

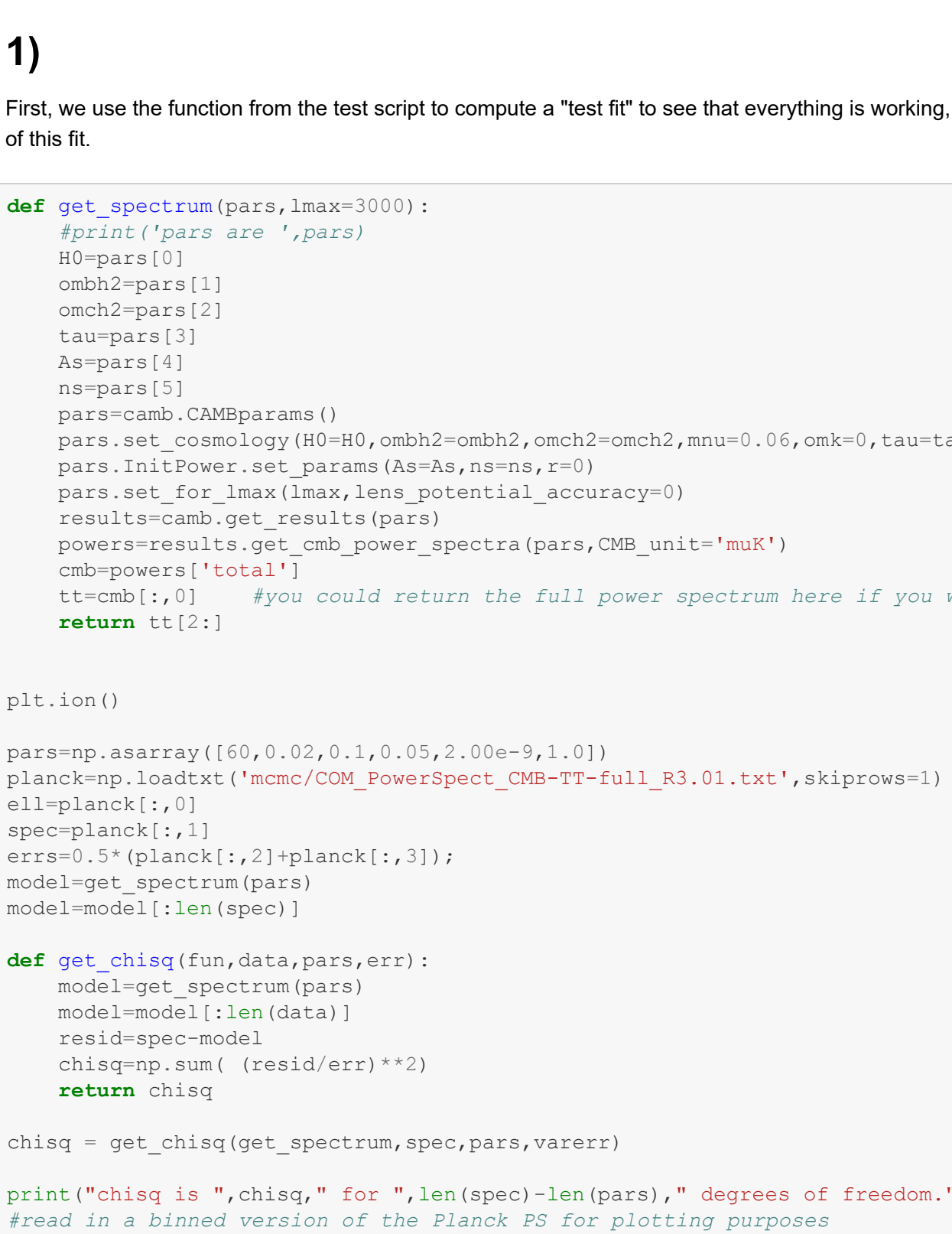
```
In [1]: import matplotlib.pyplot as plt
import numpy as np
import cmc
from cmc import model, initialpower
from tqdm.notebook import tqdm
import corner
from IPython.display import display, Math
cmc.__version__, os.path.dirname(cmc.__file__)

Out[1]: ('1.3.6', 'C:\Users\lmara\anaconda3\lib\site-packages\cmc')

In [2]: data = np.loadtxt('cmc/COM_PowerSpect_CMB-TT-Full_R3.01.txt')

In [3]: l = data[:,0]
var = data[:,1]
varerr = 1/2*(data[:,2]+data[:,3]) #error on datapoints is taken to be the average of the upper and low
er errors
N = np.diag(varerr**2) #N matrix
Ninv = np.linalg.inv(N)

In [4]: #taking a look at the data
fig, ax = plt.subplots()
ax.plot(l,var,'.')
ax.errorbar(l,var,varerr,color = 'k',alpha = 0.5)
ax.set_xlabel(r'Multipole $\ell$')
ax.set_ylabel('Variance')
fig.tight_layout()
```



1)

First, we use the function from the test script to compute a "test fit" to see that everything is working, and we can also compute the χ^2 value of this fit.

```
In [6]: def get_spectrum(pars,lmax=3000):
    #print('pars are ',pars)
    H0=pars[0]
    omh2=pars[1]
    omch2=pars[2]
    tau=pars[3]
    As=pars[4]
    ns=pars[5]
    pars=cmc.COMparams(l)
    pars.set_comology(H0=H0,omh2=omh2,omch2=omch2,mnu=0.06,omk=0,tau=tau)
    pars.InitPower.set_params(As=As,ns=ns,r=0)
    pars.set_for_lmax(lmax,lens_potential_accuracy=0)
    results=cmc.get_results(pars)
    powers=results.get_cmb_power_spectrum(pars,CMB_unit="muK")
    cmb=powers['total']
    cmcmb=0 #you could return the full power spectrum here if you wanted to do say EE
    return tt[1:]

plt.ion()
pars=np.asarray([69, 0.022, 0.12,0.06, 2.1e-9, 0.95])
planck=np.loadtxt('cmc/COM_PowerSpect_CMB-TT-binned_R3.01.txt',skiprows=1)
ell=planck[:,0]
spec=planck[:,1]
err=5*(planck[:,2]+planck[:,3])
model=get_spectrum(pars)
model=model[:len(spec)]

def get_chisq(fun,data,pars,err):
    model=get_spectrum(pars)
    model=model[:len(data)]
    resid=spec-model
    chisq=np.sum( (resid/err)**2)
    return chisq

chisq = get_chisq(get_spectrum,spec,pars,varerr)

print("chisq is \"%chisq,\" for \",len(spec)-len(pars),\" degrees of freedom.")
#read a truncated version of the Planck SS for plotting purposes
planck_binned=np.loadtxt('cmc/COM_PowerSpect_CMB-TT-binned_R3.01.txt',skiprows=1)
err_binned=0.5*(planck_binned[:,2]+planck_binned[:,3])
fig,ax = plt.subplots()
ax.plot(ell,spec)
ax.errorbar(planck_binned[:,0],planck_binned[:,1],err_binned,fmt='.')

chisq is 15267.937150261654 for 2501 degrees of freedom.
```



```
Out[6]: <ErrorbarContainer object of 3 artists>
```

We see that the value of χ^2 is around 15000 for 2501 degrees of freedom, which indicates that these parameters are not a good fit for the data we have. If the fit was good, χ^2 would be on the order of 2500. Now, let us compute the value of χ^2 for the parameters suggested in the assignment.

```
In [7]: pars = np.asarray([69, 0.022, 0.12,0.06, 2.1e-9, 0.95])
chisq = get_chisq(get_spectrum,spec,pars,varerr)
print("chisq is \"%chisq,\" for \",len(spec)-len(pars),\" degrees of freedom.")
chisq is 3272.2053559202204 for 2501 degrees of freedom.
```

This fit is slightly better, but still not such a good fit.

2)

We now perform a new fit, using Newton's method, using the numerical differentiator from last week's problem set.

```
In [8]: def ndiff_multi(fun,p,lmax=3000):
    fun0 = fun(p,lmax)
    et = 1e-16
    dps = et**(1/3)*np.abs(p) # computing the optimal dps
    #the following code adds the dp corresponding to each parameter and evaluates the function at the n
    ew
    #in parameter space, then it computes the derivative, and repeats it for all parameters in fun
    dps = np.diag(dps)
    grad = np.zeros((len(fun0),p.size))
    for i in tqdm(range(len(p)),leave = False):
        grad[:,i] = (fun(p+dps[i],lmax)-fun0)/dps[i][i]
    return fun0,grad

In [9]: def calc_spectrum(p):
    y,grad = ndiff_multi(get_spectrum,p)
    return y,grad

iter = 5
p0=np.asarray([69, 0.022, 0.12,0.06, 2.1e-9, 0.95])
p=p0.copy()
new_fit = np.zeros([iter+1,p.size+1])
new_fit[0][-1] = get_chisq(get_spectrum,spec,p0,varerr)
new_fit[0][-1] = p0

for i in tqdm(range(iter)):
    pnew,grad=calc_spectrum(p)
    resid,grad = pnew[:len(spec)],grad[:len(spec)]
    resid=spec-pnew
    r=resid.T
    lhs=grad.T@Ninv@grad
    rhs=grad.T@Ninv*r
    cov = np.linalg.inv(lhs)
    dp=cov@rhs
    for ii in range(p.size):
        p[ii]=p[ii]+dp[ii]
    chisq=np.sum(resid(varerr)**2)
    new_fit[ii][-1] = chisq
    new_fit[ii+1][-1] = p
np.savetxt('planck_fit_params.txt',new_fit)
```

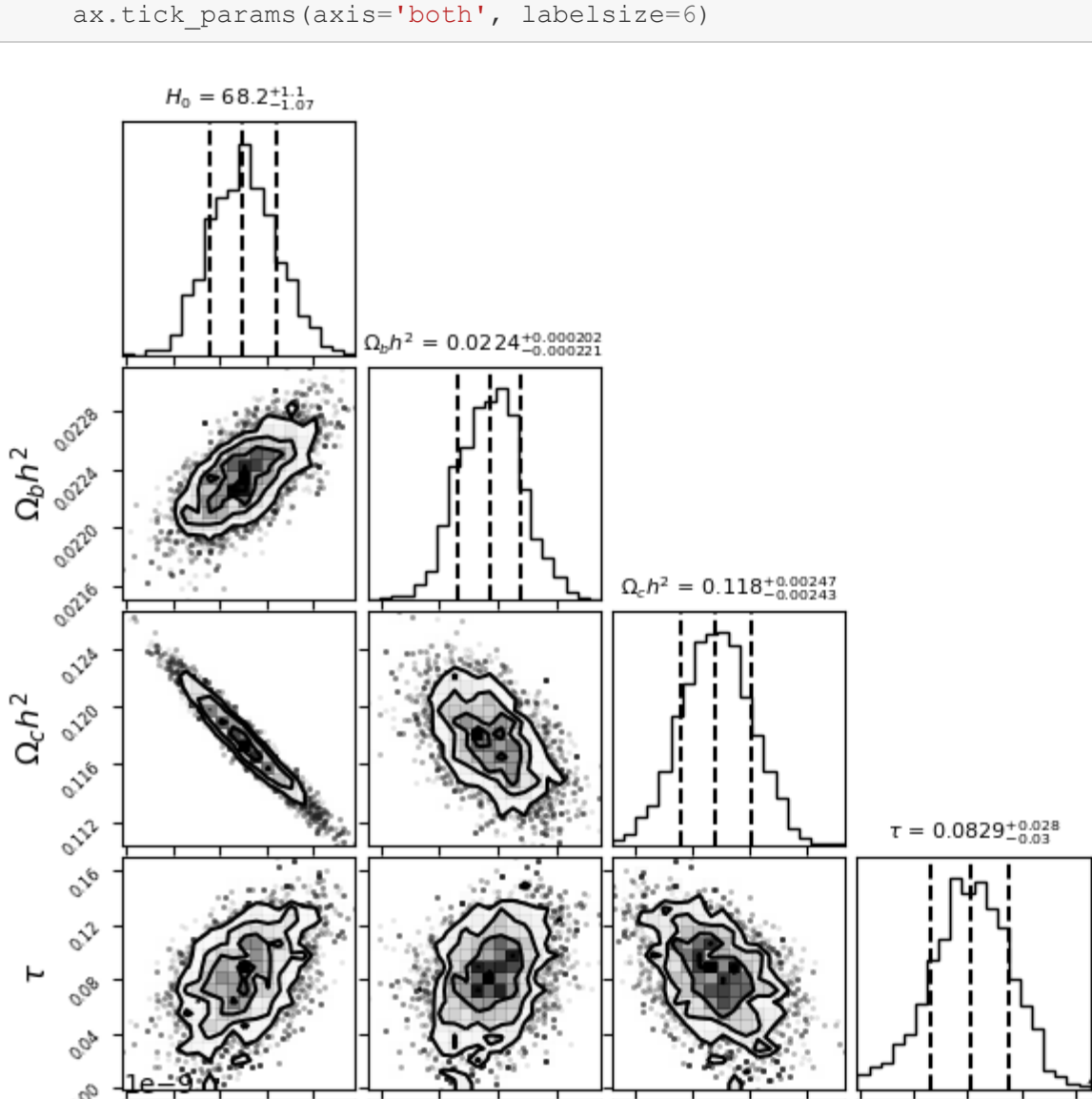
We can verify that Newton's method has converged by looking at the difference between the last 2 χ^2 values:

```
In [10]: np.abs(new_fit[-1][-1]-new_fit[-2][-1])

Out[10]: 0.00209910299500794
```

Because this value is $\ll 1$, we can be confident that Newton's method has converged. We can now look at our improved fit.

```
In [11]: fig,ax = plt.subplots()
ax.plot(ell,model,label = 'Fit at starting parameters')
ax.errorbar(planck_binned[:,0],planck_binned[:,1],err_binned,fmt='.',label = 'Data')
model2=get_spectrum(model)
model2=model2[:len(spec)]
ax.plot(ell,model2,label = 'Fit at Newton's method parameters')
ax.legend()
noise = np.mean(np.abs(model2-spec))
chisq = get_chisq(get_spectrum,spec,p,varerr)
print("chisq is \"%chisq,\" for \",len(spec)-len(pars),\" degrees of freedom.")
```



chisq is 2576.305219680515 for 2501 degrees of freedom.

```
In [12]: p_err = np.sqrt(np.diag(cov))
params = [r'%H_0%',r'%\Omega_{bh}^{2\sigma}%',r'%\Omega_{ch}^{2\sigma}%',r'%\tau%',r'%A_s%',r'%n_s%']
print("Best fit parameters using Newton's method :n")
for i in range(len(p)):
    display(Math(params[i]+'% = %' % (p[i],p_err[i])))

Best fit parameters using Newton's method :
```

$H_0 = 67.81986034221636 \pm 0.8093944887984065$
 $\Omega_b h^2 = 0.0229227267997955 \pm 0.0001629673725677291$
 $\Omega_c h^2 = 0.11858628843965942 \pm 0.002004267895025102$
 $\tau = 0.07939488797547513 \pm 0.030997412686674459$
 $A_s = 2.1970825928571528e-09 \pm 1.3248871781645257e-10$
 $n_s = 0.9712056558498744 \pm 0.005163496601096247$

3)

Now, we run an MCMC to estimate our parameters. As last week's problem set, for each iteration of the parameters, we generate a trial step from the covariance matrix of the parameters from Newton's method above. Then, we compute the value of χ^2 for these new parameters. If the value for the new parameters is lower, we accept the step. If not, we only accept it with a probability $e^{-\frac{1}{2}\Delta\chi^2}$.

```
In [13]: def get_step(pars,cov,scale):
    return np.random.multivariate_normal(np.zeros(len(pars)),cov)*scale

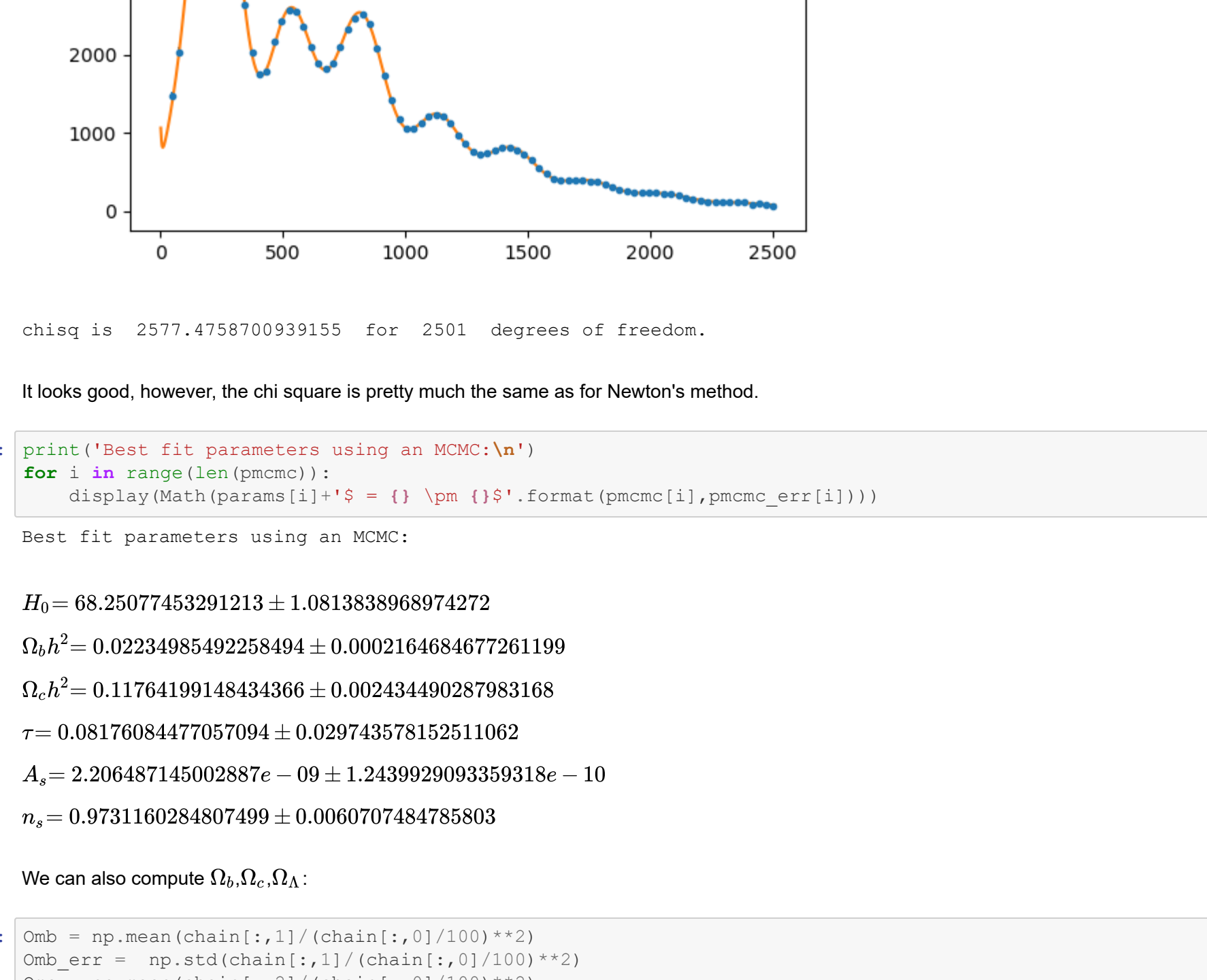
def run_chain(fun,pars,err,cov,data,scale,file_to_save,nstep=20000,T=1,include_tauprior = False,tau_pri
or = 0.05,tau_err = 0.0074):
    accepted = 0
    npar=len(pars)
    chain=np.zeros((nstep,npar+1))
    chain[0,:-1]=pars
    chi_cur=get_step(fun,data,pars,err)
    chain[0][-1]=chi_cur
    for i in tqdm(range(1,nstep)):
        pp=get_step(pars,cov,scale)
        new_chisq=get_chisq(fun,data,pp,err)
        if include_tauprior:
            new_chisq+=pp[3]-tau_prior)**2/tau_prior_err**2
        accept_prob=np.exp(-0.5*(new_chisq-chi_cur)/T)
        if np.random.rand(1)<accept_prob:
            accepted+=1
            pars=pp
            chi_cur=new_chisq
            chain[i,:-1]=pars
            chain[i][-1]=chi_cur
            path = file_to_save
            np.savetxt(path,chain)
            accrate = accepted/nstep
            chain = chain[:i,-1]
            chain = chain[:i,-1]
    return chain,chain,accrate

In [ ]: nstep = 15000
chain,chain,accrate = run_chain(get_spectrum,p,varerr,cov,spec,scale = 1,file_to_save = 'chains/planck_
chain_1.txt',file_to_save = 'chains/planck_chain_tauprior_1.txt',nstep = nstep)
```

Once our chain has run, we can load it up and look at it:

```
In [18]: chainload = np.loadtxt('chains/planck_chain_1.txt').format(15000)
chain = chainload[:,1:]

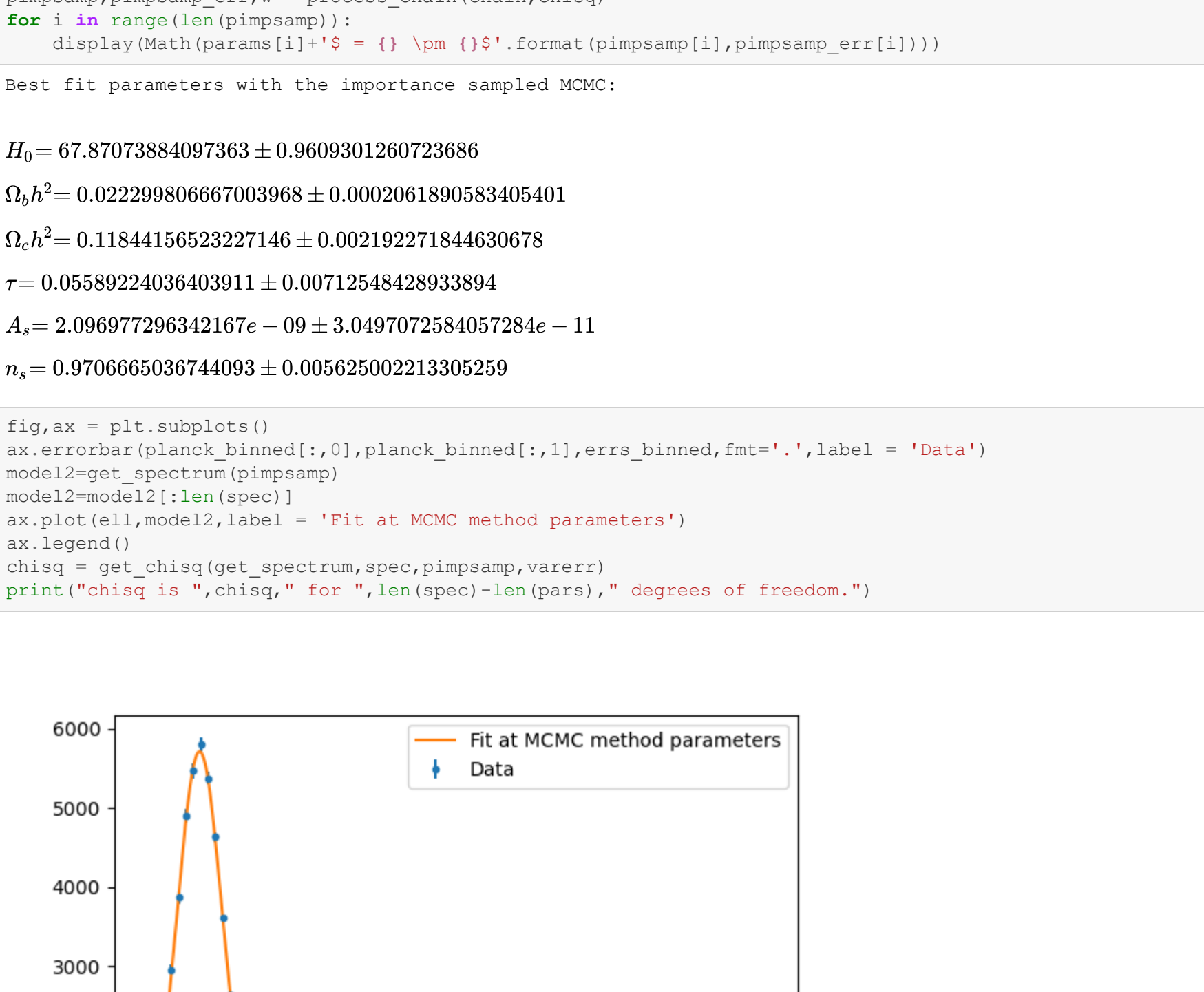
In [19]: fig = corner.corner(chain,labels = params,label_kwards=dict(fontsize=12),...,title_kwards = dict(font
size = 8))
fig.set_size_inches((8,5,8,5))
for ax in fig.get_axes():
    ax.tick_params(axis='both', file_to_save = 'chains/planck_chain_tauprior_1.txt',nstep = nstep)
```



We can look at the trace of each parameter to verify the convergence.

```
In [20]: pmcmc = np.mean(chain,axis = 0)
pmcmc_err = np.std(chain,axis = 0)

fig,ax = plt.subplots(np.shape(chain)[1],1,figsize = (8,2*np.shape(chain)[1]))
for i in range(len(chain[1:])):
    ax[i].plot(chain[:,i],linewidth = 1)
    ax[i].set_ylabel(params[i])
    ax[i].hlines(pmcmc[i],0,len(chain),linestyle = '--',alpha = 0.5,xorder = -1)
    ax[i].set_xlabel('Iteration')
fig.tight_layout()
```



We see that our chains have indeed converged. We can also look at the power spectrum of these chains. If they have converged, the spectrum should be flat at low k.

```
In [23]: fig, ax = plt.subplots()

for i in range(len(pmcmc)):
    p0 = np.abs(np.fft.rfft(chain[:,i]))
    ax.loglog(p0,p,figsize=(8,2*np.shape(chain)[1]))
    ax.legend()
ax.set_xlabel('k')
ax.set_ylabel('Power')
```



```
Out[23]: Text(0, 0.5, 'Power')
```

We see that the power spectra for each parameter looks like what we expect for converged chains. Let us now look at the actual fit.

```
In [24]: fig,ax = plt.subplots()
ax.errorbar(planck_binned[:,0],planck_binned[:,1],err_binned,fmt='.',label = 'Data')
model2=get_spectrum(pmcmc)
model2=model2[:len(spec)]
ax.plot(ell,model2,label = 'Fit for MCMC parameters')
ax.legend()
chisq = get_chisq(get_spectrum,spec,pmcmc,varerr)
print("chisq is \"%chisq,\" for \",len(spec)-len(pars),\" degrees of freedom.")

chisq is 2577.4758700939155 for 2501 degrees of freedom.
```

It looks good, however, the chi square is pretty much the same as Newton's method.

```
In [25]: print("Best fit parameters using an MCMC:\n")
for i in range(len(pmcmc)):
    display(Math(params[i]+'% = %' % (pmcmc[i],pmcmc_err[i])))

Best fit parameters using an MCMC:
```

$H_0 = 68.25077453291213 \pm 1.0813838968974272$
 $\Omega_b h^2 = 0.02234985492258494 \pm 0.000216484677261199$
 $\Omega_c h^2 = 0.11764199148434366 \pm 0.002434490287983168$
 $\tau = 0.08176084477057494 \pm 0.029743578152511062$
 $A_s = 2.206487145002887e-09 \pm 1.2439929093359318e-10$
 $n_s = 0.9731160284807499 \pm 0.006070748785803$

We can also compute $\Omega_b, \Omega_c, \Omega_A$:

```
In [26]: Omb = np.mean(chain[:,1]/(chain[:,0]/100)**2)
Omb_err = np.std(chain[:,1]/(chain[:,0]/100)**2)
Omc = np.mean(chain[:,2]/(chain[:,0]/100)**2)
Omc_err = np.std(chain[:,2]/(chain[:,0]/100)**2)
OmA = 1-(Omb+Omc)
OmA_err = Omb_err+Omc_err

densities = [r'%\Omega_b%',r'%\Omega_{ch}^{2\sigma}%',r'%\Omega_{bh}^{2\sigma}%',r'%\Lambda_{\rm dm}^{2\sigma}%',r'%\Lambda_{\rm dm}^{2\sigma}%',r'%\Lambda_{\rm dm}^{2\sigma}%']
dens = [Omb,Omc,OmA]
dens_err = [Omb_err,Omc_err,OmA_err]

for i in range(len(dens)):
    display(Math(dens[i]+'% = %' % (dens[i],dens_err[i])))

\Omega_b=0.048006246421904236 \pm 0.0012596286031152644
\Omega_c=0.2529004281250636 \pm 0.01313483317721375
\Omega_A=0.6990933254521322 \pm 0.01439446172083664
```

4)

We now add the constraint from the polarization data that the distribution of τ should have a mean of 0.054 and a standard deviation of 0.0074. First, we will improve the sample our previous chain with that constraint. This effectively comes back to assigning a weight on each iteration of parameters of the chain such that this weight is proportional to how close the parameter τ from that iteration was to the prior. Quantitatively, each weight is $e^{-\frac{1}{2}(\tau-\tau_0)^2/\sigma^2}$. This gives us a new set of parameters that agree with the prior knowledge on τ .

```
In [27]: def process_chain(chain,chisq,T=1.0,tau_prior = 0.054,tau_err = 0.0074):
    dtau = chain[:,3]-tau_prior
    w=np.exp(-0.5*(tau_prior**2/tau_err**2))
    npar=chain.shape[1]
    tot=np.zeros(npar)
    totsq=np.zeros(npar)
    for i in range(npar):
        tot[i]=np.sum(wt*chain[:,i])
        totsq[i]=np.sum(wt*chain[:,i]**2)
    #divide by sum of weights
    mean=tot/np.sum(wt)
    meansq=totsq/np.sum(wt)

    #variance is <x^2>-<x>^2
    var=meansq-mean**2
    return mean,np.sqrt(var),wt

In [28]: chisq = chainload[-1,-1]
print("Best fit parameters with the importance sampled MCMC:\n")
pimpsamp,pimpsamp_err,w = process_chain(chain,chisq)
for i in range(len(pimpsamp)):
    display(Math(params[i]+'% = %' % (pimpsamp[i],pimpsamp_err[i])))

Best fit parameters with the importance sampled MCMC:
```

$H_0 = 67.87073884057363 \pm 0.9609301260723686$
 $\Omega_b h^2 = 0.02229806607003968 \pm 0.000206189058273405401$
 $\Omega_c h^2 = 0.11844156623227146 \pm 0.00219227184463078$
 $\tau = 0.05589224036403911 \pm 0.0071254828933894$
 $A_s = 2.09697296324167e-09 \pm 3.0497072584055284e-11$
 $n_s = 0.9706665036744093 \pm 0.005625002213305259$

```
In [29]: fig,ax = plt.subplots()
ax.errorbar(planck_binned[:,0],planck_binned[:,1],err_binned,fmt='.',label = 'Data')
model2=get_spectrum(pimpsamp)
model2=model2[:len(spec)]
ax.plot(ell,model2,label = 'Fit at MCMC method parameters')
ax.legend()
chisq = get_chisq(get_spectrum,spec,pimpsamp,varerr)
print("chisq is \"%chisq,\" for \",len(spec)-len(pars),\" degrees of freedom.")

chisq is 2577.0796104116343 for 2501 degrees of freedom.
```

Again, the fit looks sensible, but now the other parameters have "adjusted" such that χ^2 remains pretty much unchanged, but our parameter τ now agrees with its constraints from the polarization data. We can run a new chain using this constraint to compare the resulting parameters to those of the importance sampled chain. We will do so by slightly modifying our likelihood function, where as before, it was defined as $e^{-\frac{1}{2}\chi^2}$. It is now $e^{-\frac{1}{2}\chi^2} \cdot e^{-\frac{1}{2}(\tau-\tau_0)^2/\sigma^2}$. However, we will now compute our covariance matrix from the weighted chain such that we obtain a better fit. We will also start our guess of τ at the value of the prior. As we did from the previous chain, we look at the traces of the parameters to verify convergence, we look at the corner plots because they're cool, and we look at the value of our parameters.

```
In [30]: pmcmcov = np.cov(chain.T,weights=w)

p0_tau=pmcmc.cov.copy()
p0_tau[3] = 0.054

chain_tau,chisq_tau,accrate_tau = run_chain(get_spectrum,p0_tau,varerr,pmcmcov,spec,scale = 1,
include_tauprior = True)

In [31]: chainload = np.loadtxt('chains/planck_chain_tauprior_1.txt').format(20000)

In [32]: chain = chainload[:,1:]

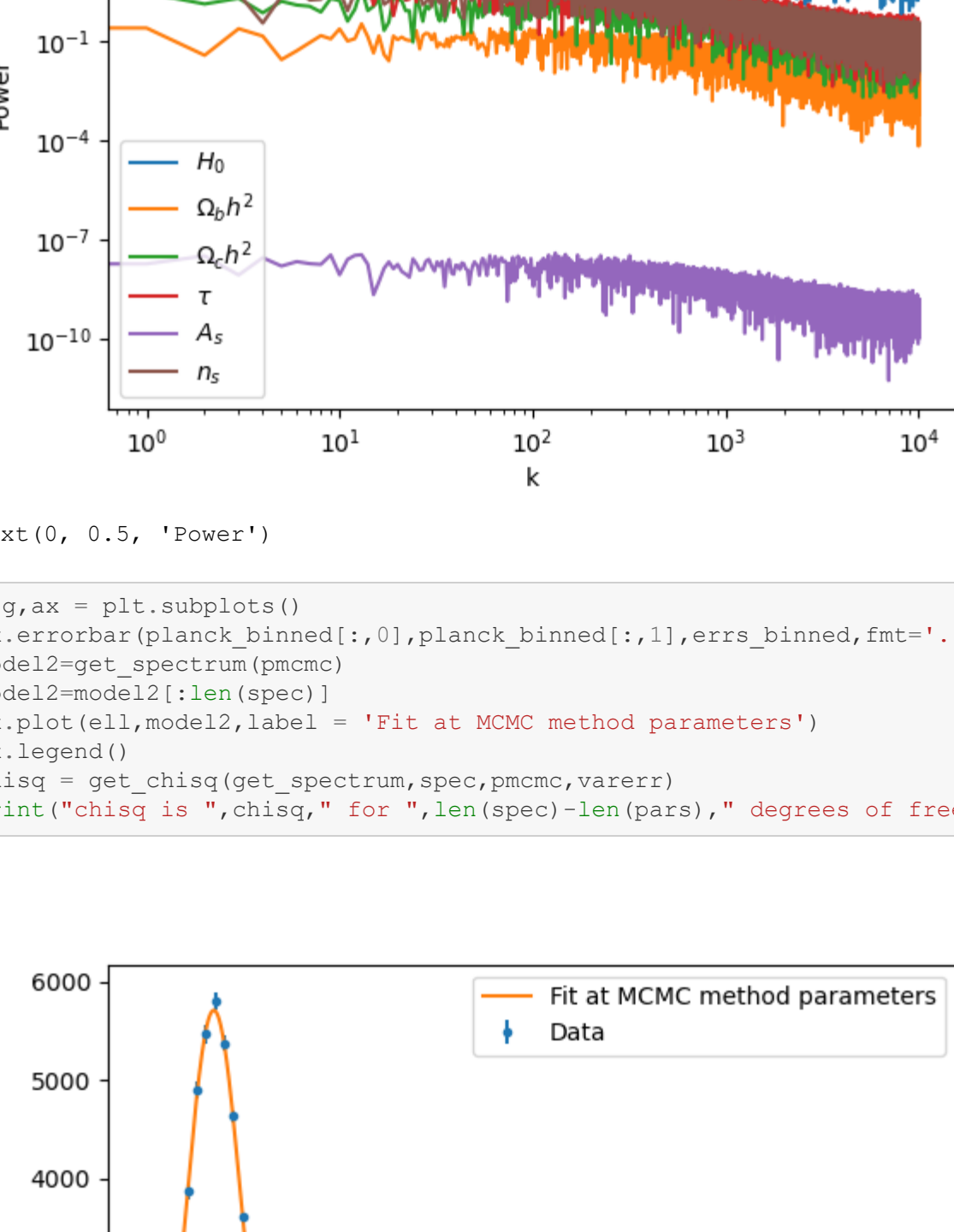
In [33]: pmcmc = np.mean(chain,axis = 0)
pmcmc_err = np.std(chain,axis = 0)

fig,ax = plt.subplots(np.shape(chain)[1],1,figsize = (8,2*np.shape(chain)[1]))
for i in range(np.shape(chain)[1]):
    ax[i].plot(chain[:,i],linewidth = 1)
    ax[i].set_ylabel(params[i])
    ax[i].hlines(pmcmc[i],0,len(chain),linestyle = '--',alpha = 0.5,xorder = -1)
    ax[i].set_xlabel('Iteration')
fig.tight_layout()
```



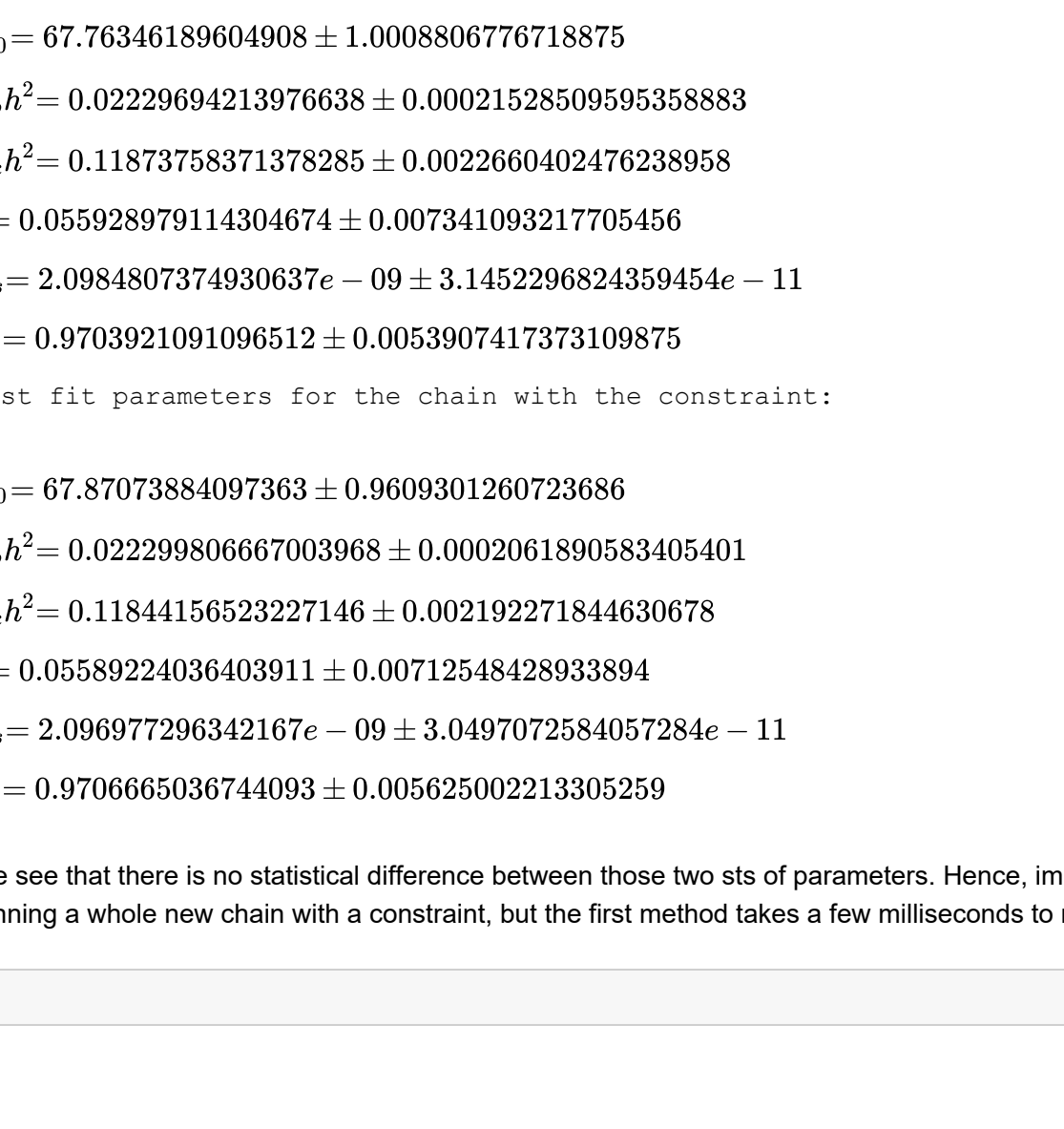
```
[34]: fig, ax = plt.subplots()

for i in range(len(pmcml)):
    pad = np.abs(np.fft.rfft(chain[:,i]))
    ax.loglog(pad,label=params[i])
ax.legend()
ax.set_xlabel('k')
ax.set_ylabel('Power')
```



Out[34]: Text(0, 0.5, 'Power')

```
In [35]: fig,ax = plt.subplots()
ax.errorbar(planck_binned[:,0],planck_binned[:,1],errs_binned,fmt='.',label = 'Data')
model2=get_spectrum(pmcml)
model2=model2[:len(spec)]
ax.plot(e11,model2,label = 'Fit at MCMC method parameters')
ax.legend()
chisq = get_chisq(get_spectrum,spec,pmcml,varerr)
print("chisq is ",chisq," for ",len(spec)-len(pars)," degrees of freedom.")
```



chisq is 2577.043102636848 for 2501 degrees of freedom.

```
In [36]: print('Best fit parameters for the chain with the constraint:\n')
for i in range(len(pmcml)):
    display(Math(params[i]+'r'+'$= {} \pm {}'.format(pmcml[i],pmcml_err[i])))

print('\nBest fit parameters for the chain with the constraint:\n')
for i in range(len(pmcml)):
    display(Math(params[i]+'r'+'$= {} \pm {}'.format(pimpcamp[i],pimpcamp_err[i])))

print("chisq is ",chisq," for ",len(spec)-len(pars)," degrees of freedom.")
```

Best fit parameters for the chain with the constraint:

$$H_0 = 67.76346189604908 \pm 1.0008806776718875$$

$$\Omega_b h^2 = 0.02229694213976638 \pm 0.00021528509595358863$$

$$\Omega_c h^2 = 0.11873758371378285 \pm 0.0022660402476238958$$

$$\tau = 0.055928979114304674 \pm 0.007341093217705456$$

$$A_s = 2.0984807374930637e-09 \pm 3.1452296824359454e-11$$

$$n_s = 0.9703921091096512 \pm 0.0053907417373109875$$

Best fit parameters for the chain with the constraint:

$$H_0 = 67.87073884097363 \pm 0.9609301260723686$$

$$\Omega_b h^2 = 0.022298806667003968 \pm 0.0002061890583405401$$

$$\Omega_c h^2 = 0.11844156523227146 \pm 0.002192271844630678$$

$$\tau = 0.05589224036403911 \pm 0.00712548428933894$$

$$A_s = 2.096977296342167e-09 \pm 3.0497072584057284e-11$$

$$n_s = 0.9706665036744093 \pm 0.005625002213305259$$

We see that there is no statistical difference between those two sts of parameters. Hence, importance sampling has the same effect as running a whole new chain with a constraint, but the first method takes a few milliseconds to run, and the other takes a couple of hours.

```
In [ ]:
```