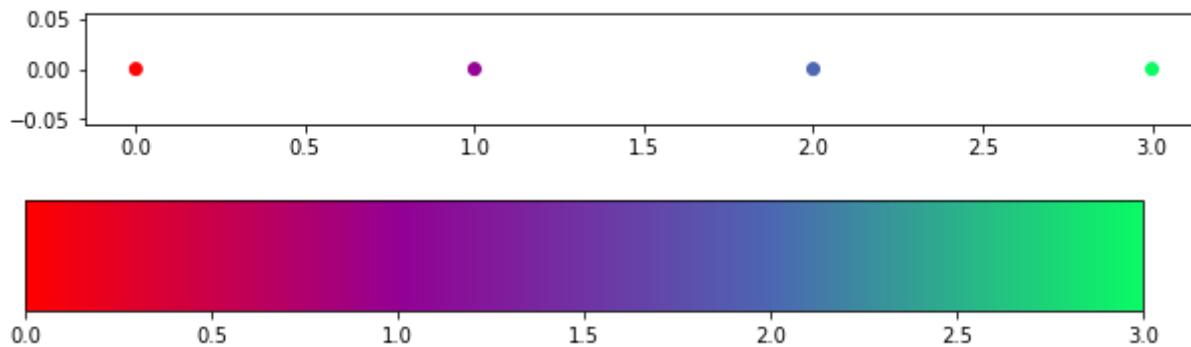
- An array-like containing float-like values (colors are taken from a matplotlib colormap corresponding to the passed `colormap` argument. Defaults to "`RdYIBu_r`".)

```
values = np.random.rand(10) * 10
cmap = pmv.ColorMap(values, colormap="viridis")
plot_colors(cmap, values)
```



- An array-like containing single colors (see above)

```
cmap = pmv.ColorMap(["red", "I", [0.3, 0.4, 0.7], [10, 250, 100]])
plot_colors(cmap, range(4))
```



### Linear Segmented Color Input

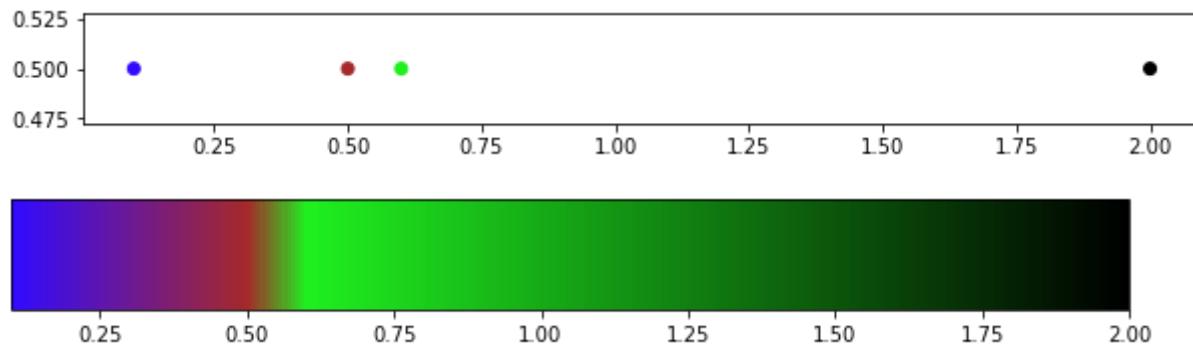
If you want to assign certain colors to certain values, you can pass a list of tuples to the ColorMap, with each tuple (value, color) containing the value and the corresponding single color (see above).

Alternatively tuples of (value, color\_value) pairs can be passed. In this case color\_value may be a float between 0 and 1 or an integer between 0 and 255 indicating the color based on the passed *colormap* keyword.

Linear Segmented Color Inputs can be:

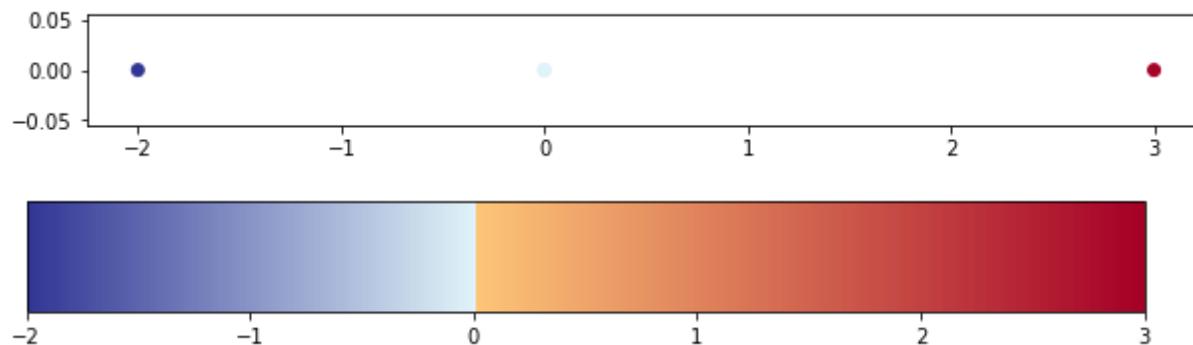
- An array-like containing tuples of (float-like, single color (see above)).

```
values = [0.1, 0.5, 0.6, 2]
colors = [(50, 10, 255), "Br", "C1", "black"]
cmap = pmv.ColorMap(list(zip(values, colors)))
plot_colors(cmap, values)
```



- An array-like containing tuples of (float-like, color-indicator) with color-indicator being a float between 0 and 1. The colors are then determined by passing the color-indicator to the matplotlib colormap corresponding to the passed *colormap* argument (Defaults to "RdYlBu\_r").

```
values = [-2, 0, 0, 3]
color_values = [0, 0.4, 0.65, 1]
cmap = pmv.ColorMap(list(zip(values, color_values)))
plot_colors(cmap, values)
```



## Meshes and Primitives

# Meshes

In addition to the basic data representations presented thus far, PyMOLViz also provides an Interface to the Mesh representation in PyMOL. Such a mesh has, in addition to points and colors also faces and vertex normals.

**Faces** should be a list or array of 3 dimensional indices into vertices. Faces indicate which 3 vertices should be connected to generate an opaque triangle. If faces are not given, every 3 consecutive points are assumed to form a triangle.

As a mesh will display an actual surface the additional information of the direction of the surface is used to compute lighting on the surface. For this, **vertex normals** can be provided which should for every provided vertex indicate the surface normal at that vertex. If you have no information of vertex normals you can either compute them from surrounding vertices or just pass zero vectors.

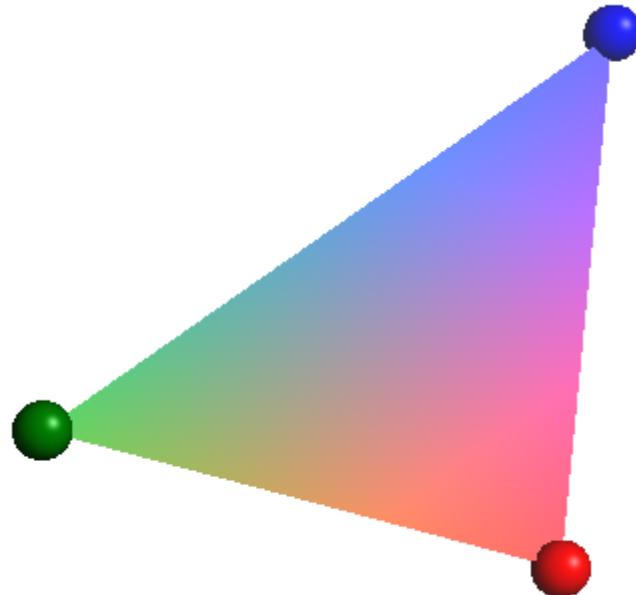
```
import pymolviz as pmv
import numpy as np

# creating dummy points
points = np.array([[0, 0, 0], [0, 0, 1], [0, 1, 0]])
colors = np.array(["red", "green", "blue"])

# creating a point mesh of the dummy points, rendering the points as spheres
p = pmv.Points(points, color = colors, name ="points")

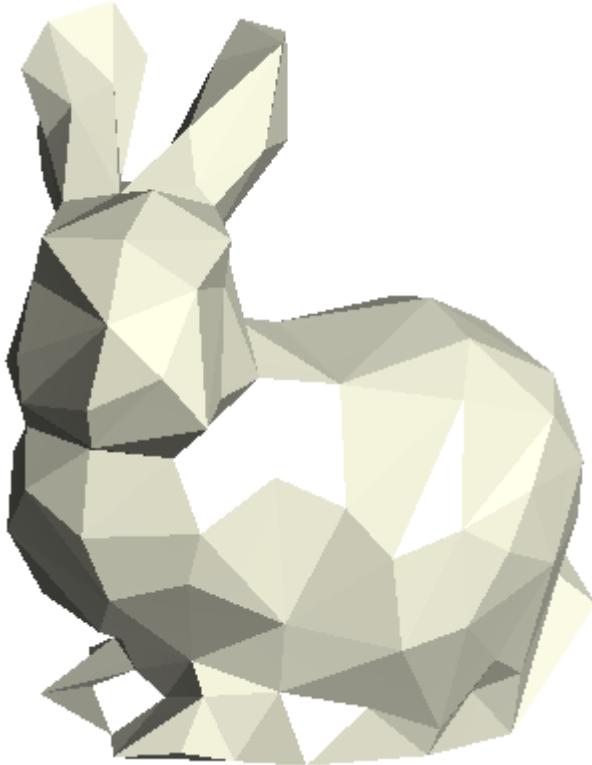
# creating the actual mesh. As we dont know the vertex normals, we set them to
# 0 vectors. The faces input means, the points at index 0, 1 and 2 should be
# connected to create a triangle. Any color between vertices is interpolated (by
# PyMOLs shaders).
m = pmv.Mesh(points, faces = [[0, 1, 2]], normals = np.zeros_like(points),
color = colors, name = "mesh")

pmv.Script([m, p]).write("out/test_mesh.py")
```



We can also load larger meshes into PyMOL, to display arbitrary objects:

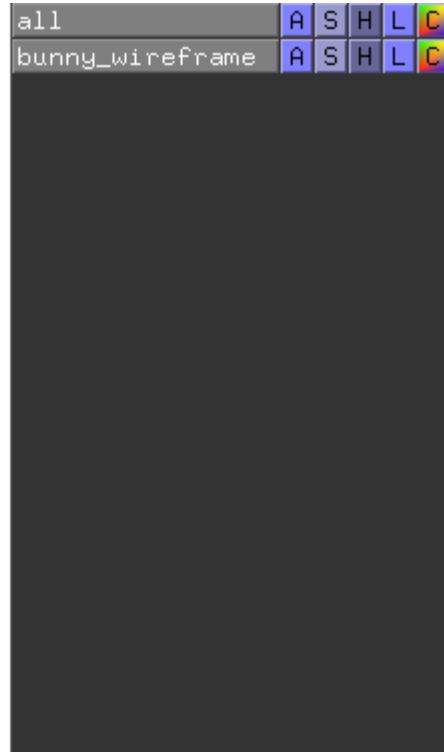
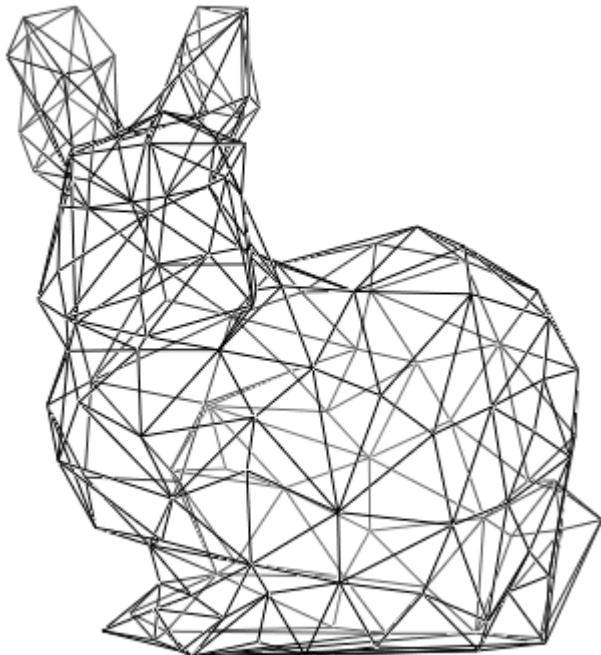
```
bunny_points = np.load('../data/Bunny.npy')
m2 = pmv.Mesh(bunny_points, color = "beige", name = "bunny")
m2.write("out/bunny.py")
```



## Wireframes

Any mesh can be turned into a wireframe via the `to_wireframe` method. Note that this is different from an IsoMesh that is created using volumetric data, which is explained further below.

```
bunny_points = np.load('../data/Bunny.npy')
l = m2.to_wireframe(name = "bunny_wireframe")
l.colormap = pmv.ColorMap("black")
l.write("out/bunny_wireframe.py")
```



## Mesh Primitives

PyMOLViz currently also provides the `Plane` and `Sphere` classes, which allow to instantiate plane and sphere meshes more easily.

- The `Plane` class represents a mesh consisting of two triangles which are placed at a given `position` and with a given `plane normal`. The size of the triangles is controlled by the `scale` parameter.
- The `Sphere` class allows to create a sphere directly as a mesh (allowing to e.g. extract its wireframe representation). If you want to represent many points as spheres, you should use the `Points` class instead. The `sphere` is defined by its `position`, `radius` and its `resolution`, determining how many points are approximating a circle.

```

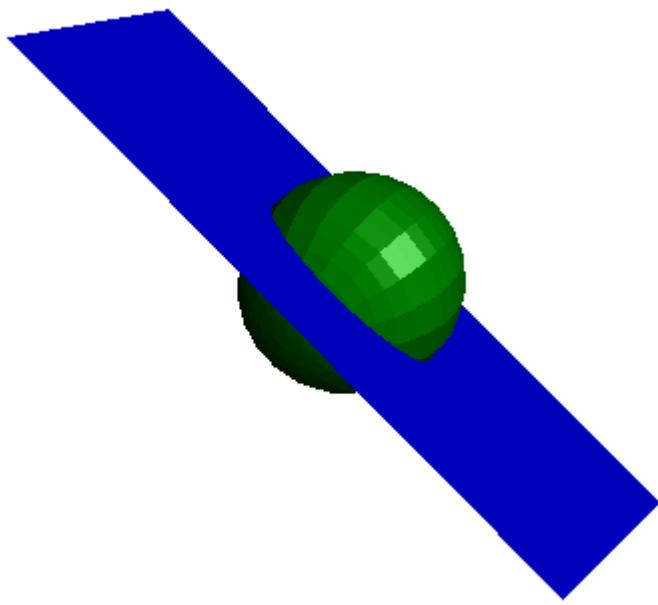
start_point = np.array([1,1,1])

# creating plane
normal = np.array([1,1,-1])
plane = pmv.Plane(start_point, normal, scale = 2, color = "blue", name =
"plane")

# creating sphere
sphere = pmv.Sphere(start_point, 0.3, color = "green", name = "sphere")

# joining meshes into a script
s = pmv.Script([plane, sphere])
s.write("test_primitives.py")

```



## Collections, Groups and Scripts

Up to now we basically always created a *Displayable* and used its *write* method to generate a corresponding script. In reality we will usually want to combine different *Displayables* and write them to a single script. The classes *CGOCollection*, *Group*, and *Script* all allow to gather different *Displayables* but have distinct use cases.

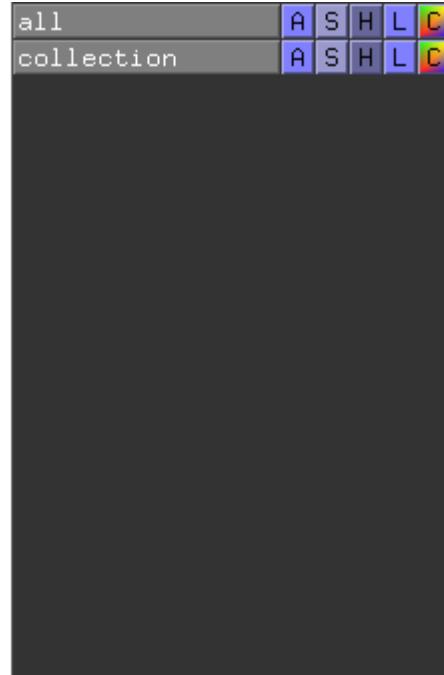
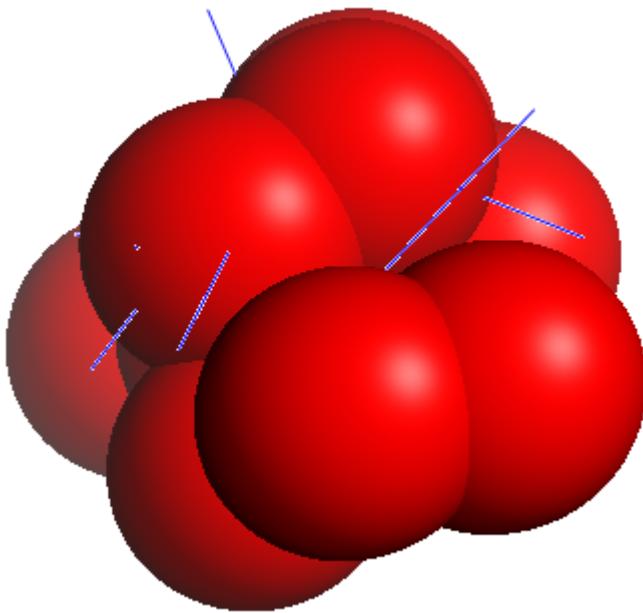
### CGOCollection

*CGOCollections*, as the name indicates are collections of CGOs, **Compiled Graphics Objects**. In PyMOLViz this corresponds to every class that inherits from *Points*. This

includes every class except for the ColorMap that has been presented thus far. However it specifically excludes any volumetric class.

CGOCollections are *Displayables* and have therefore a *name* and a *write* function. They are special in that all *Displayables* that are part of a *CGOCollection* will be combined and appear in PyMOL as the **same** *Displayable* under the name of the Collection (unless they are also added by different means).

```
points = pmv.Points(np.random.rand(10,3), color = (1,0,0), name = "points")
lines = pmv.Lines(np.hstack([np.random.rand(10,3), np.random.rand(10,3)]),
color = (0,1,0), name = "lines")
collection = pmv.CGOCollection([points, lines], name = "collection")
collection.write("basic_collection.py")
```



## Groups

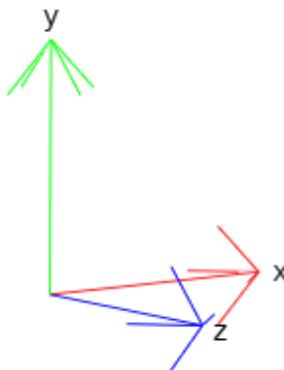
Groups are used to gather multiple *Displayables*. Other than with *CGOCollections*, any other *Displayable* **that is not a Group** can be gathered. They are part of PyMOLs GUI. They are themselves also *Displayables* and therefore a *name* and a *write* function. Any *Displayable* that is part of a *Group* will also be loaded into PyMOL itself. We made use of the *Group* class when implementing the coordinate axes.

```
start = np.zeros((3,3))
end = np.eye(3)
a3 = pmv.Arrows(np.hstack([start, end]), name = "coordinate_axes_arrows",
```

```

color = end)
labels = pmv.Labels(end * 1.1, name = "coordinate_axes_labels", labels = ["x",
"y", "z"])
g = pmv.Group([a3, labels], "coordinate_axes")
g.write("out/coordinate_axes.py")

```



all	A	S	H	L	C
- coordinate_axes	A	S	H	L	C
coordinate_axes_arrows	A	S	H	L	C
coordinate_axes_labels 1	A	S	H	L	C

## Scripts

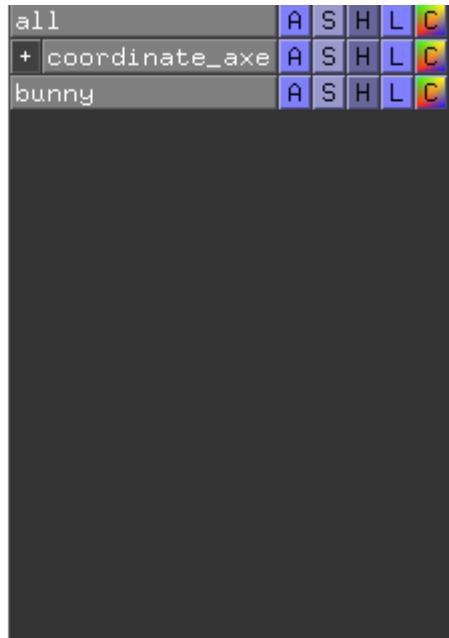
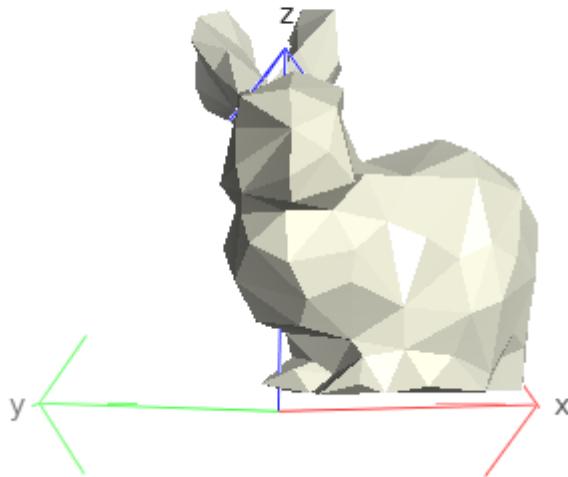
Scripts lie at the root of the implementation of PyMOLViz as any *Displayable* is converted to a *Script* when its *write* function is called. The *Script* class is used to actually convert its *Displayables* into runnable python scripts. It can be used to gather different *Displayables* which should be loaded with a single script. **Scripts themselves are not Displayables but rather represent a collection of Displayables that should be converted into a single python script.**

We could use the *Script* class to write the coordinate axes and the bunny to a single script:

```

bunny_points = np.load('../data/Bunny.npy')
m2 = pmv.Mesh(bunny_points, color = "beige", name = "bunny")
s = pmv.Script([g, m2])
s.write("out/bunny_with_coordinates.py")

```



## Volumetric Displays

PyMOL has different capabilities for displaying volumetric data, such as electrostatic potentials or electron density. These all are based on data on a three dimensional grid, which is why the interface to volumetric displays in PyMOLViz is always based on the *GridData* class.

### GridData

Volumetric Displays are all based on the *GridData* class. As the name implies it stores data on a grid. The grid can either be specified by its *positions* or by an *origin*, *step\_sizes* and *step\_counts*, each being a 3-dimensional vector. **step\_counts here means the number of steps taken from origin, specifically not counting origin as a step. Thus, the number of grid points along one axis i is step\_counts[i] + 1.**

At least currently, non-orthogonal Grids are not supported. *GridData* is a *Displayable*, and thus can be loaded into PyMOL on its own.

As a simple example we create a 1 by 1 cube at [0, 0, 0] and assign values as the manhattan distance from origin.

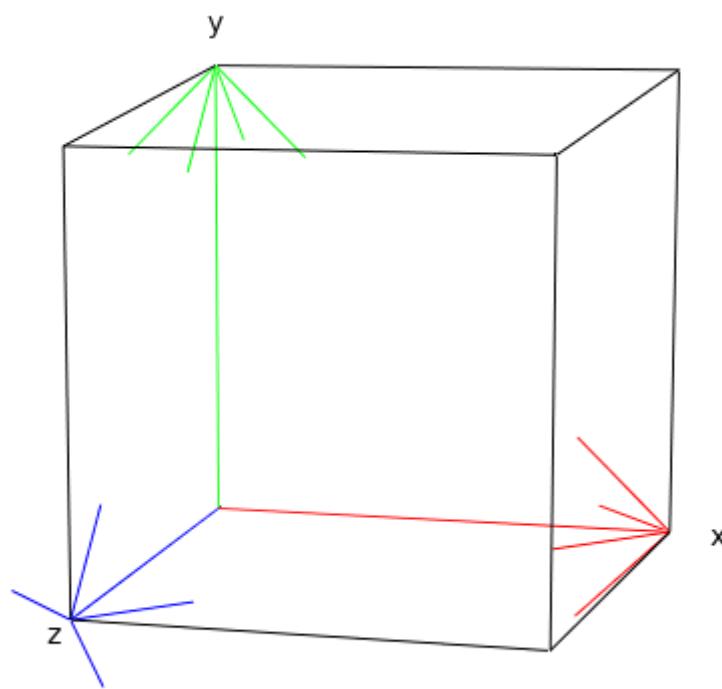
```
grid = np.array([[0, 0, 0],
    [0, 0, 1],
    [0, 1, 0],
    [0, 1, 1],
    [1, 0, 0],
```

```

[1, 0, 1],
[1, 1, 0],
[1, 1, 1]])

values = np.sum(grid, axis=1) # manhattan distance from origin
grid_data = pmv.GridData(values, grid, name = "basic_grid_data")
grid_data.write("basic_grid_data.py")

```



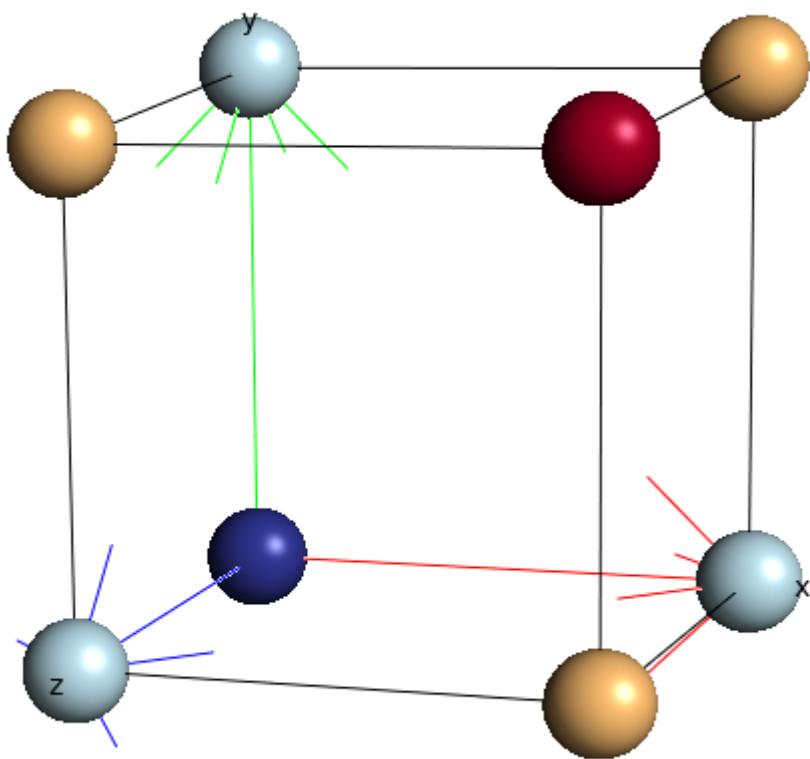
As no display type has been added yet, PyMOL will only show the bounding box of the loaded 3d-grid. For better comprehensiveness, the coordinate axes from the section before was added.

If you like to see the points of the *GridData*, you can convert them into a *Points* class using the *to\_points* method.

```

points = grid_data.to_points(name = "grid_data_points", radius = 0.1)
points.write("out/basic_grid_data_points.py")

```



all	A	S	H	L	P
grid_data	A	S	H	L	C
+ coordinate_axis	A	S	H	L	C
grid_data_points	A	S	H	L	C

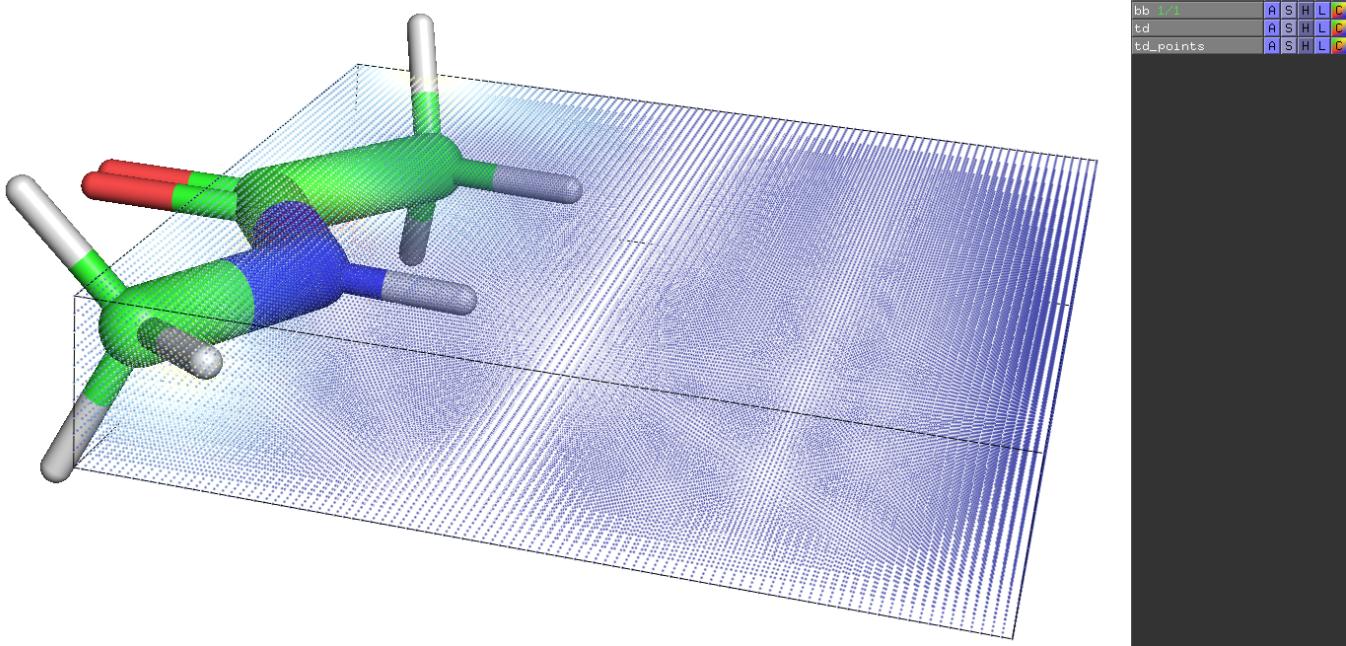
## Reading external volumetric data

PyMOLViz currently supports reading xyz files containing volumetric data created by turbomole, as well as mtz files using [gemmi](#). With time and demand additional formats will follow.

### Reading xyz files

One example was already in the *Points* chapter:

```
td_data = pmv.GridData.from_xyz("../data/td.xyz", name = "td")
points = td_data.to_points(name = "td_points", radius = 0.1, render_as="Dots")
pmv.Script([td_data, points]).write("out/td_points.py")
```



The `from_xyz` function has the argument `in_bohr` which defaults to True. This signifies that the data from the xyz file is in Bohr (as is the default for turbomole outputs), but we want to see it in Angström. If you want to leave the data in its original form you need to pass

```
in_bohr = False.
```

## Reading mtz files

Reading mtz files is more complicated, since they usually hold a lot of information and you need to pick what information you would like to display. If you want more than a quick way to display the information you need to take a deeper look into the documentation, e.g. for the [MTZ Format](#) or how to handle them with [gemmi](#).

PyMOLViz allows to specify the structure factor column and the phase column from the mtz file to compute the grid data. additionally you can specify the sample rate and the area in which to display the data via the `min_pos` and `max_pos` keywords.

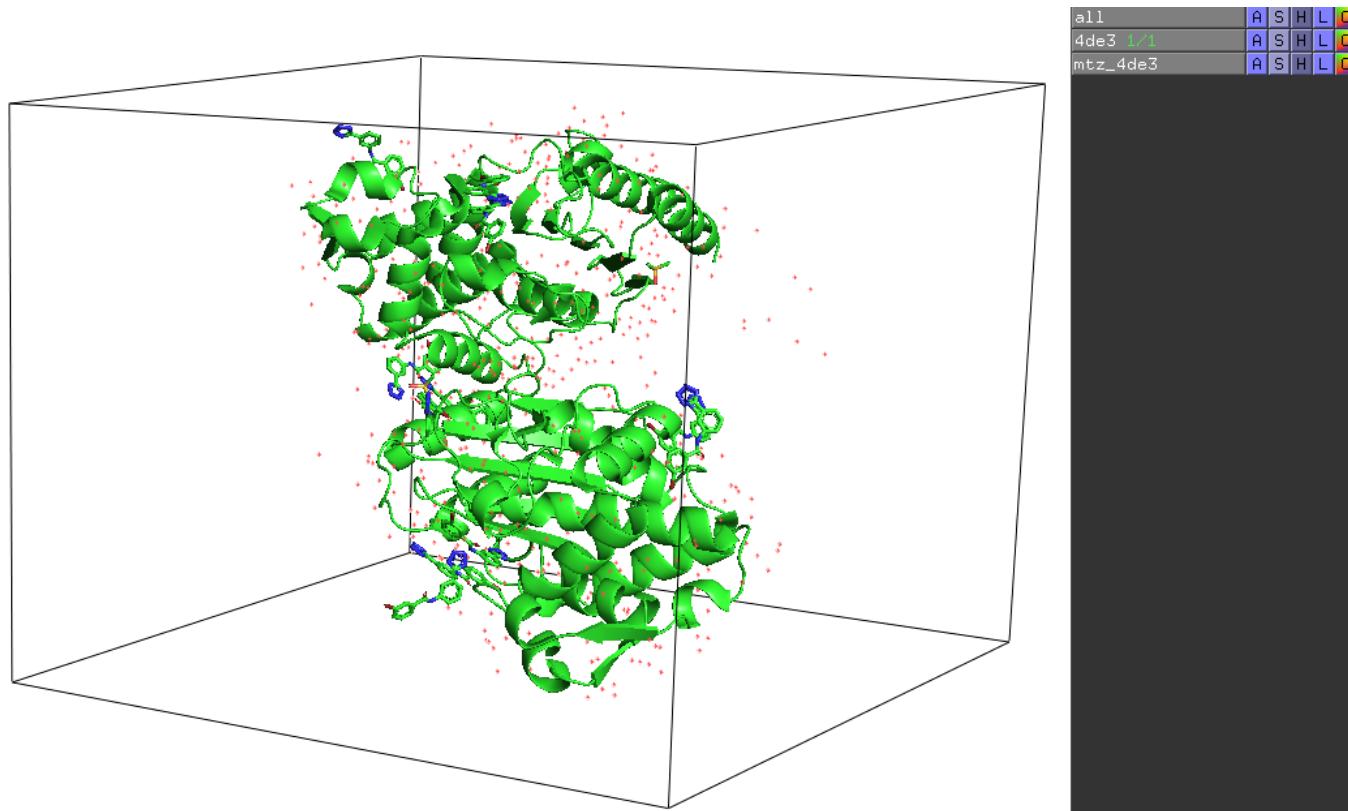
For standard files you want the following structure factors and phases (see <https://www.globalphasing.com/buster/wiki/index.cgi?MTZcolumns>, <https://www.ccp4.ac.uk/html/refmac5/keywords/xray-general.html>):

- 2mFo-dFc: Factor: "FWT", Phase: "PHWT"
- mFo-dFc: Factor: "DELFWT", Phase: "PHDELWT"
- Fc: Factor: "FC", Phase: "PHIC"
- Fo: Factor: "FP", Phase: usually N/A

```

from rdkit import Chem
prot = Chem.MolFromPDBFile('../data/4de3.pdb')
positions = prot.GetConformer().GetPositions()
buffer = 5
min_pos = np.min(positions, axis = 0) - buffer
max_pos = np.max(positions, axis = 0) + buffer
mtz_data = pmv.GridData.from_mtz('../data/4de3_phases.mtz', min_pos = min_pos,
max_pos = max_pos, step_sizes = [1, 1, 1], name = 'mtz_4de3')
mtz_data.write("out/mtz_4de3.py")

```



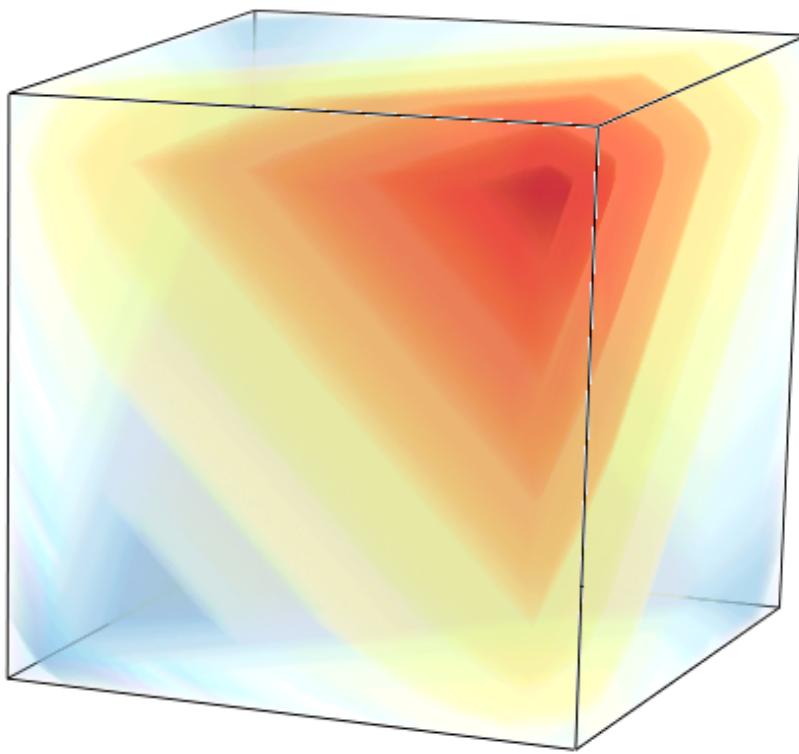
## Volumes

Once the data is available there are two major types of displaying them. Via transparent *Volumes* or via *IsoSurfaces*. First we will show how to use *Volumes*. *Volumes* are *Displayables* and therefore have a *name* and can be written directly as a script via the *write* method.

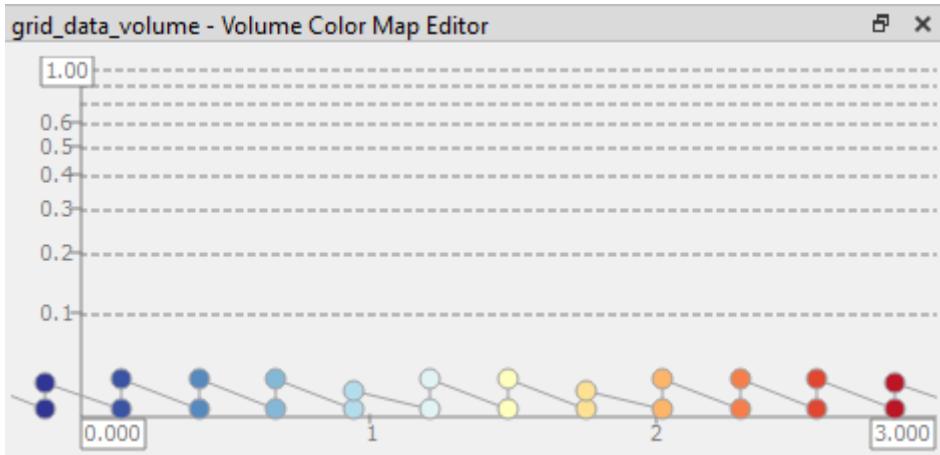
```

v1 = pmv.Volume(grid_data, name = "grid_data_volume")
v1.write("out/basic_volume.py")

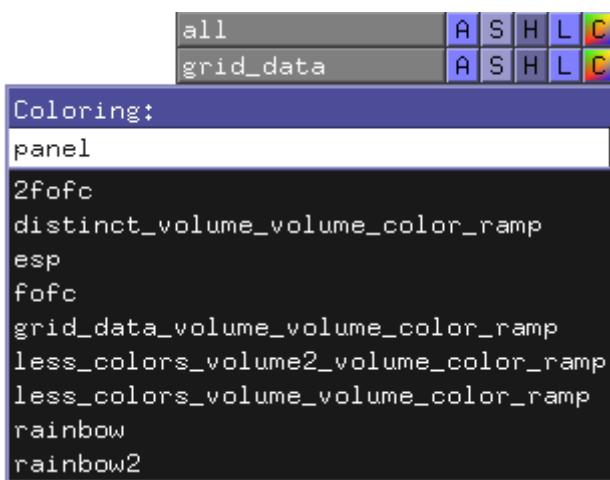
```



With the volume panel looking like:



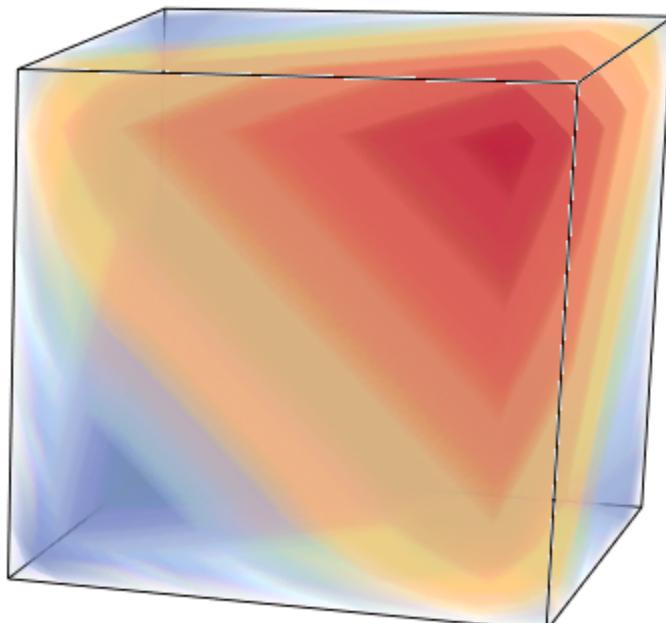
To refine the coloring you can access the volume color map panel via the color of the volumes:



A *Volume* is defined by values which are mapped to (color, alpha) value pairs, with the color for every point inbetween being interpolated. In PyMOLViz, this is done by specifying the *alphas* and *clims* keywords for the *Volume*. The *clims* define the values at which a new color is used by passing the clim to the *Volume*'s *ColorMap*, which can be specified using the *colormap* keyword in a similar fashion to the *Points* class.

As an example we will try to show a clearer distinction between points below 1.5 and above 1.5 by adjusting our colormap:

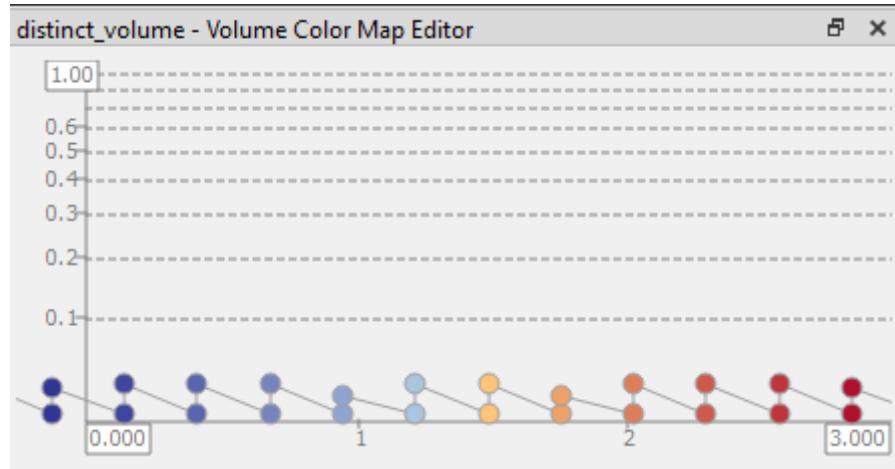
```
values = [np.min(grid_data.values), 1.5, 1.5, np.max(grid_data.values)]
color_values = [0, 0.35, 0.65, 1]
cmap = pmv.ColorMap(list(zip(values, color_values)), name="distinct_colormap")
v2 = pmv.Volume(grid_data, name = "distinct_volume", colormap = cmap)
pmv.Script([v2, cmap]).write("out/distinct_volume.py")
```



all	A	S	H	L	C
grid_data	A	S	H	L	C
distinct_volume	A	S	H	L	C
distinct_colorma	A	S	H	L	C

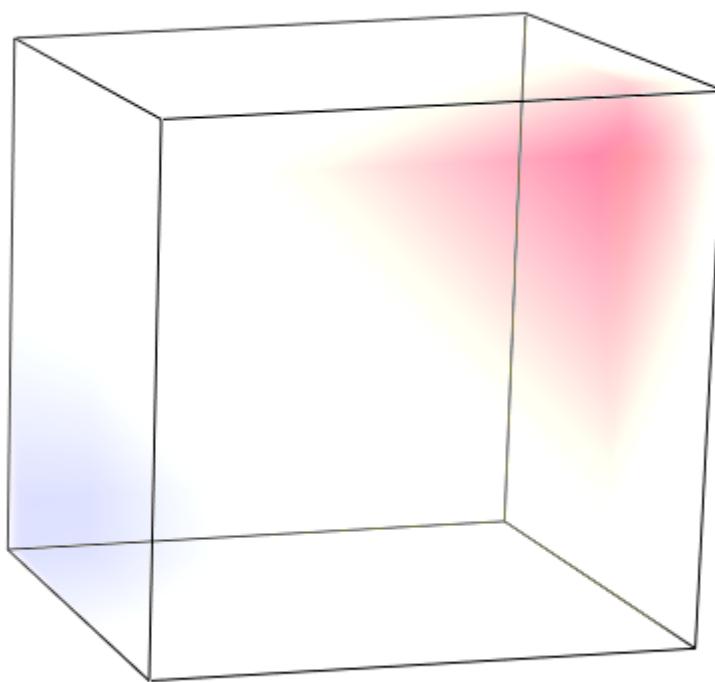


With the volume panel looking like:

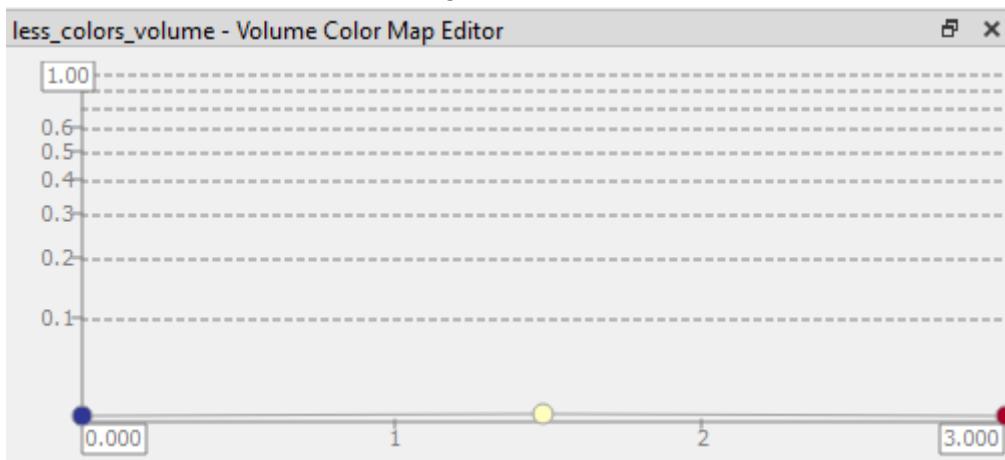


If we don't want to distinguish so many colors, we can pass different *clims* to the *Volume* constructor:

```
clims = [
    np.min(grid_data.values),
    np.mean(grid_data.values),
    np.max(grid_data.values)
]
v3 = pmv.Volume(grid_data, name = "less_colors_volume", clims = clims)
v3.write("out/less_colors_volume.py")
```



With the volume panel looking like:

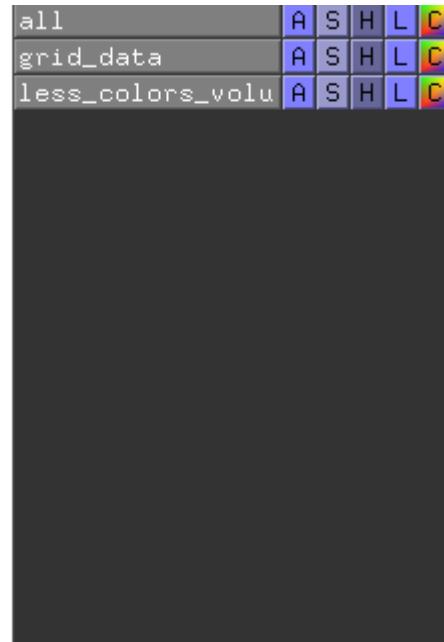
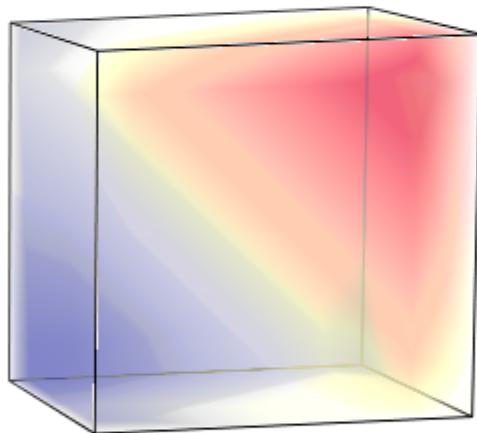


This doesn't look perfect. The way that the alpha values are determined by default, it is assumed that the first clim is at a high alpha value and the second goes down to a low alpha value. Thus, the follow would be more correct:

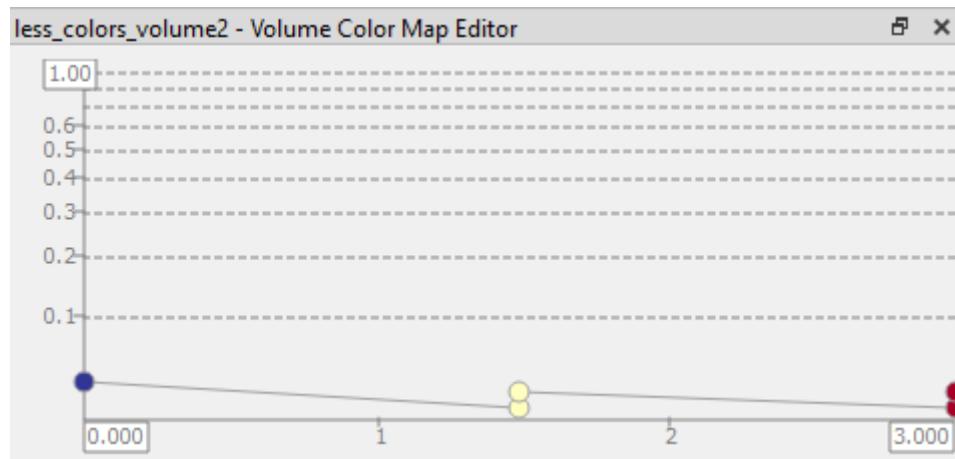
```
clims = [
    np.min(grid_data.values),
    np.mean(grid_data.values),
    np.mean(grid_data.values),
    np.max(grid_data.values),
    np.max(grid_data.values)
]
```

```
v4 = pmv.Volume(grid_data, name = "less_colors_volume2", clims = clims)

v4.write("out/less_colors_volume2.py")
```



With the volume panel looking like:



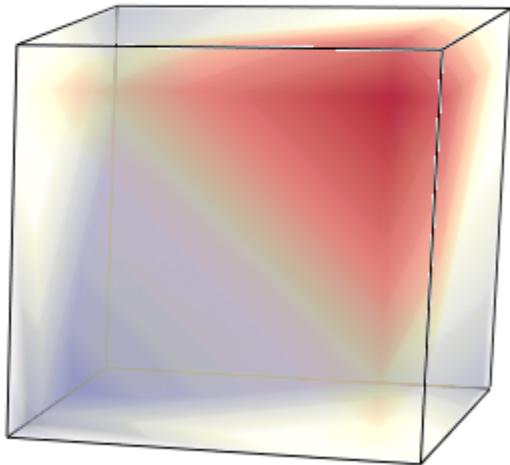
Instead we can also pass the alpha values ourselves:

```
clims = [
    np.min(grid_data.values),
    np.mean(grid_data.values),
    np.max(grid_data.values)
]

alphas = [0.03, 0.005, 0.03]

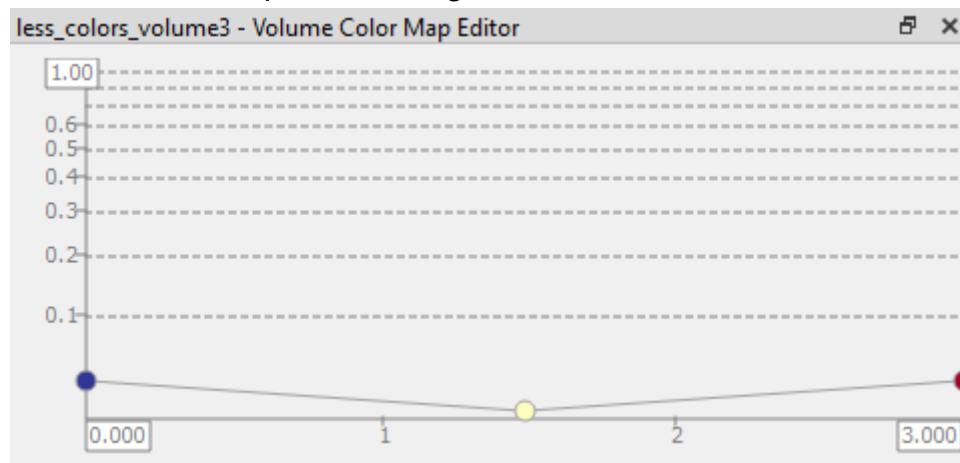
v3 = pmv.Volume(grid_data, name = "less_colors_volume3", clims = clims, alphas
= alphas)

v3.write("out/less_colors_volume3.py")
```



all	A	S	H	L	C
grid_data	A	S	H	L	C
less_colors_volum	A	S	H	L	C

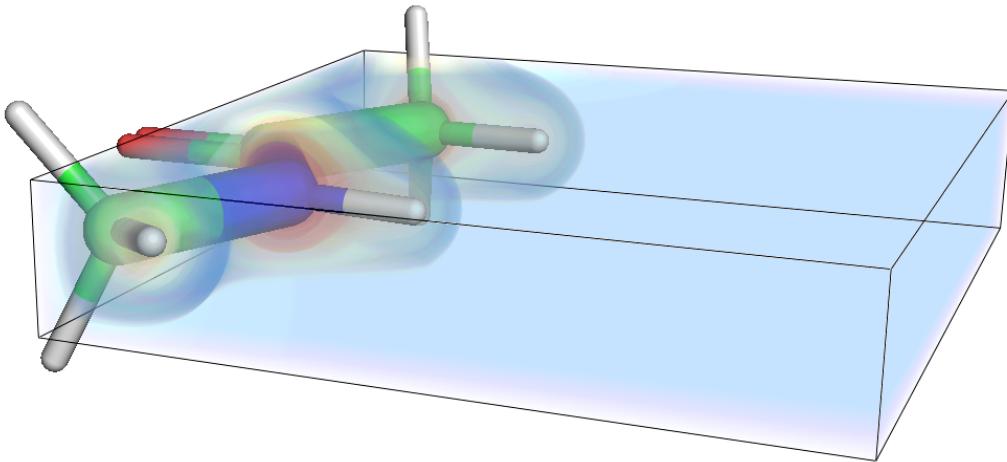
With the volume panel looking like:



By default the clim's are chosen as 33 even spaced values between mean plus/minus 5 standard deviations. The alpha values are chosen based on the point densities between the points in that region.

As a more practical example we will show the density around the N-methyl acetamide:

```
data = pmv.GridData.from_xyz("../data/td.xyz", name = "td")
cmap = pmv.ColorMap([0, 0.5])
v4 = pmv.Volume(data, name = "td_volume", colormap = cmap)
v4.write("out/td_volume.py")
```

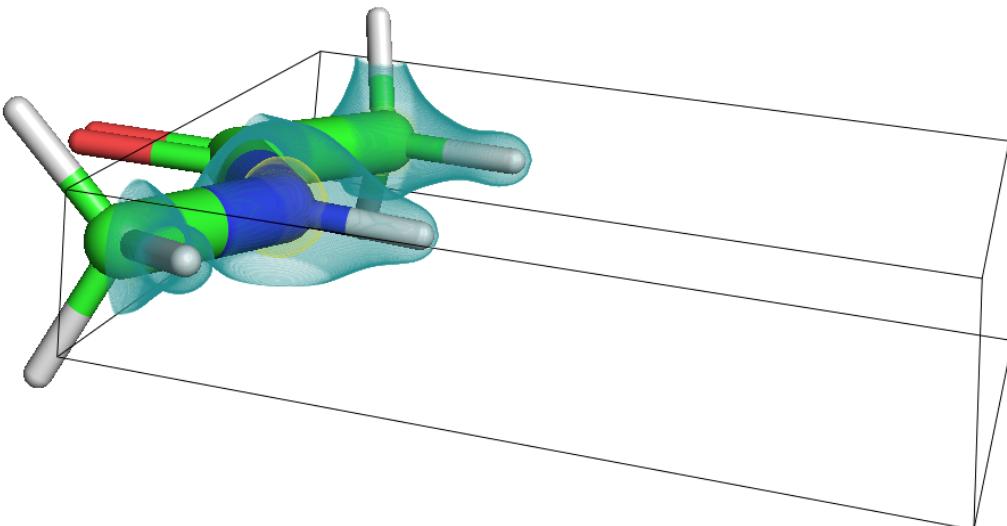


all	A	S	H	L	C
td	A	S	H	L	C
td_isovolume	A	S	H	L	C
bb_tdi	A	S	H	L	C

## IsoVolumes

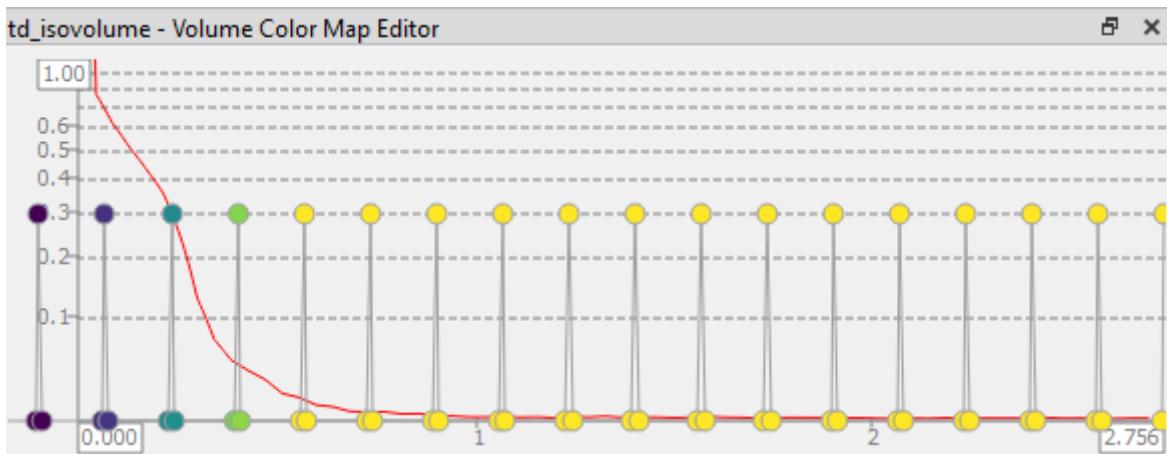
Sometimes it is hard to see what is going on using Volumes (at least in their default setting). In order to simplify generating Volumes showing iso-surfaces PyMOLViz has the class *IsoVolume*. It still makes use of the PyMOLs volume functionality but creates "coloring peaks" at the given values.

```
cmap = pmv.ColorMap([0, 0.5], colormap = "viridis")
v5 = pmv.IsoVolume(data, name = "td_isovolume", colormap = cmap)
v5.write("out/td_isovolume.py")
```



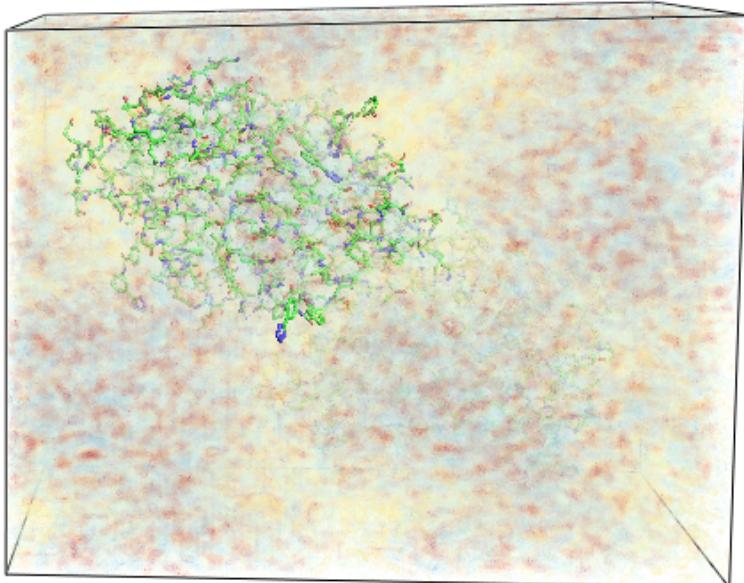
all	A	S	H	L	C
td	A	S	H	L	C
td_isovolume	A	S	H	L	C
bb_tdi	A	S	H	L	C

With the volume panel looking like:



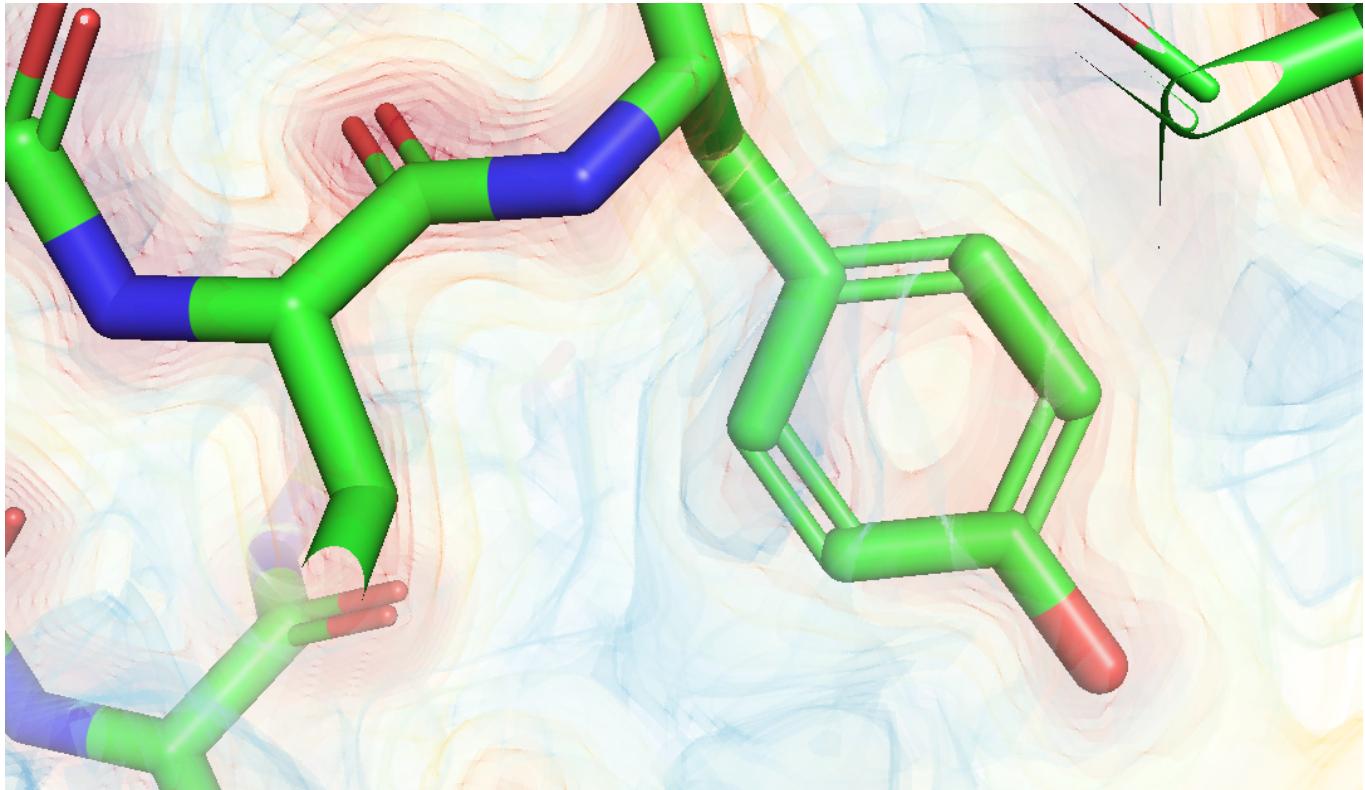
Displaying the 2mFo-dFc map from before we get:

```
from rdkit import Chem
prot = Chem.MolFromPDBFile('../data/4de3.pdb')
positions = prot.GetConformer().GetPositions()
buffer = 5
min_pos = np.min(positions, axis = 0) - buffer
max_pos = np.max(positions, axis = 0) + buffer
data = pmv.GridData.from_mtz('../data/4de3_phases.mtz', min_pos = min_pos,
max_pos = max_pos, step_sizes = [1, 1, 1], name = 'mtz_4de3')
cmap = pmv.ColorMap([-1, 1])
v6 = pmv.IsoVolume(data, name = "mtz_4de3_volume", colormap = cmap)
v6.write("out/mtz_4de3_isovolume.py")
```



all	A	S	H	L	D
4de3 1/1	A	S	H	L	D
mtz_4de3	A	S	H	L	D
mtz_4de3_volume	A	S	H	L	D

Zooming in, we can see some detail, but it is still hard to make out, due to the everything beeing quite dense:

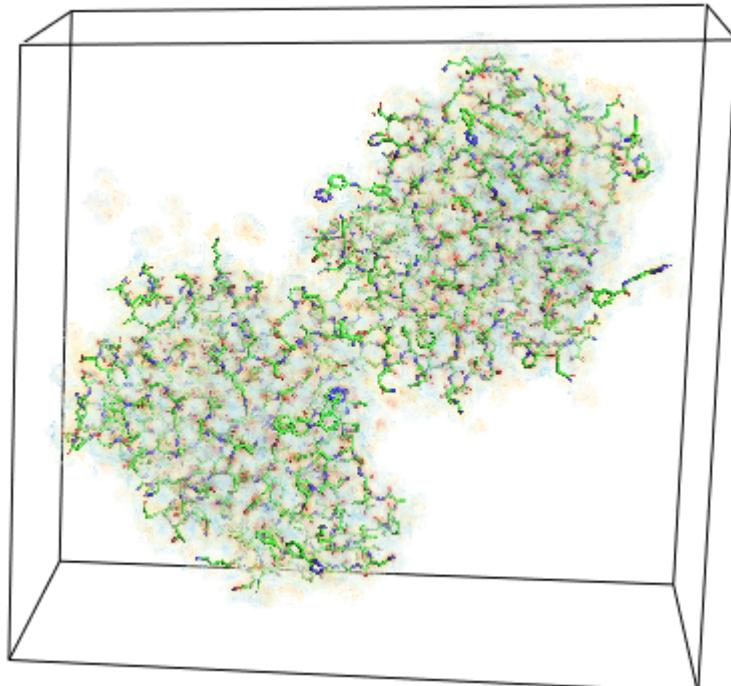


## Carve

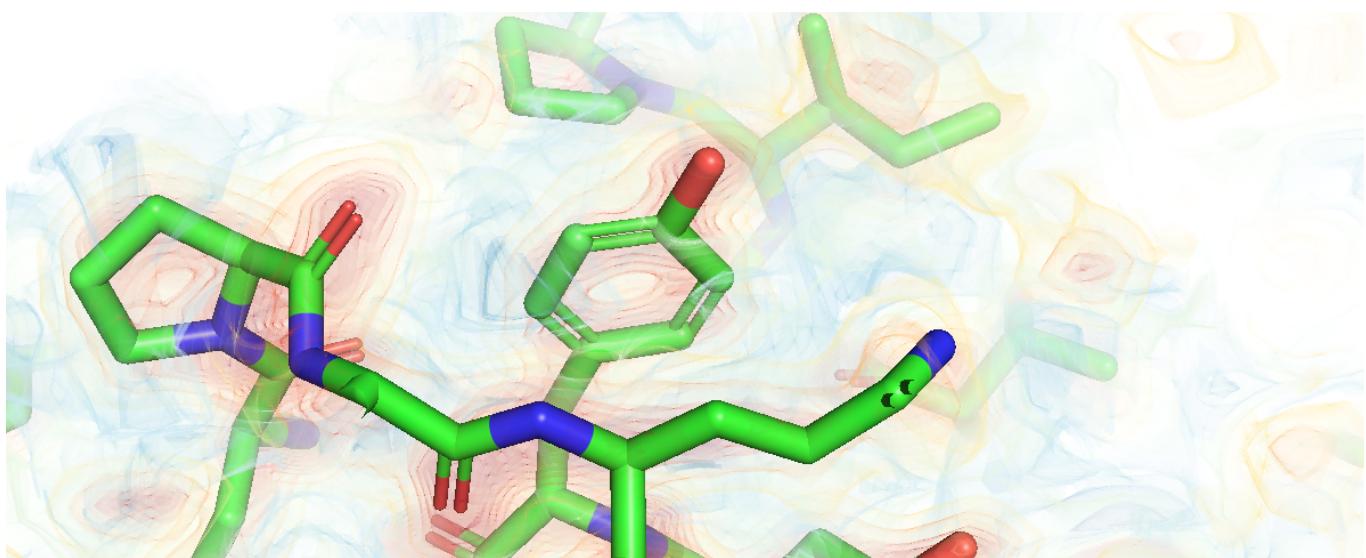
In order to limit where the volume is displayed, we can pass a name of a PyMOL object (that should exist at the time we load the script), and a radius around that object to display

the volume. The name is passed via the keyword `selection` and the carve radius via the keyword `carve`.

```
v7 = pmv.IsoVolume(data, name = "mtz_4de3_volume", colormap = cmap, carve = 2,
selection = "4de3")
v7.alphas[v6.alphas > 0] = 1
v7.write("out/mtz_4de3_isovolume_carved.py")
```

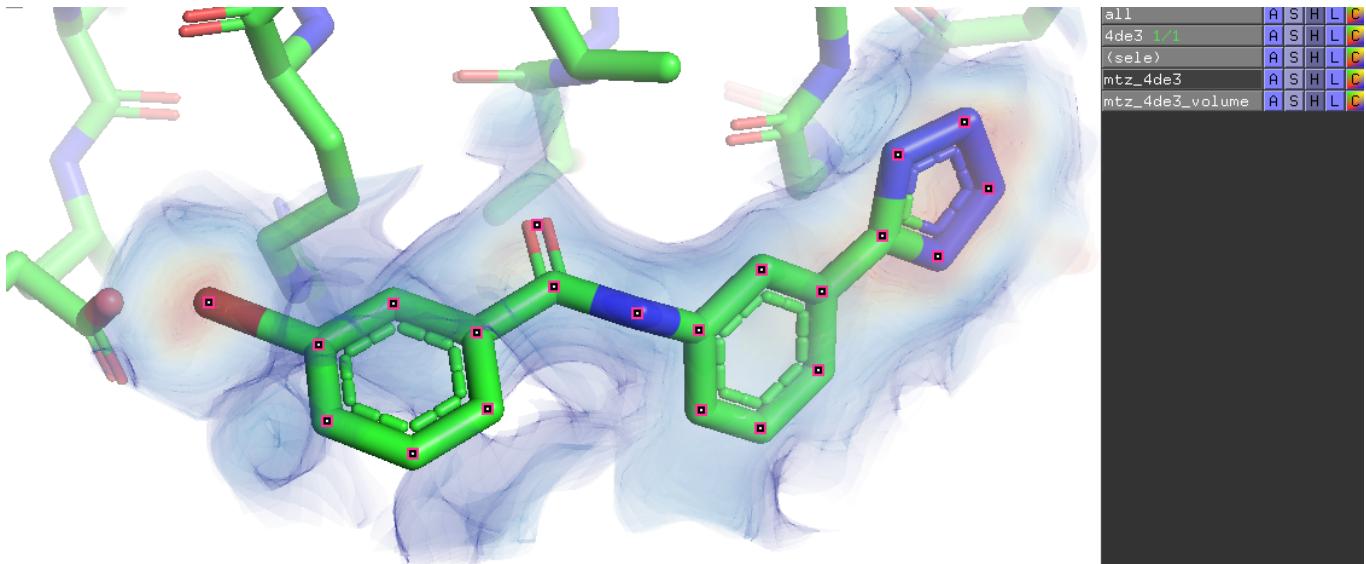


	A	S	H	L	C
all					
4de3 1/1	A	S	H	L	C
(sele)	A	S	H	L	C
mtz_4de3	A	S	H	L	C
mtz_4de3_volume	A	S	H	L	C



To show the volume within 2 Ångström around the selection at the time the script is loaded we can use the following:

```
cmap = pmv.ColorMap([0, .7])
v8 = pmv.IsoVolume(data, clims = np.linspace(0, 1, 32), name =
"mtz_4de3_volume", colormap = cmap, carve = 2, selection = "sele")
v8.alphas[v8.alphas > 0] = 1
v8.alphas[v8.alphas == 0] = 0.05
v8.write("out/mtz_4de3_isovolume_carved_sele.py")
```



```
cmap.get_figure(orientation = "horizontal", figsize = (12, 1))
```



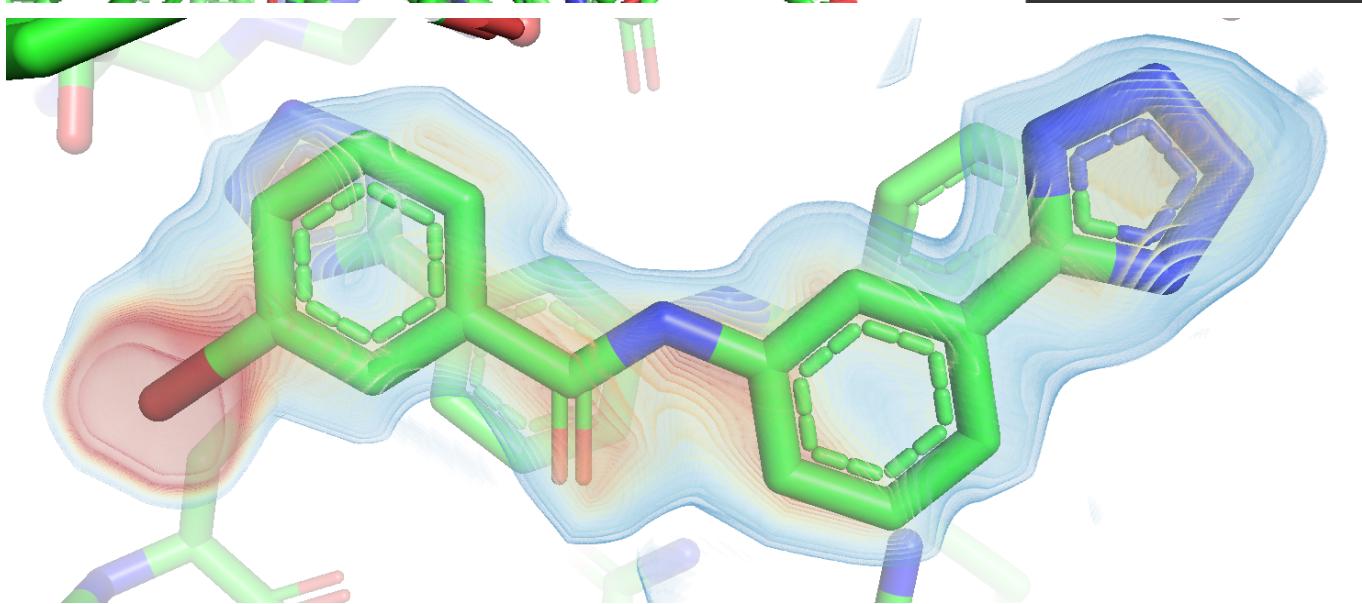
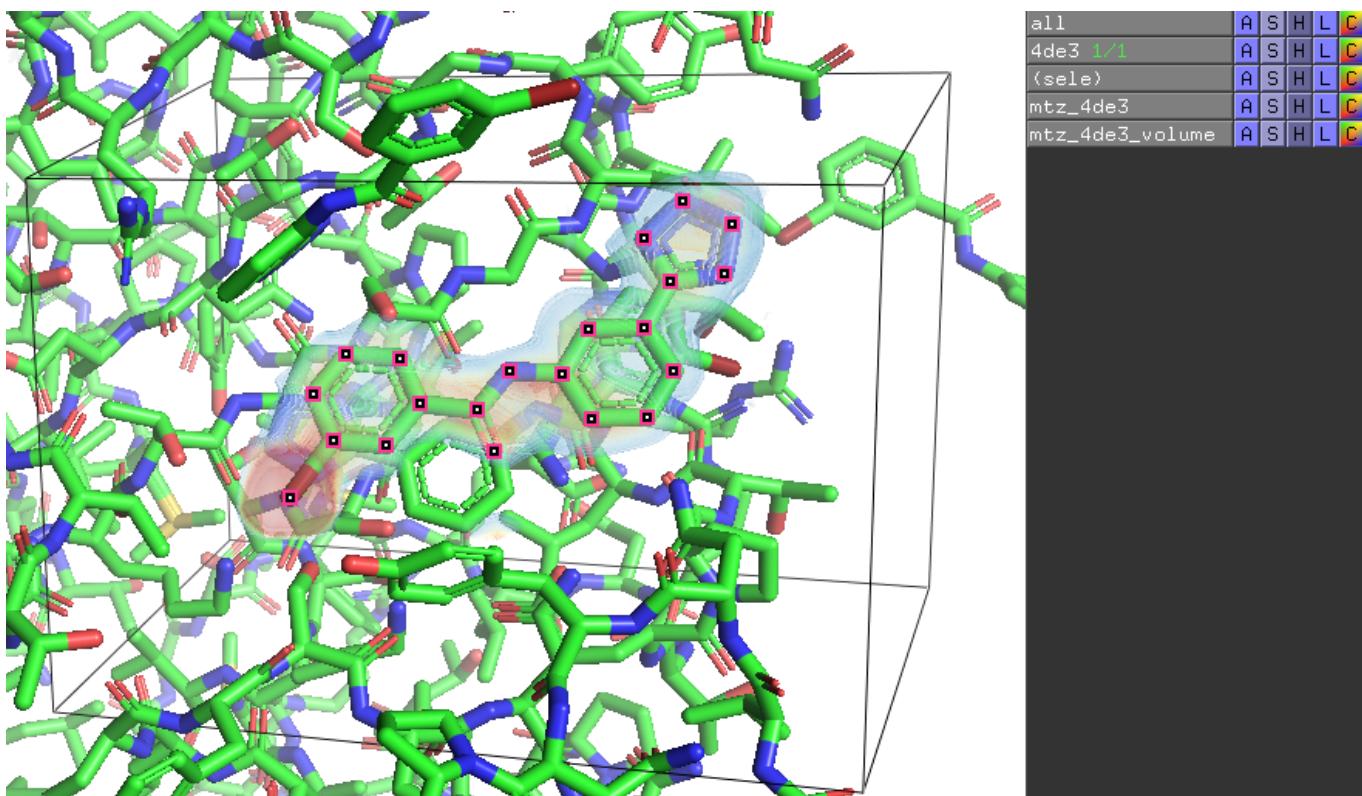
Here we had selected the entire region of the protein when reading in the mtz file and then carved down the display to the selection. A better way to do it would be to restrict the selection of the read in of the mtz file to the region you are interested in.

```
# bfs from a bromine
bromine = [a for a in prot.GetAtoms() if a.GetAtomicNum() == 35][0]
cur_indices = [bromine.GetIdx()]; found_indices = [bromine.GetIdx()]
while(len(cur_indices) > 0):
    next_indices = [a.GetIdx() for a in
prot.GetAtomWithIdx(cur_indices[0]).GetNeighbors() if a.GetIdx() not in
found_indices]
    found_indices.extend(next_indices)
    cur_indices.extend(next_indices)
    cur_indices = cur_indices[1:]
```

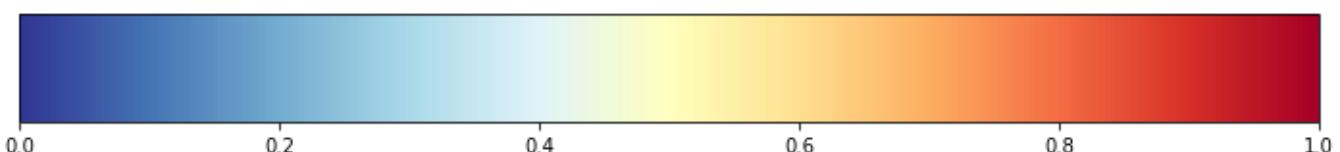
```
# determine box
used_positions = np.array([positions[i] for i in found_indices])
min_pos = np.min(used_positions, axis = 0) - buffer
max_pos = np.max(used_positions, axis = 0) + buffer

#read in data
data = pmv.GridData.from_mtz('../data/4de3_phases.mtz', min_pos = min_pos,
max_pos = max_pos, step_sizes = [1, 1, 1], name = 'mtz_4de3')

#create Volume
cmap = pmv.ColorMap([0, 1])
clims = np.linspace(0, 2, 32)
v9 = pmv.IsoVolume(data, name = "mtz_4de3_volume", colormap = cmap, selection
= "sele", carve = 2, clims = clims)
v9.alphas[v9.alphas > 0] = 1
v9.write("out/mtz_4de3_isovolume_small.py")
```



```
cmap.get_figure(orientation = "horizontal", figsize = (12, 1))
```



## IsoSurfaces

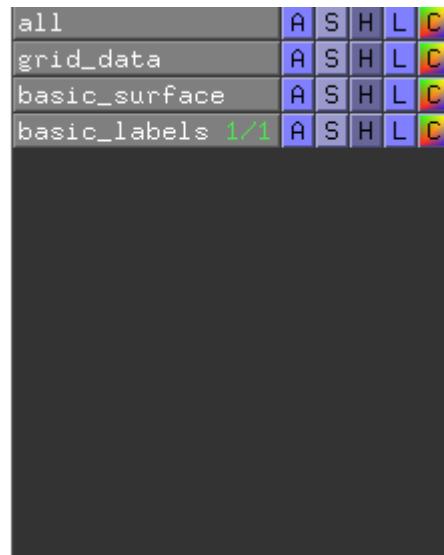
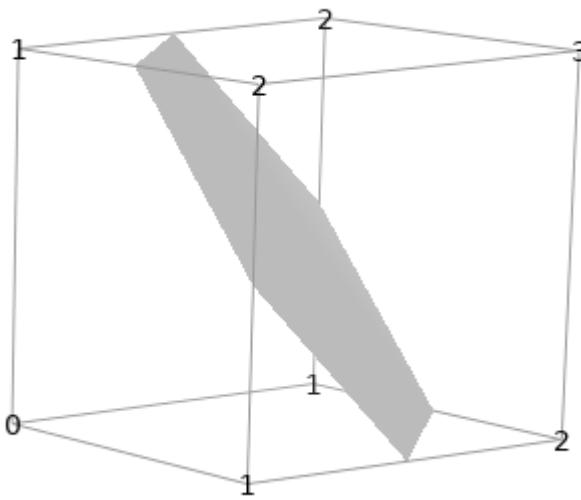
While transparent volumes are a good tool to show volumetric data, we are sometimes not interested in all of the volumetric data or we want to combine two different volumetric information. For this we can use *IsoSurfaces*. They are defined by *GridData* and a *level*. The surface that is drawn is then determined by the points where the values of the *GridData* correspond to the *level*. As those points generally do not fall onto the grid points themselves, [PyMOL uses a form of marching cubes to determine the surface](#).

*IsoSurfaces* are *Displayables* and therefore have a *name* and can be written directly as a script via the *write* method.

We'll start with our simple cube example to get a feeling for the *IsoSurfaces*:

```
grid = np.array([[0, 0, 0],
                [0, 0, 1],
                [0, 1, 0],
                [0, 1, 1],
                [1, 0, 0],
                [1, 0, 1],
                [1, 1, 0],
                [1, 1, 1]])
values = np.sum(grid, axis=1)

grid_data = pmv.GridData(values, grid, name = "grid_data")
s1 = pmv.IsoSurface(grid_data, 1.5, name = "basic_surface")
labels1 = pmv.Labels(grid, values, name = "basic_labels")
pmv.Script([s1, labels1]).write("out/basic_surface.py")
```

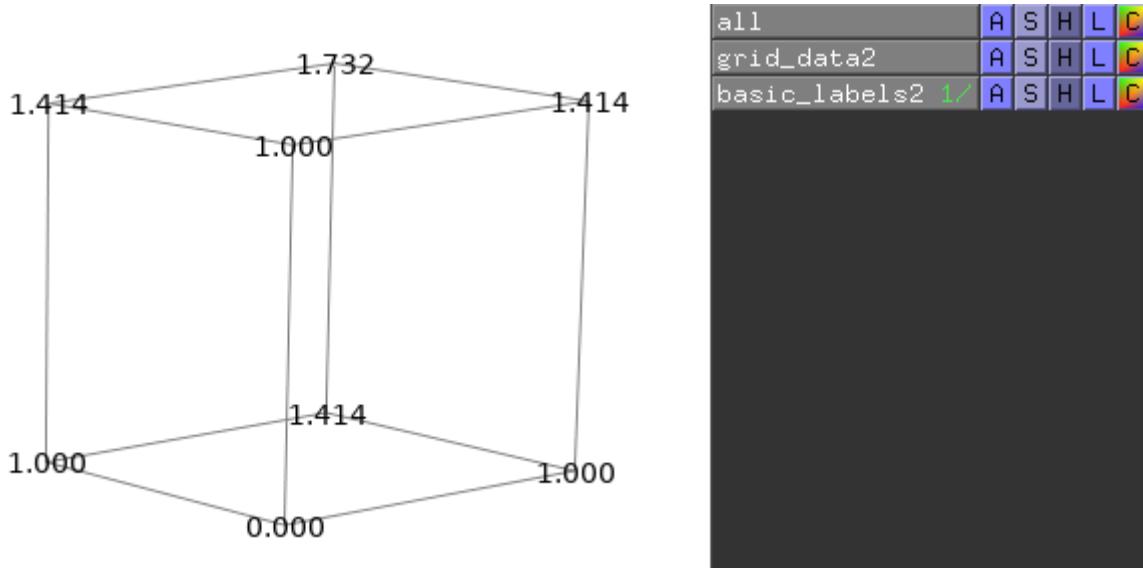


We can see that the surface is drawn exactly at the level 1.5 given a linear interpolation between grid points.

## ColorRamps

One important use-case of *IsoSurfaces* is to map data from different *GridData* onto it. For now we will create another mock-data giving the (euclidean) distance to [0, 0, 1].

```
values2 = np.linalg.norm(grid - np.array([0,0,1]), axis=1)
grid_data2 = pmv.GridData(values2, grid, name = "grid_data2")
labels2 = pmv.Labels(grid, [f"{v:.3f}" for v in values2], name =
"basic_labels2")
pmv.Script([grid_data2, labels2]).write("out/grid_data2.py")
```



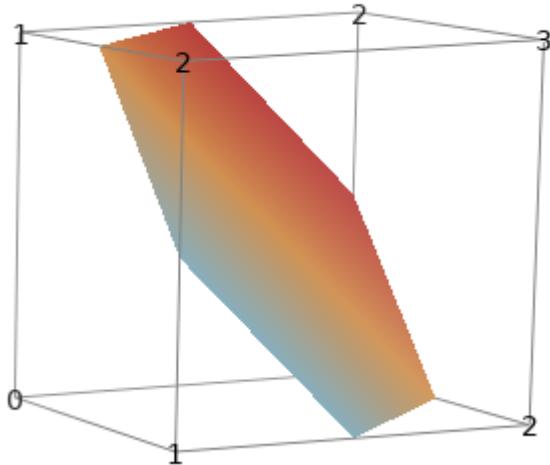
In order to color an *IsoSurface* from another *GridData*, we now need to create a *ColorRamp* object. *ColorRamps* assign a color from a *ColorMap* to every point of a *GridData* based on its value on that point (similar to what is done with *Points*).

Thus a *ColorRamp* takes in a *GridData* object under the keyword *data*, detailing the grid points and their values as well as a *colormap* (which again can be a string mapping onto matplotlib colormaps, a matplotlib colormap itself or a PyMOLViz *ColorMap*).

*ColorRamps* are *Displayables* and therefore have a *name* and can be written directly as a script via the *write* method.

As an example, we will create a *ColorRamp* from the euclidean distance data and map it onto the *IsoSurface* for the manhattan distance.

```
c_ramp = pmv.ColorRamp(grid_data2, name = "color_ramp")
s2 = pmv.IsoSurface(grid_data, 1.5, name = "colored_surface", color = c_ramp)
pmv.Script([s2, labels]).write("out/colored_surface.py")
```

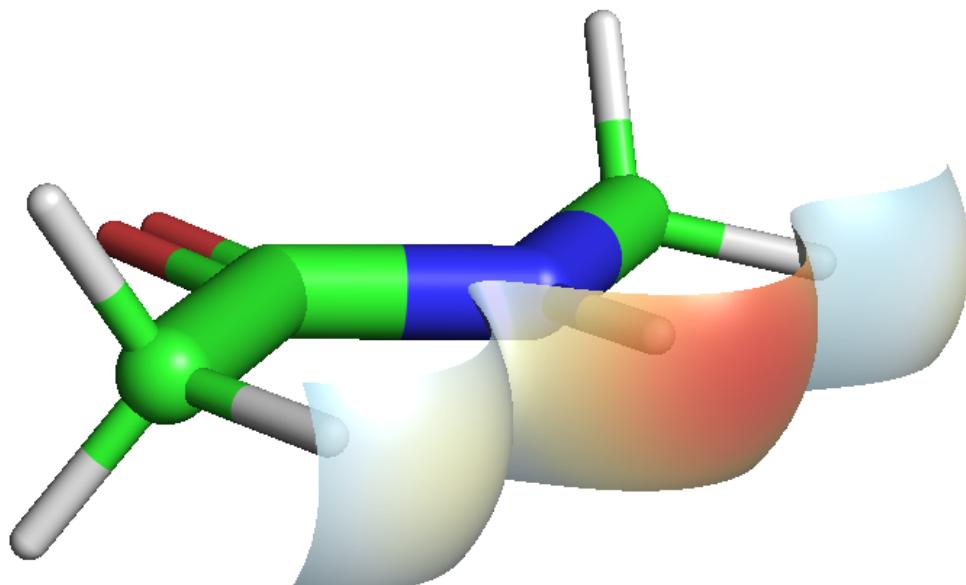


all	A	S	H	L	C
grid_data	A	S	H	L	C
grid_data2	A	S	H	L	C
color_ramp	A	S	H	L	C
colored_surface	A	S	H	L	C
basic_labels 1/1	A	S	H	L	C

Using the N-methyl acetamide example, we can draw an IsoSurface at a density level of 0.01

and color it by the electrostatic potential. To set a surface's transparency, we can use the *transparency* keyword.

```
density_data = pmv.GridData.from_xyz("../data/td.xyz", name = "density_data")
potential_data = pmv.GridData.from_xyz("../data/tp.xyz", name =
"potential_data")
cmap = pmv.ColorMap([0, 0.2])
c_ramp2 = pmv.ColorRamp(potential_data, name = "color_ramp2", colormap = cmap)
s3 = pmv.IsoSurface(density_data, 0.01, name = "potential_surface", color =
c_ramp2, transparency = 0.2)
s3.write("out/potential_surface.py")
```

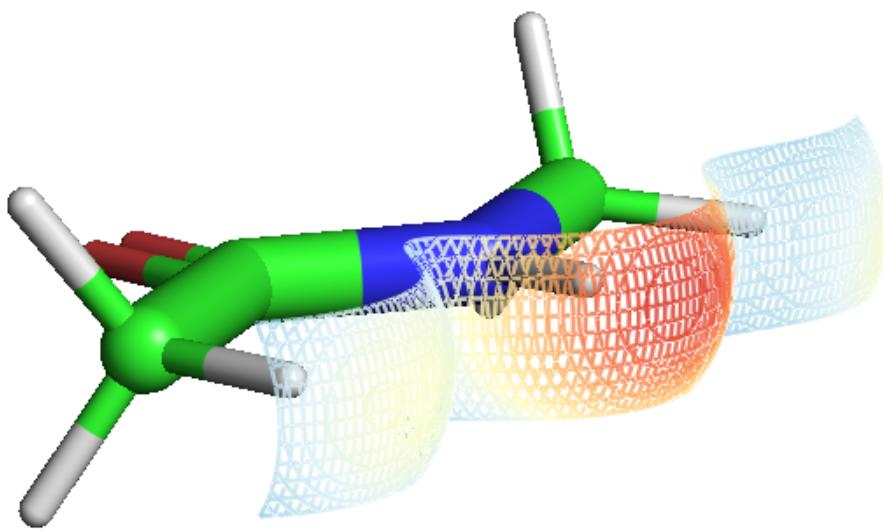


all	A	S	H	L	C
density_data	A	S	H	L	C
potential_data	A	S	H	L	C
color_ramp2	A	S	H	L	C
potential_surface	A	S	H	L	C
bb 1/1	A	S	H	L	C

# IsoMeshes

Sometimes *IsoSurfaces* are unclear and a less obtrusive visualization is preferred. For this, *IsoMeshes* can be used. *IsoMeshes* effectively show the result of the Marching Cubes algorithm as a wireframe. They inherit from *IsoSurfaces* and accept the same arguments, only differing in the way they are displayed.

```
m3 = pmv.IsoMesh(density_data, 0.01, name = "potential_mesh", color = c_ramp2)
m3.write("out/potential_mesh.py")
```



	A	S	H	L	C
all	A	S	H	L	C
bb 1/1	A	S	H	L	C
density_data	A	S	H	L	C
potential_data	A	S	H	L	C
color_ramp2	A	S	H	L	C
potential_mesh	A	S	H	L	C

This can also be used to show the 2mFo-dFc density:

```
from rdkit import Chem
prot = Chem.MolFromPDBFile('../data/4de3.pdb')
positions = prot.GetConformer().GetPositions()
buffer = 5

# bfs from a bromine
bromine = [a for a in prot.GetAtoms() if a.GetAtomicNum() == 35][0]
cur_indices = [bromine.GetIdx()]; found_indices = [bromine.GetIdx()]
while(len(cur_indices) > 0):
    next_indices = [a.GetIdx() for a in
    prot.GetAtomWithIdx(cur_indices[0]).GetNeighbors() if a.GetIdx() not in
    found_indices]
    found_indices.extend(next_indices)
    cur_indices.extend(next_indices)
    cur_indices = cur_indices[1:]

# determine box
```

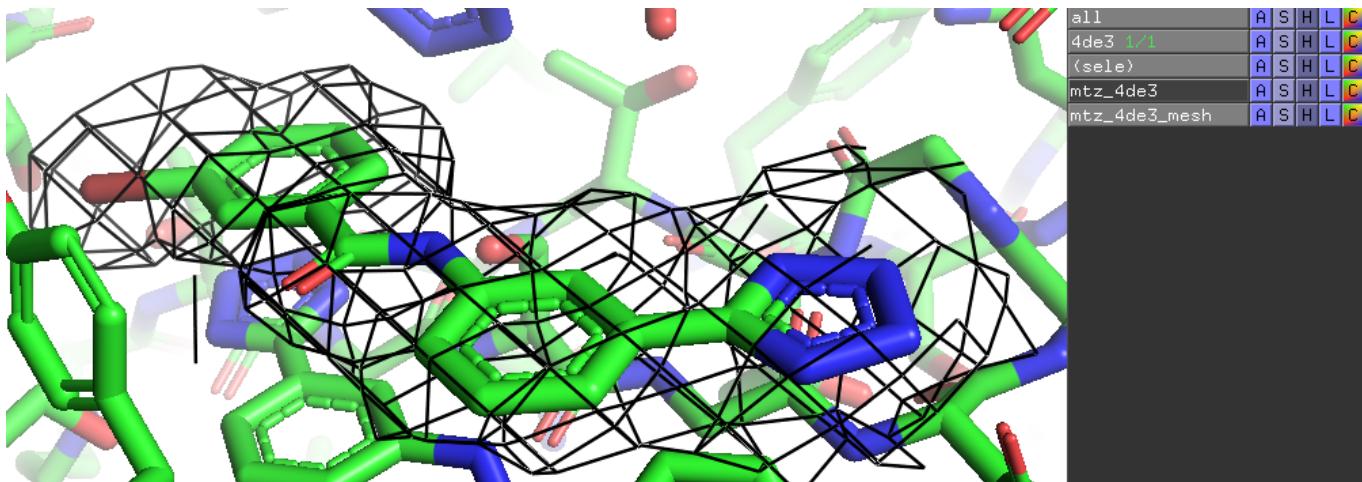
```

used_positions = np.array([positions[i] for i in found_indices])
min_pos = np.min(used_positions, axis = 0) - buffer
max_pos = np.max(used_positions, axis = 0) + buffer

data = pmv.GridData.from_mtz('../data/4de3_phases.mtz', min_pos = min_pos,
max_pos = max_pos, step_sizes = [1, 1, 1], name = 'mtz_4de3')

m4 = pmv.IsoMesh(data, name = "mtz_4de3_mesh", level = 0, selection = "sele",
carve = 2, color = "black")
m4.write("out/mtz_4de3_mesh.py")

```



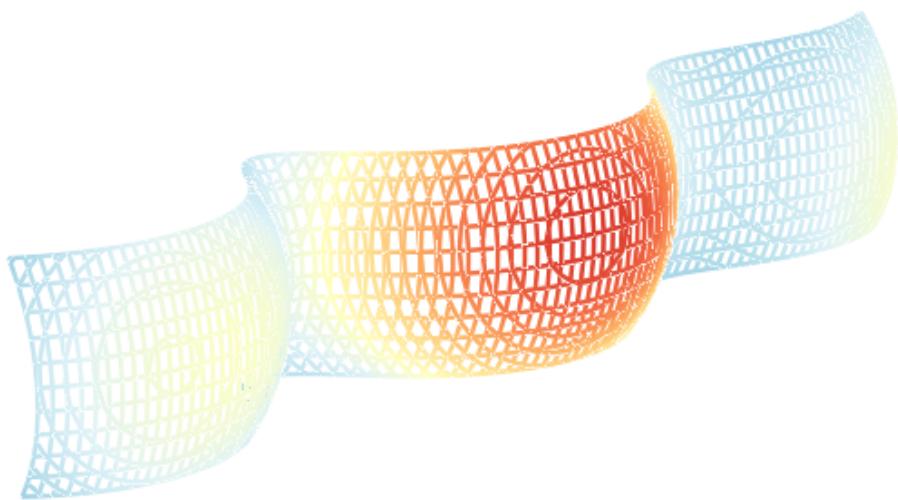
## Dependencies between Displayables

For more complex *Displayables* multiple other *Displayables* are required to draw them properly. Generally this is handled automatically, e.g. when writing a *Volume*, the corresponding *GridData* is written as well. If you want to organize these in *Groups*, you need to explicitly add all dependencies to the *Group*.

```

g = pmv.Group([density_data, potential_data, c_ramp2, m3], name =
"potential_mesh_group")
g.write("out/potential_mesh_group.py")

```



all	A	S	H	L	C
- potential_mesh	A	S	H	L	C
density_data	A	S	H	L	C
potential_data	A	S	H	L	C
color_ramp2	A	S	H	L	C
potential_mesh	A	S	H	L	C