#### overview

June 15, 2021

```
[29]: %load_ext autoreload
      %autoreload 2
      %aimport
      from pathlib import Path
      import numpy as np
      import matplotlib.pyplot as plt
      import re
      from astropy.table import Table
      import astropy.table
      from relaxed import halo_parameters, halo_catalogs
      from relaxed.halo_parameters import get_hparam
     The autoreload extension is already loaded. To reload it, use:
       %reload ext autoreload
     Modules to reload:
     all-except-skipped
     Modules to skip:
[20]: plt.rc('text', usetex=True)
[21]: %matplotlib inline
```

# 1 Plot style

```
[22]: import numpy as np
  import matplotlib.pyplot as plt
  import matplotlib as mpl
  from cycler import cycler
  plt.style.use('seaborn-colorblind')
[23]: mpl.rcParams.update(
{
```

```
# figure
    'figure.figsize': (10, 10),
    # axes
    'axes.labelsize': 24,
    # ticks
    'xtick.major.size': 5,
    'xtick.minor.size': 2.5,
    'xtick.major.width': 0.8,
    'xtick.minor.width': 0.6,
    'xtick.labelsize':
    'ytick.major.size': 5,
    'ytick.minor.size': 2.5,
    'ytick.major.width': 0.8,
    'ytick.minor.width': 0.6,
    'ytick.labelsize':
    #legend
    'legend.fontsize': 24,
})
```

```
[24]: colors = plt.rcParams['axes.prop_cycle'].by_key()['color']
```

# 2 Load catalog

```
[7]: # load catalog we know and love

fpath = Path('/home/imendoza/nbody-relaxed/data/Bolshoi/minh/hlist_1.00035.

→minh')

name = 'Bolshoi'

# this command just sets up the attributes and filters. Catalog is loaded in

→the next cell from the *.minh file.

hcat = halo_catalogs.HaloCatalog(name, fpath)
```

```
[8]: hcat.load_cat_minh()
```

```
[9]: # Load catalog from minh and apply default filters on-the-fly.
print('rows in catalog: ', len(hcat.cat))
```

rows in catalog: 337438

### 3 Add f sub

```
[11]: from relaxed.subhaloes.catalog import create_subhalo_cat
[12]: subhalo_cat = create_subhalo_cat(np.array(hcat.cat['id']), fpath)

[13]: # add column to original catalog
    assert np.all(subhalo_cat['id'] == hcat.cat['id'])
    hcat.cat.add_column(subhalo_cat['f_sub'], name='f_sub')
```

## 4 Different samples

```
[25]: from relaxed.halo_filters import HaloFilter, get_bound_filter, ___ 
→get_relaxed_filters
```

```
[26]: # use halo filters to create additional halo catalogs for analysis.
      hcat_m11 = HaloFilter(get_bound_filter('mvir', high=11.22, modifier=np.log10),_u
      → 'M11') (hcat)
      hcat_m12 = HaloFilter(get_bound_filter('mvir', 12,12.2, modifier=np.log10),_
      → 'M12') (hcat)
      hcat_m13 = HaloFilter(get_bound_filter('mvir',13,14,modifier=np.log10),__
      →'M13')(hcat)
      power_cat = HaloFilter(get_relaxed_filters('power2011'), 'power2011')(hcat)
      neto_cat = HaloFilter(get_relaxed_filters('neto2007'), 'neto2007')(hcat)
      # for easy of access
      dcats = {
          'm11': hcat_m11,
          'm12': hcat_m12,
          'm13': hcat_m13,
          'power': power_cat,
          'neto': neto_cat,
          'all': hcat,
      }
```

```
[27]: # make sure length of catalogs make sense
print(len(hcat))

print(len(hcat_m11), len(hcat_m12), len(hcat_m13))

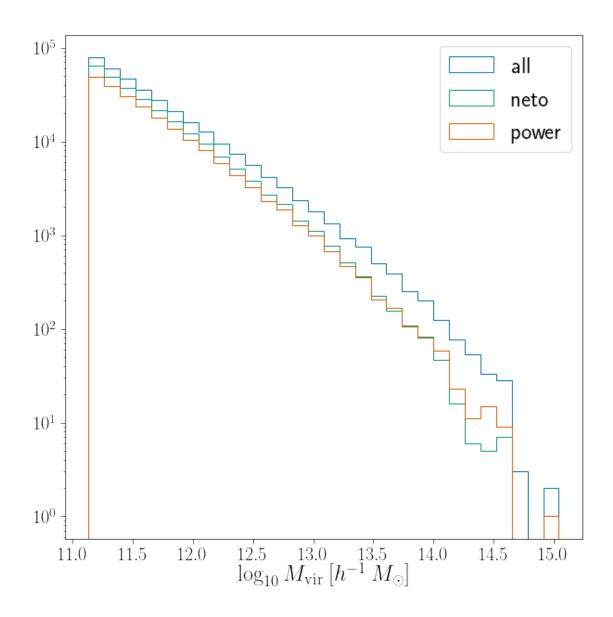
# 500 haloes are so > 13.75
print(len(power_cat), len(neto_cat))
```

```
337438
56076 19726 5507
213058 263039
```

## 5 Histograms

## 5.1 Histogram of Mvir for different samples

```
[34]: names = ['all', 'neto', 'power']
      fig, ax = plt.subplots(1, 1)
      n_bins = 30
      all mvirs = np.hstack([np.log10(dcats[name].cat['mvir']) for name in names])
      bins = get_bins(all_mvirs, n_bins)
      for i, name in enumerate(names):
          c = colors[i]
          legend_label = f'{name}'
          draw_histogram(ax, np.log10(dcats[name].cat['mvir']), bins=bins, color=c,__
       →legend_label=name, vline=None)
      # fix axes and legend.
      param_mvir = halo_parameters.get_hparam('mvir', log=True)
      ax.set_xlabel(param_mvir.get_text())
      plt.yscale('log')
      ax.legend()
      plt.show()
```



#### 5.2 Mean-centered and normalized log parameters

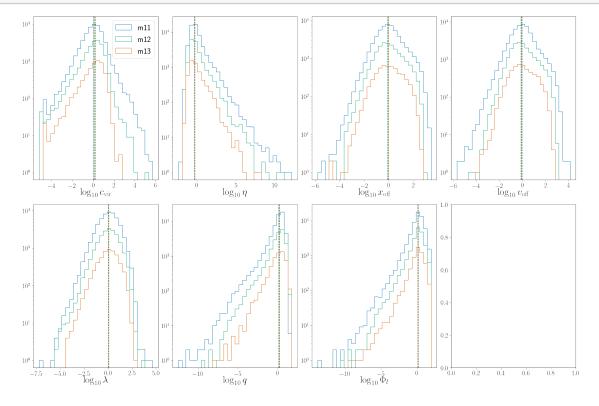
```
[61]: # maybe need to do a specific mass bin to have meaningful results here.
def make_mean_centered_histograms(n_bins=30):
    params = ["cvir", "eta", "x0", "v0", "spin", "q", "phi_l"]
    names = ['m11', 'm12', 'm13']
    fig, axes = plt.subplots(2, 4, figsize=(24, 16))
    normalize = lambda x: (x - np.mean(x)) / np.std(x)
    axes = axes.flatten()

for i, (param, ax) in enumerate(zip(params, axes)):
```

```
hparam = halo_parameters.get_hparam(param, log=True,_
→modifiers=[normalize])
       xlabel = hparam.get_text()
       all_values = np.hstack([hparam.get_values(dcats[name].cat) for name in_
→names])
      bins = get_bins(all_values, n_bins)
       for c, name in zip(colors, names):
          hcat = dcats[name]
           x = hparam.get_values(hcat.cat)
           draw_histogram(ax, x, bins=bins, vline='median', legend_label=name,_
ax.set_yscale('log')
       ax.set_xlabel(xlabel, size=30)
       if i==0:
           ax.legend()
  plt.tight_layout()
```

[62]: # TODO: add title → all haloes for each of the samples, add legend to the → first plot, add xlabel

make\_mean\_centered\_histograms()



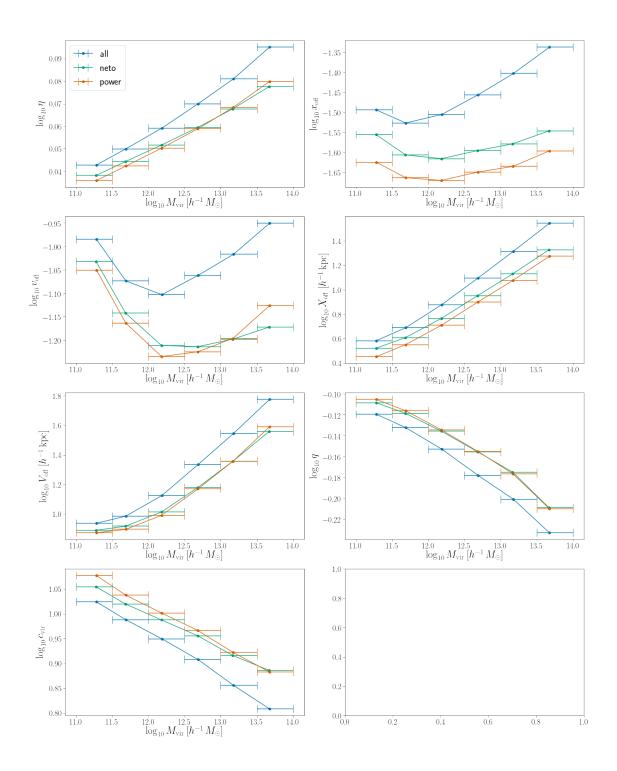
## 6 Scatter binning

#### 6.1 Relaxed parameters as a function of mass bin

```
[66]: def make_scatter_binning(ax, x, y, n_xbins=30, bin_bds=None, show_bands=True,_
      if bin_bds is not None:
              # ignore n xbins
             size = len(bin_bds) - 1
             x_bds = np.array([(bin_bds[i], bin_bds[i + 1]) for i in range(size)])
         else:
              # divide uniformly.
             xs = np.linspace(np.min(x), np.max(x), n_xbins)
              x_bds = np.array([(xs[i], xs[i + 1]) for i in range(len(xs) - 1)])
         masks = [((x_bd[0] < x) & (x < x_bd[1]))  for x_bd  in x_bds]
         xbins = [x[mask]] for mask in masks if len(x[mask]) > 0] # remove empty__
      \hookrightarrow ones.
         ybins = [y[mask]] for mask in masks if len(x[mask]) > 0 and len(y[mask]) > 0
         xmeds = np.array([np.median(xbin) for xbin in xbins])
         ymeds = np.array([np.median(ybin) for ybin in ybins])
         xdiffs = abs(x bds.reshape(-1, 2) - xmeds.reshape(-1, 1))
         ax.errorbar(
             xmeds,
             ymeds,
             xerr=xdiffs.T,
             fmt="o-",
             color=color,
             label=label,
             capsize=10,
         )
         y1 = np.array([np.quantile(ybin, 0.25) for ybin in ybins])
         y2 = np.array([np.quantile(ybin, 0.75) for ybin in ybins])
         if show bands:
              ax.fill_between(xmeds, y1, y2, alpha=0.2, linewidth=0.001, color=color)
```

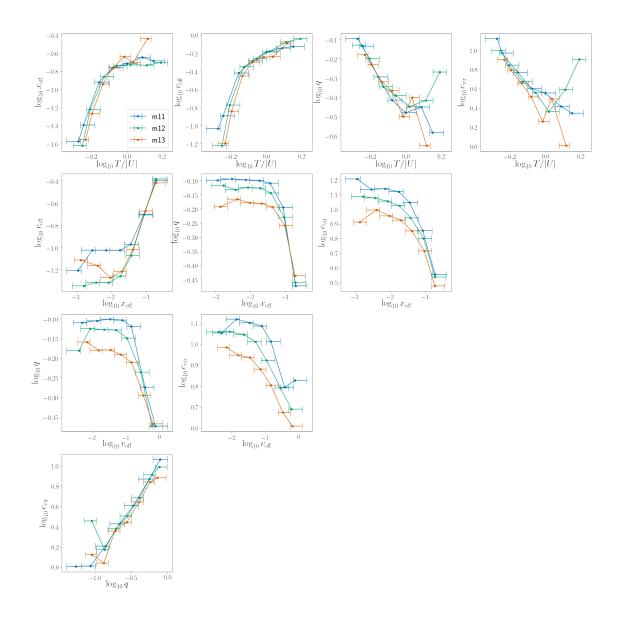
```
[70]: mass_bin_bds = np.arange(11, 14.5, 0.5)
names = ['all', 'neto', 'power']
params = ["eta", "x0", "v0", "xoff", "voff", "q", "cvir"]
hparams = {param: get_hparam(param, log=True) for param in params}
```

```
hparams['mvir'] = get_hparam('mvir', log=True)
fig, axes = plt.subplots(4, 2, figsize=(20, 25))
axes = axes.flatten()
for i, (ax, param) in enumerate(zip(axes, params)):
   for c, name in zip(colors, names):
       hcat = dcats[name]
       xlabel = hparams['mvir'].get_text()
       ylabel = hparams[param].get_text()
       x = hparams['mvir'].get_values(hcat.cat)
       y = hparams[param].get_values(hcat.cat)
       make_scatter_binning(ax, x, y, bin_bds=mass_bin_bds, show_bands=False,_u
ax.set_xlabel(xlabel, size=26)
       ax.set_ylabel(ylabel, size=26)
   if i==0:
       ax.legend()
plt.tight_layout()
plt.show()
```



### 6.2 Correlations of pairs of relaxed parameters at fixed mass

```
[161]: figsize = (24, 24)
       fig = plt.figure(figsize=figsize)
       for (param1, param2) in pos:
           i = pos[(param1, param2)]
           ax = fig.add_subplot(4, 4, i)
           for c, name in zip(colors, names):
               x = hparams[param1].get_values(dcats[name].cat)
               y = hparams[param2].get_values(dcats[name].cat)
               xlabel = hparams[param1].get_text()
               ylabel = hparams[param2].get_text()
               make_scatter_binning(ax, x, y, n_xbins=8, bin_bds=None,_
       →show_bands=False, color=c, label=name)
               ax.set_xlabel(xlabel, size=28)
               ax.set_ylabel(ylabel, size=28)
               ax.tick_params(axis='both', which='major', labelsize=20)
           if i==1:
               ax.legend(loc='best')
       plt.tight_layout()
       plt.show()
```



## 7 Correlation Matrix

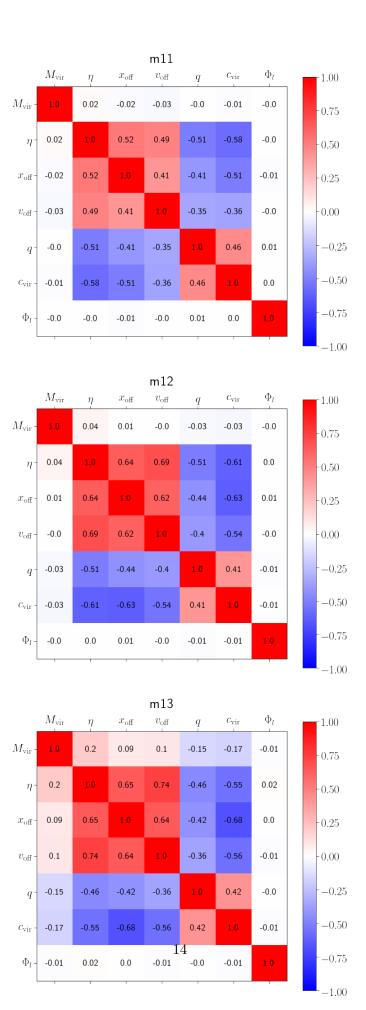
```
[113]: from scipy.stats import spearmanr

def plot_correlation_matrix(ax, values, cell_text_size=14):
    # values: list of values of ech para
    n_params = len(values)
    matrix = np.zeros((n_params, n_params))

for i, value1 in enumerate(values):
    for j, value2 in enumerate(values):
        matrix[i, j] = spearmanr(value1, value2)[0]
```

```
[115]: params = ["mvir", "eta", "x0", "v0", "q", "cvir", "phi_l"]
       hparams = {param: get_hparam(param, log=True) for param in params}
       names = ['m11', 'm12', 'm13']
       fig, axes = plt.subplots(3, 1, figsize=(10, 30))
       for ax, name in zip(axes, names):
           latex_params = [
               hparams[param].get_text(only_param=True)
               for param in params
           values = [
               hparams[param].get_values(dcats[name].cat)
               for param in params
           1
           plot_correlation_matrix(ax, values, cell_text_size=16)
           ax.set_xticks(range(len(latex_params)))
           ax.set_xticklabels(latex_params, size=20)
           ax.set_yticks(range(len(latex_params)))
           ax.set_yticklabels(latex_params, size=20)
           ax.set_title(name, size=25, pad=20)
       plt.show()
       plt.tight_layout()
```

<Figure size 720x720 with 0 Axes>



[]:[