

## Examining the importance of mass-matching

set up the polygon which defines the 'quenched' group

```
%x=[ 10.1379    9.8269    9.9108    10.3255    11.6090    11.0018    10.0194    10.0194];
%y=[ 2.3425    1.3433    0.0921   -0.2410    2.1714    2.3425    2.3785    2.3785];

% x =[ 11.1202    11.0018    10.5476    10.3057    10.0293    10.0737    10.1626    11.1202 ];
% y =[ 2.1624    0.9922    0.3531    0.0291    0.3351    1.7034    2.3695    2.1624 ];

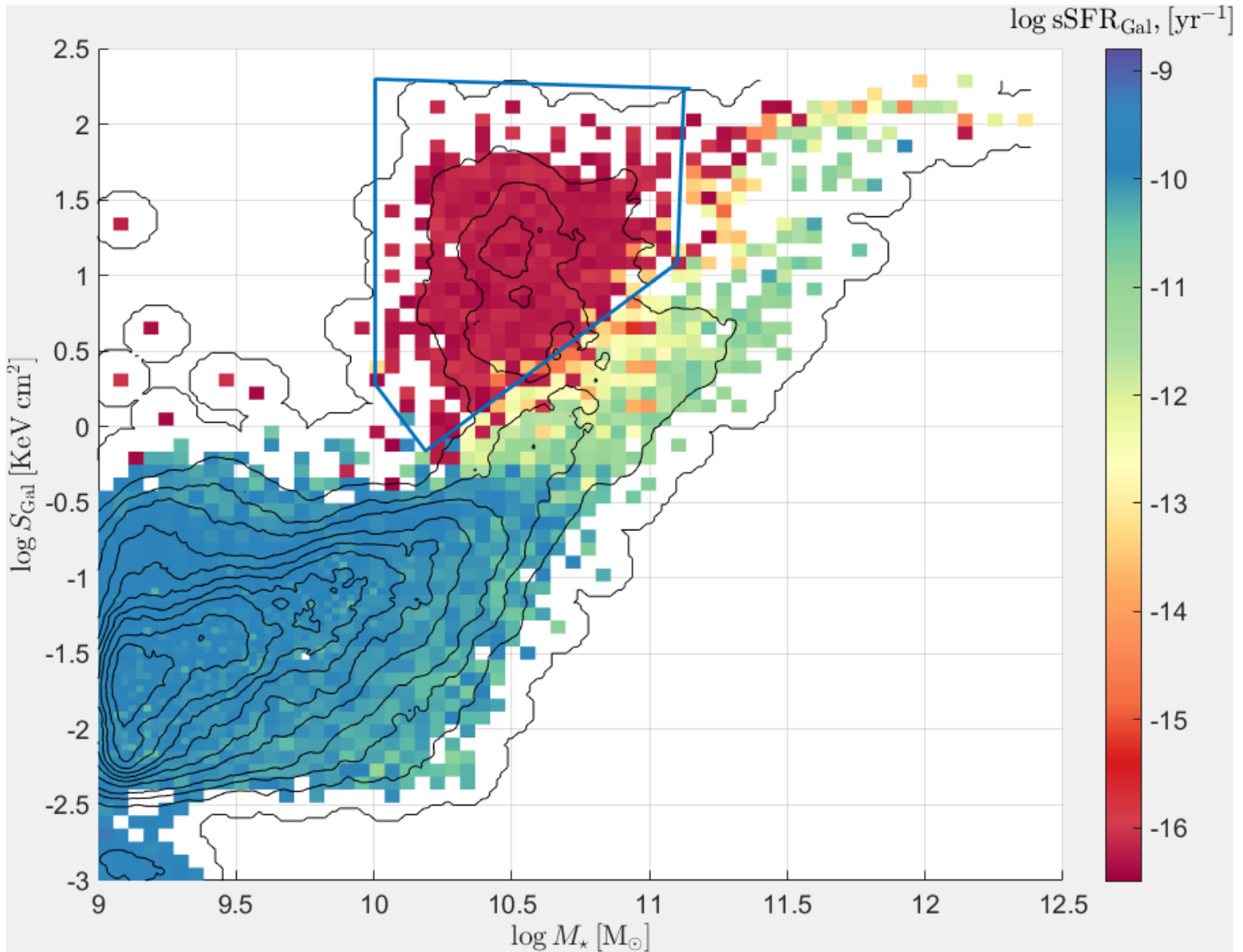
x=[11.1499    10.0046    10.0046    10.1872    11.1005    11.1252];
y=[2.2345    2.2975    0.2811   -0.1600    1.0822    2.2345];

% define important parameters
galMass=tCoolStruct.galMass; % galaxy stellar mass
gasMass=tCoolStruct.inGal.gasMass(1,:);
gasEnt=tCoolStruct.inGal.meanEntMW(1,:);

%centralMask= subsInfo.isCentral(tCoolStruct.galMask);

sfr=subs.SubhaloSFRinRad; % sfr in galaxy
ssfr=sfr./galMass; % + 10^0.5*1e-17.*10.^(0.5.*rand(size(sfr)));

% plot the polygon
```



### get mask from polygon

define the mass range according to the selected group (via polygon) find the rest of the population in the mass range , thus defining two distinct groups in the same mass range

```
polyMask=inpolygon(log10(galMass),log10(gasEnt),x,y);
groupMask=polyMask & subsInfo.isCentral & tCoolStruct.galMask;
qGroupInd=find(groupMask);

massRange=[min(galMass(groupMask)) max(galMass(groupMask))];
massMask=galMass>= massRange(1) & galMass<=massRange(2);

oGroupMask=massMask & subsInfo.isCentral & tCoolStruct.galMask & ~groupMask ;
oGroupInd=find(oGroupMask);
```

### show the distribution of host masses for the two groups

Here we show the distribution of the host masses for the galaxies in each group

```

qFofMass=fofs.Group_M_Crit200(subsInfo.hostFof(qGroupInd)+1).*illUnits.massUnit;
oFofMass=fofs.Group_M_Crit200(subsInfo.hostFof(oGroupInd)+1).*illUnits.massUnit;

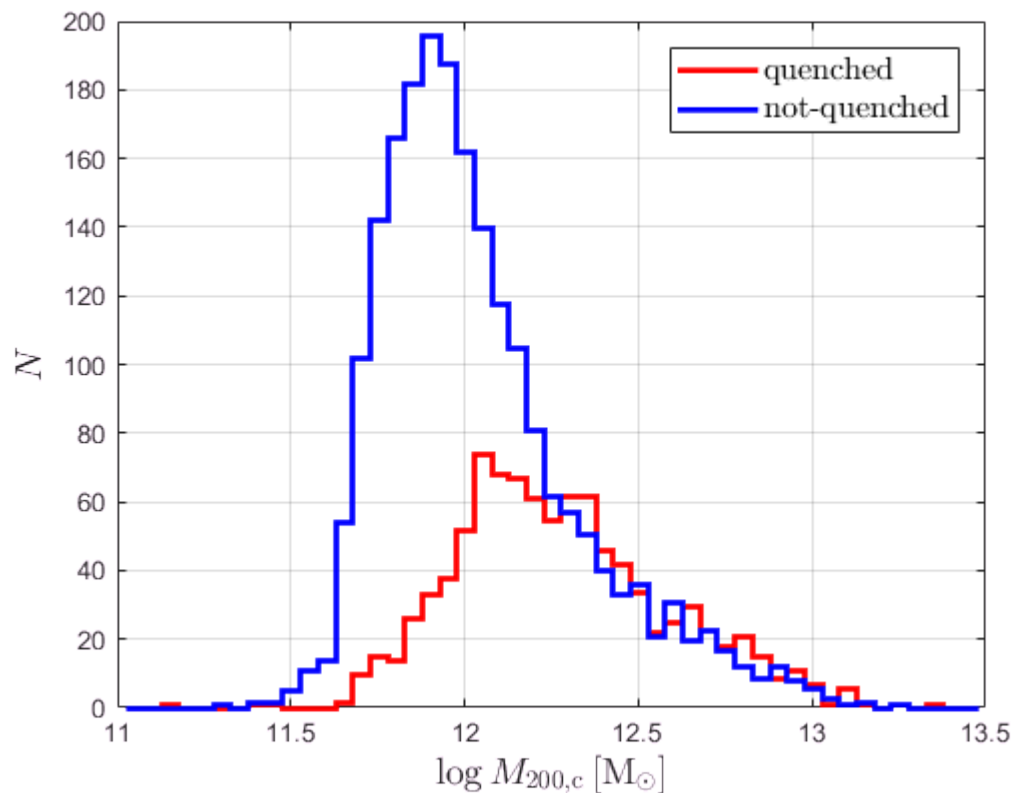
nb=50;
binEdge=linspace(11,13.5,nb+1);
bins=binEdge(1:end-1)+0.5.*diff(binEdge);

qh=histcounts(log10(qFofMass),binEdge);
oh=histcounts(log10(oFofMass),binEdge);

figure

h(1)=stairs(bins,qh,'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,oh,'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log M_{\mathrm{200,c}}\backslash,[\mathrm{M}_{\odot}]$')
ylabelmine('$N$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthEast')

```



host-mass histogram for the two group which make up the mass range.

Since there is a different number of galaxies the histogram needs to be normalized, as in the next figure.

```

figure
h(1)=stairs(bins,qh./sum(qh),'r','DisplayName','quenched','linewidth',2);

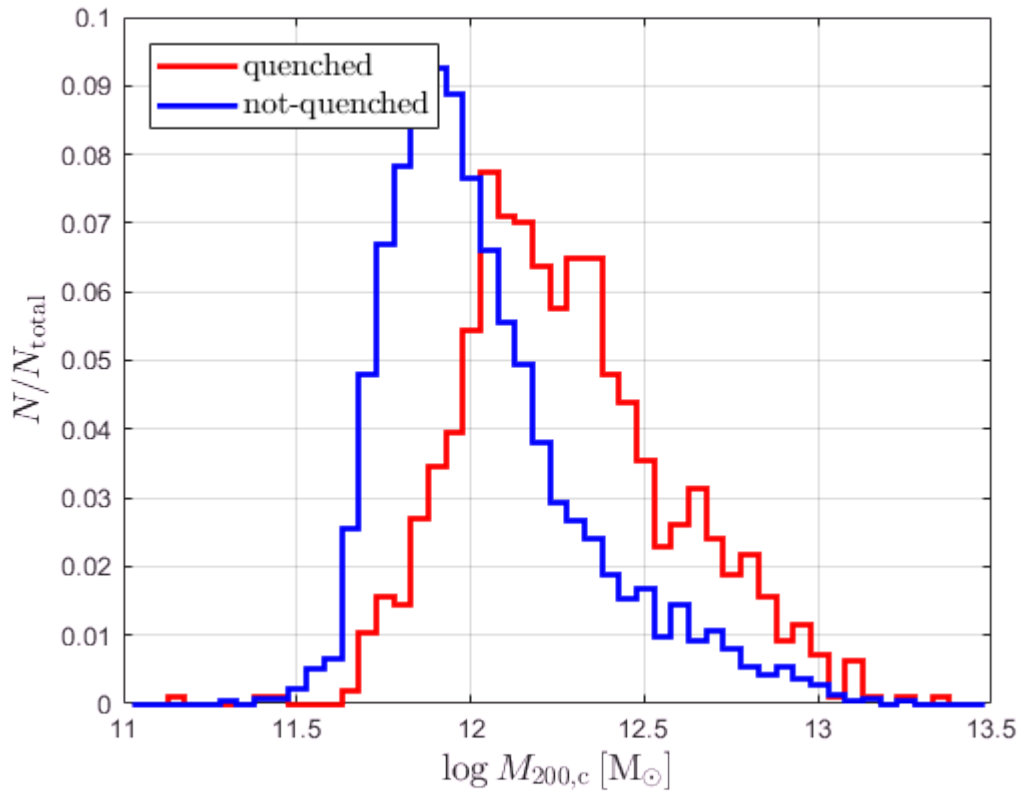
```

```

hold on
h(2)=stairs(bins,oh./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log M_{\mathrm{200,c}}\backslash, [\mathrm{M}_{\odot}]$')
ylabelmine('$N / N_{\mathrm{total}}$')
grid
hl=legend(h);

set(hl,'interpreter','latex','fontsize',12,'location','NorthWest')

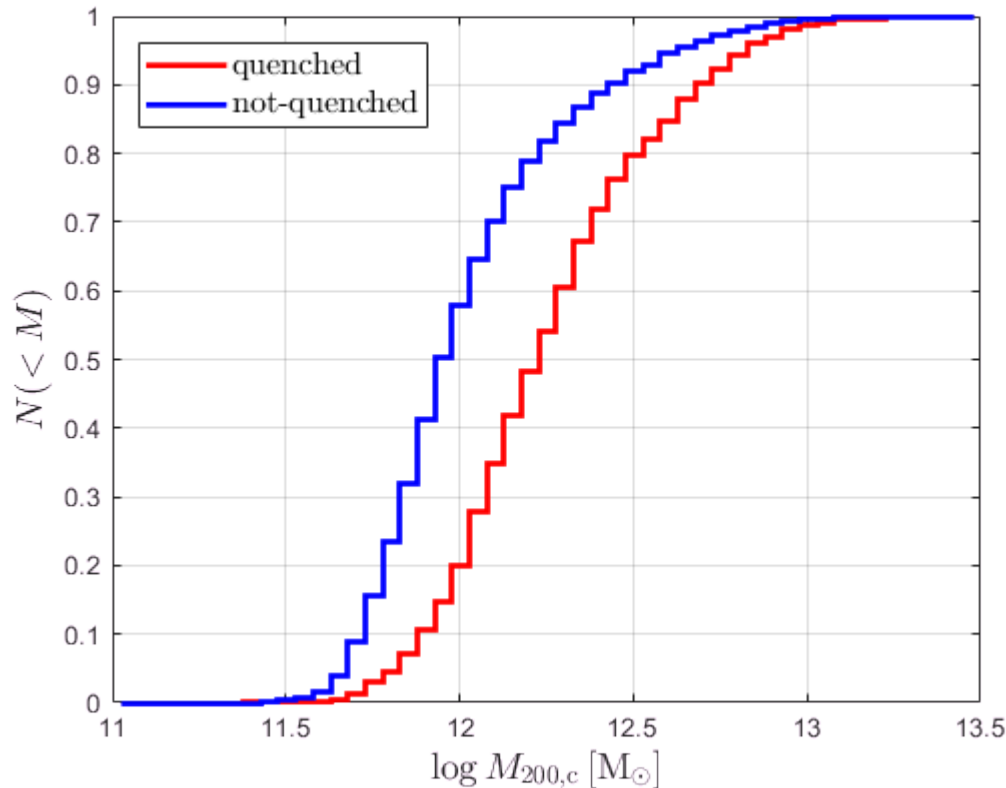
```



```

figure
h(1)=stairs(bins,cumsum(qh)./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,cumsum(oh)./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log M_{\mathrm{200,c}}\backslash, [\mathrm{M}_{\odot}]$')
ylabelmine('$N(<M)$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthWest')

```



The cumulative function is also a good way to compare the distributions.

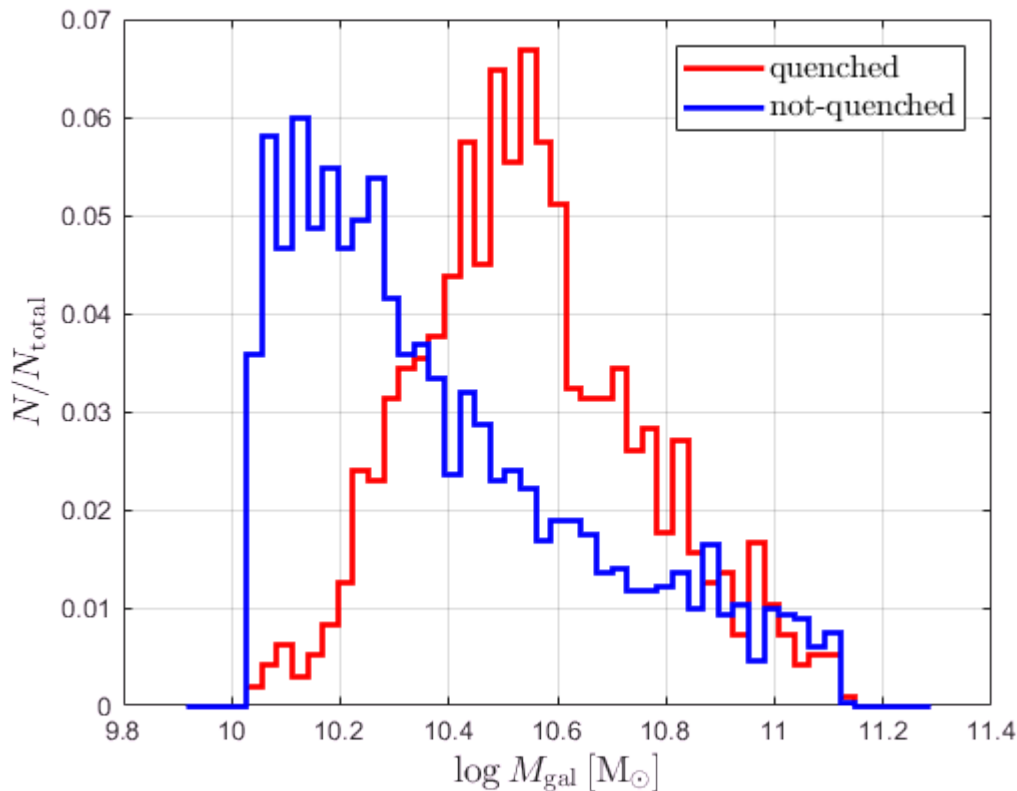
Sum-up: It appears that there is a distinct difference between the two distributions though, one must be careful - the two groups do not sample the same mass range as can be seen in the next figure:

```
nb=50;
binEdge=linspace(9.9,11.3,nb+1);
bins=binEdge(1:end-1)+0.5.*diff(binEdge);

qh=histcounts(log10(galMass(qGroupInd)),binEdge);
oh=histcounts(log10(galMass(oGroupInd)),binEdge);

figure
h(1)=stairs(bins,qh./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,oh./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabel('log M_{\mathrm{gal}} / [M_{\odot}]')
ylabel('N / N_{\mathrm{total}}')
grid
hl=legend(h);

set(hl,'interpreter','latex','fontsize',12,'location','NorthEast')
```



It is this difference which may be responsible for the different host mass distributions (since they are known to be correlated). To examine this further we examine the mass-matched sample.

### examine mass-matching

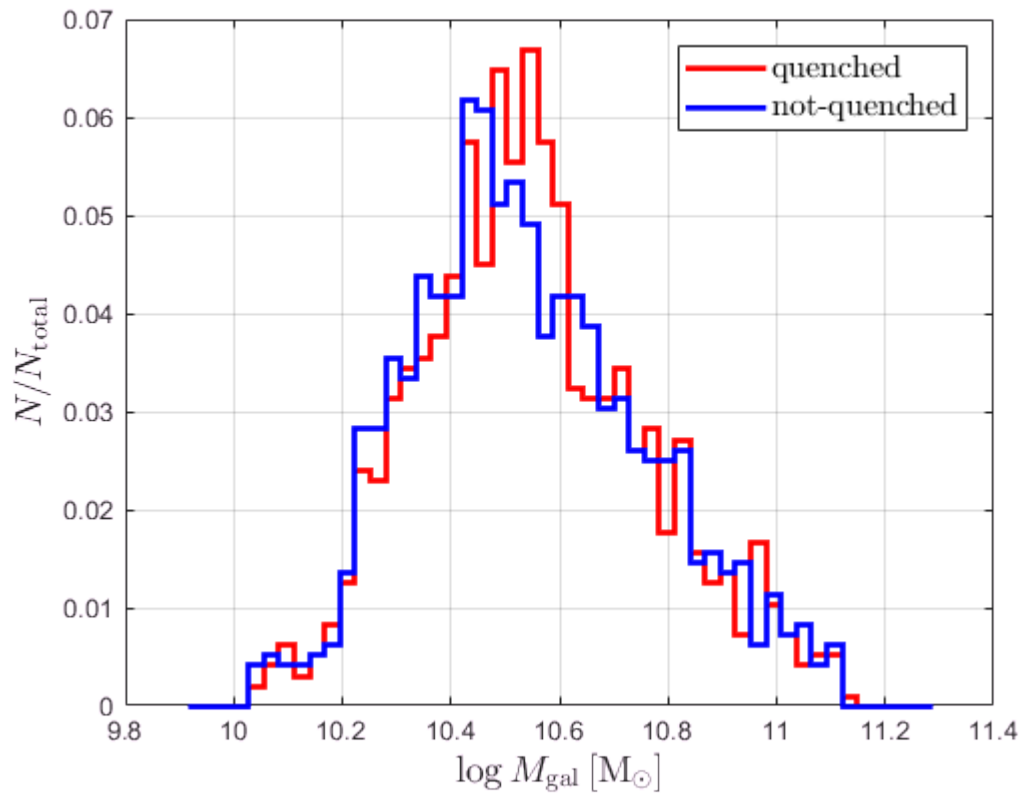
```
matched=create_matched_sample(qGroupInd,oGroupInd,galMass,'range');

nb=50;
binEdge=linspace(9.9,11.3,nb+1);
bins=binEdge(1:end-1)+0.5.*diff(binEdge);

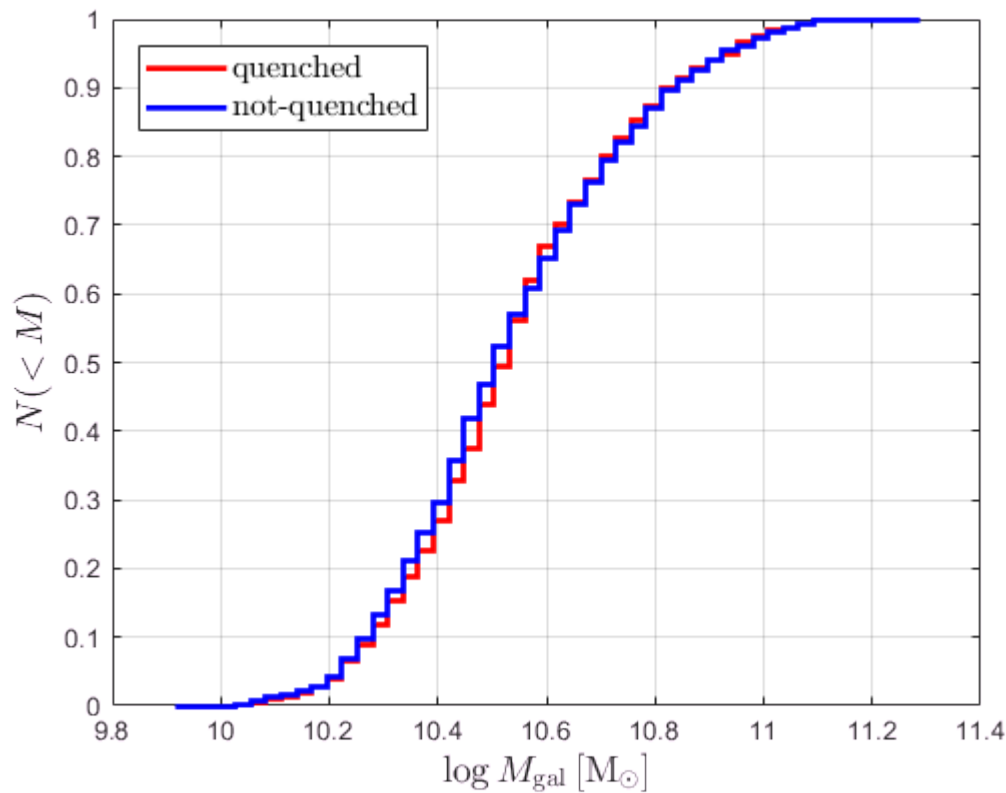
qh=histcounts(log10(galMass(qGroupInd)),binEdge);
oh=histcounts(log10(galMass(matched)),binEdge);

figure
h(1)=stairs(bins,qh./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,oh./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log M_{\mathrm{gal}}\backslash, [\mathrm{M}_{\odot}]$')
ylabelmine('$N / N_{\mathrm{total}}$')
grid
hl=legend(h);

set(hl,'interpreter','latex','fontsize',12,'location','NorthEast')
```



```
figure
h(1)=stairs(bins,cumsum(qh)./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,cumsum(oh)./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log M_{\mathrm{gal}}\backslash,[\mathrm{M}_{\odot}]$')
ylabelmine('$N(<M)$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthWest')
```



### Show host mass distributions from matched mass sample

We perform mass matching 100 times and then average the resulting histogram.

```
nb=50;
binEdge=linspace(11,13.5,nb+1);
bins=binEdge(1:end-1)+0.5.*diff(binEdge);

qh=histcounts(log10(qFofMass),binEdge);

clear ohTemp
for i=1:100

    matched=create_matched_sample(qGroupInd,oGroupInd,galMass,'range');
    oFofMass=fofs.Group_M_Crit200(subsInfo.hostFof(matched)+1).*illUnits.massUnit;

    ohTemp(i,:)=histcounts(log10(oFofMass),binEdge);
end

oh=mean(ohTemp,1);

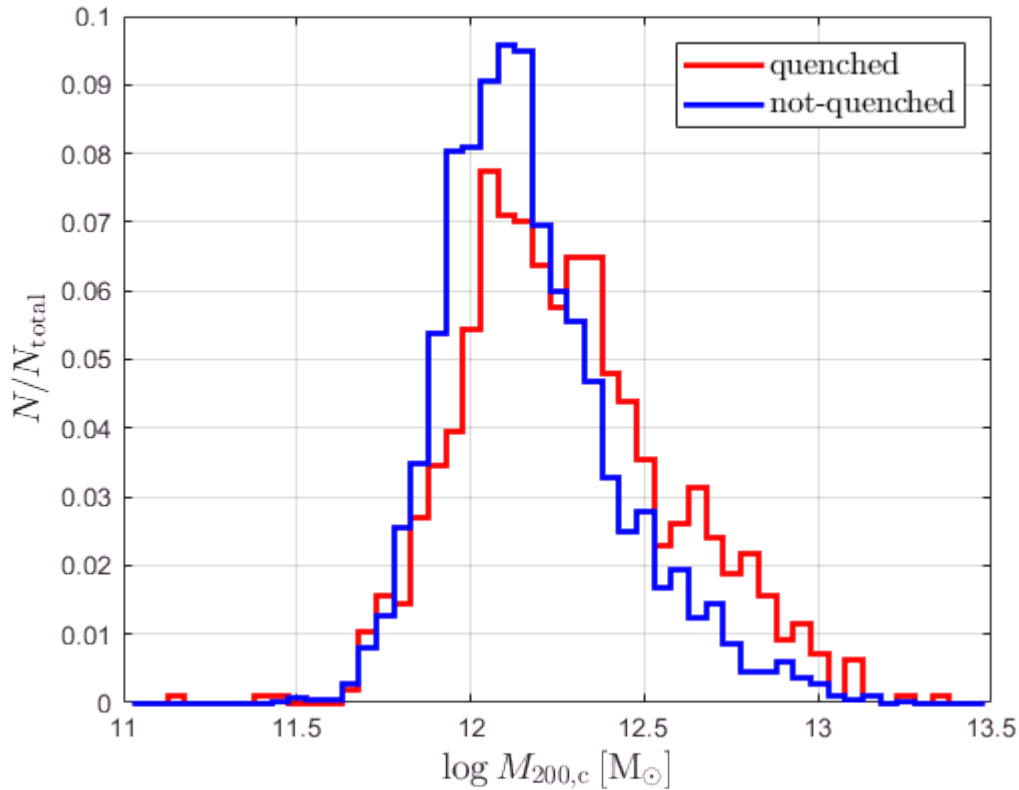
figure
h(1)=stairs(bins,qh./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
```



```

h(2)=stairs(bins,oh./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log M_{\mathrm{200,c}}\backslash, [\mathrm{M}_{\odot}]$')
ylabelmine('$N / N_{\mathrm{total}}$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthEast')

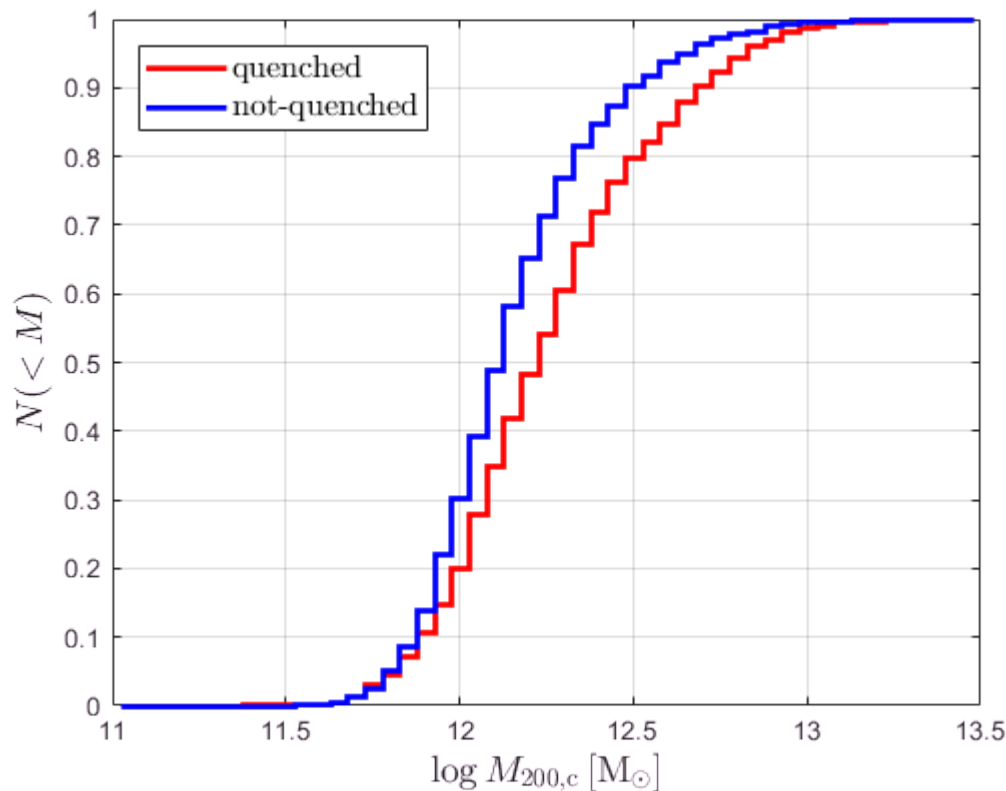
```



```

figure
h(1)=stairs(bins,cumsum(qh)./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,cumsum(oh)./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log M_{\mathrm{200,c}}\backslash, [\mathrm{M}_{\odot}]$')
ylabelmine('$N(<M)$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthWest')

```



```
%oh=
```

In the mass matched sample the difference between the host-mass distribution has become much smaller, and is probably not very significant.

## Show the distribution of BH masses for the two groups

Here we examine the difference in the BH mass distribution between the two groups. again, we begin with 2 groups which span the entire mass range, but are not mass-matched and then repeat the analysis for a mass-matched sample.

```
qBHMass=subs.SubhaloMassInRadType(illustris.partTypeEnum('bh')+1,qGroupInd).*illUnits.massUnit;
oBHMass=subs.SubhaloMassInRadType(illustris.partTypeEnum('bh')+1,oGroupInd).*illUnits.massUnit;

nb=50;
binEdge=linspace(7,9.5,nb+1);
bins=binEdge(1:end-1)+0.5.*diff(binEdge);

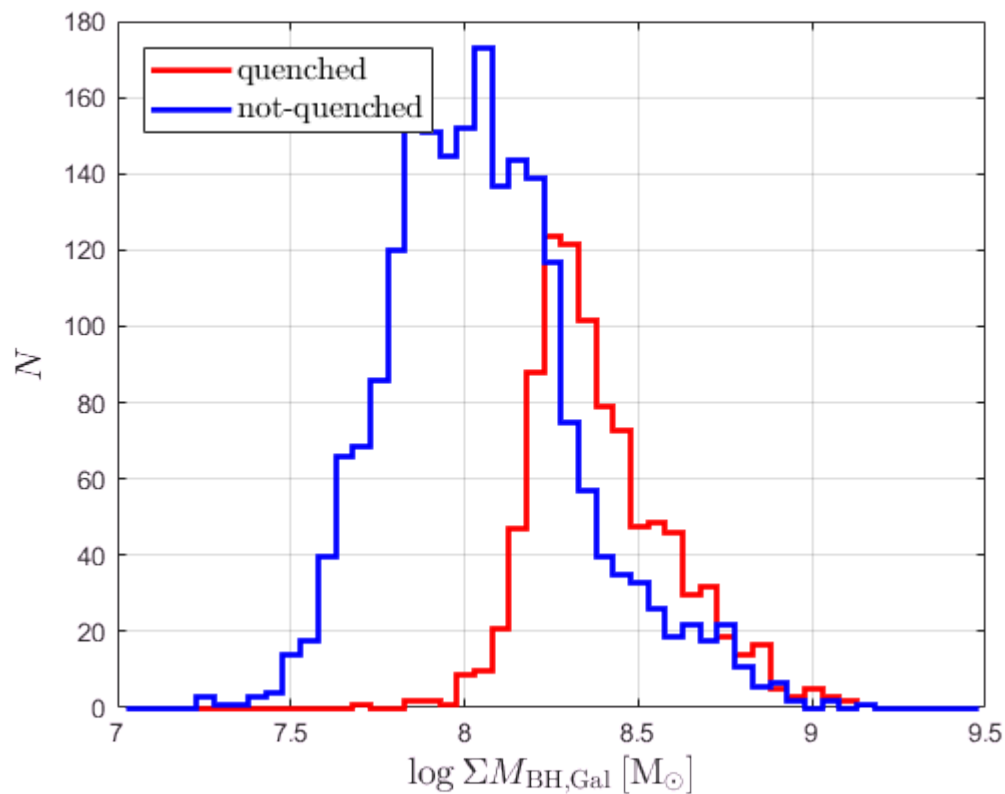
qh=histcounts(log10(qBHMass),binEdge);
oh=histcounts(log10(oBHMass),binEdge);

figure
h(1)=stairs(bins,qh,'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,oh,'b','DisplayName','not-quenched','linewidth',2);
xlabel('log Sigma M_{\mathrm{BH,Gal}} / [\mathrm{M}_{\odot}]')
```

```

ylabelmine('$N$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthWest')

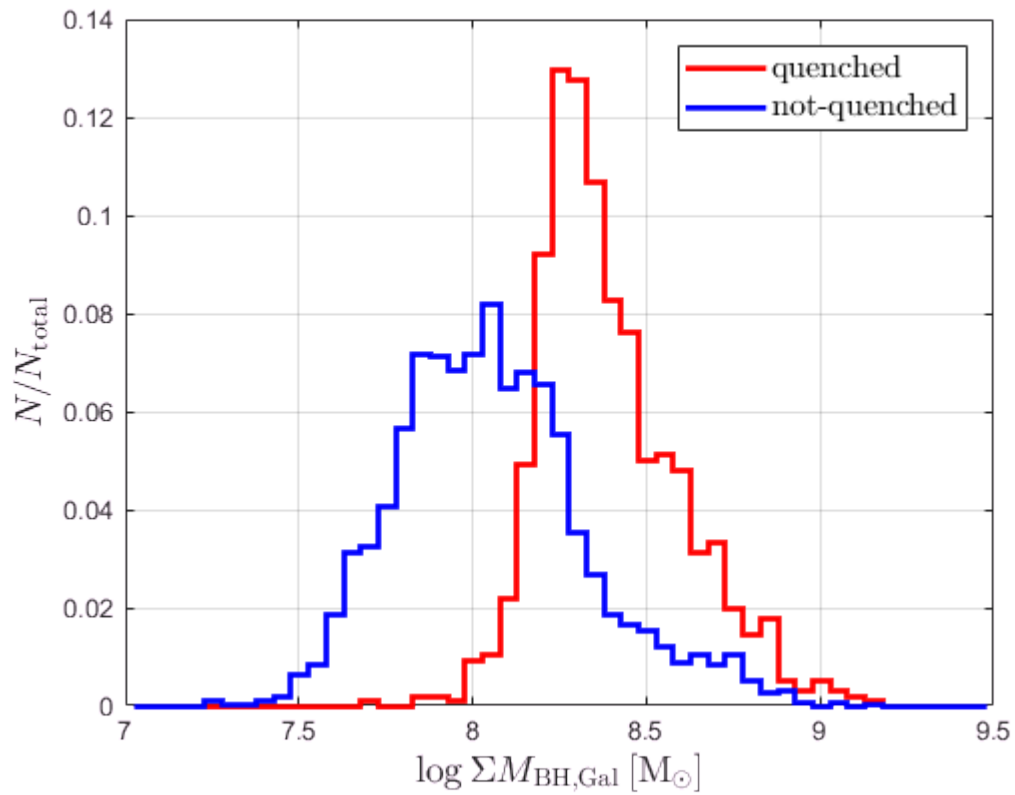
```



```

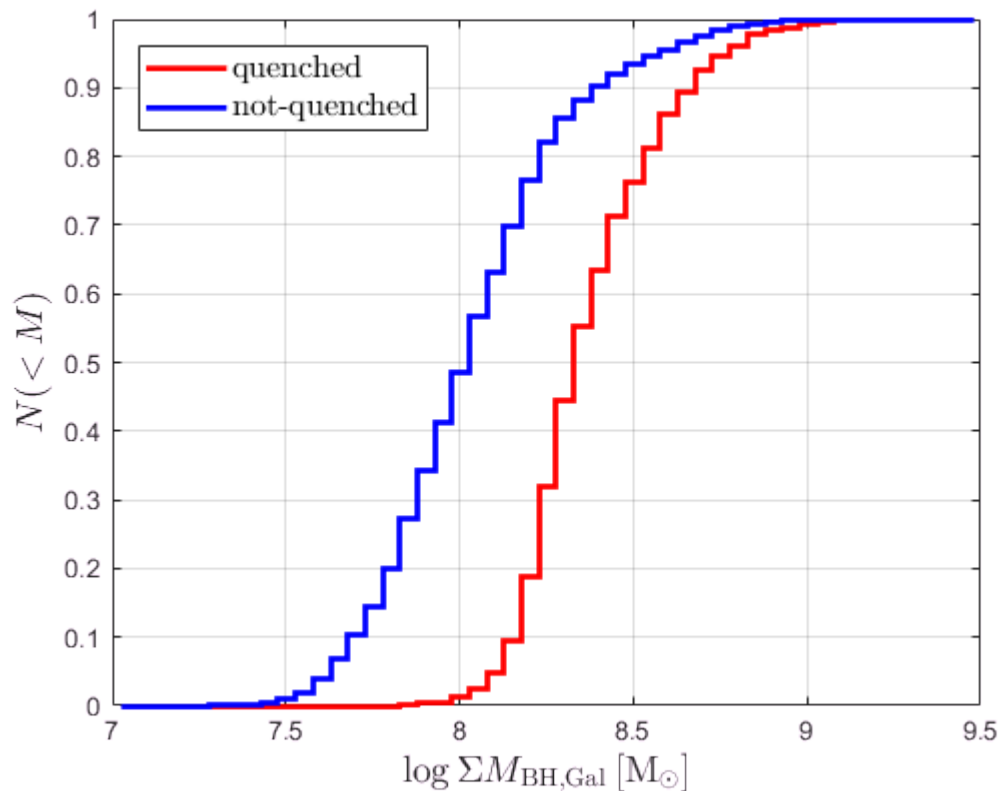
figure
h(1)=stairs(bins,qh./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,oh./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log \Sigma M_{\mathrm{BH,Gal}}\, [\mathrm{M}_\odot]$')
ylabelmine('$N / N_{\mathrm{total}}$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthEast')

```



```
figure
h(1)=stairs(bins,cumsum(qh)./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,cumsum(oh)./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log \Sigma M_{\mathrm{BH,Gal}}\, [\mathrm{M}_{\odot}]$')

ylabelmine('$N(<M)$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthWest')
```



Comparing the distributions shows a marked difference of the BH masses in the two groups. However, one must be cautious as we've seen before.

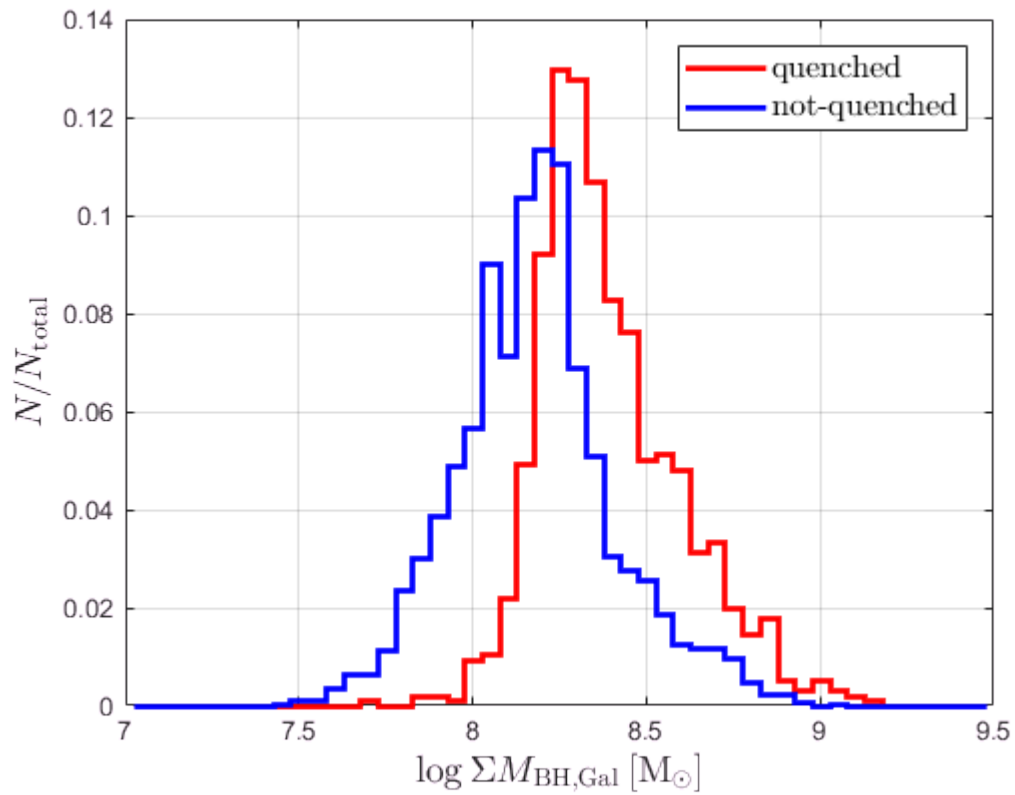
### compare with mass-matched sample

```
for i=1:100

    matched=create_matched_sample(qGroupInd,oGroupInd,galMass,'range');
    oBHMass=subs.SubhaloMassInRadType(illustris.partTypeEnum('bh')+1,matched).*illUnits.massUnit;
    ohTemp(i,:)=histcounts(log10(oBHMass),binEdge);
end

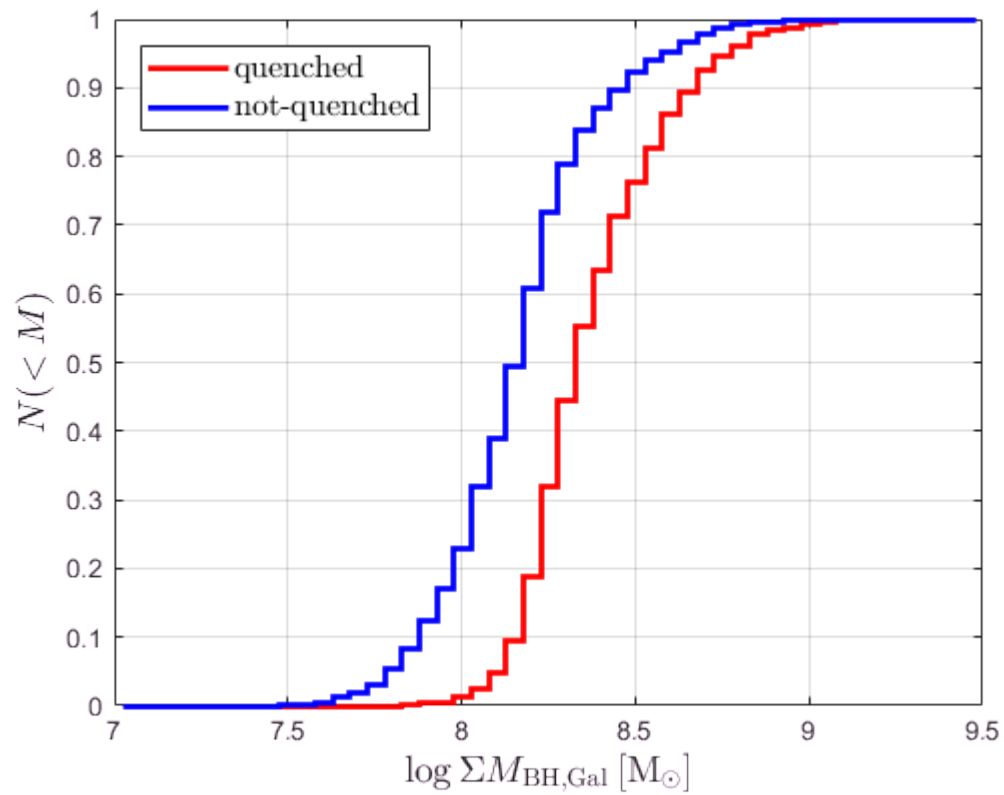
oh=mean(ohTemp,1);

figure
h(1)=stairs(bins,qh./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,oh./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log \Sigma M_{\mathrm{BH,Gal}}$',[M_{\odot}]$')
ylabelmine('$N / N_{\mathrm{total}}$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthEast')
```



```
figure
h(1)=stairs(bins,cumsum(qh)./sum(qh),'r','DisplayName','quenched','linewidth',2);
hold on
h(2)=stairs(bins,cumsum(oh)./sum(oh),'b','DisplayName','not-quenched','linewidth',2);
xlabelmine('$\log \Sigma M_{\mathrm{BH,Gal}}\backslash,[\mathrm{M}_{\odot}]$')

ylabelmine('$N(<M)$')
grid
hl=legend(h);
set(hl,'interpreter','latex','fontsize',12,'location','NorthWest')
```



Once again, comparing a mass-matched sample shows a smaller difference between the two distributions, but that difference is still there - though it may require some more rigorous analysis, it seems there is a significantly higher BH mass in the quenched galaxies versus a mass-matched sample.