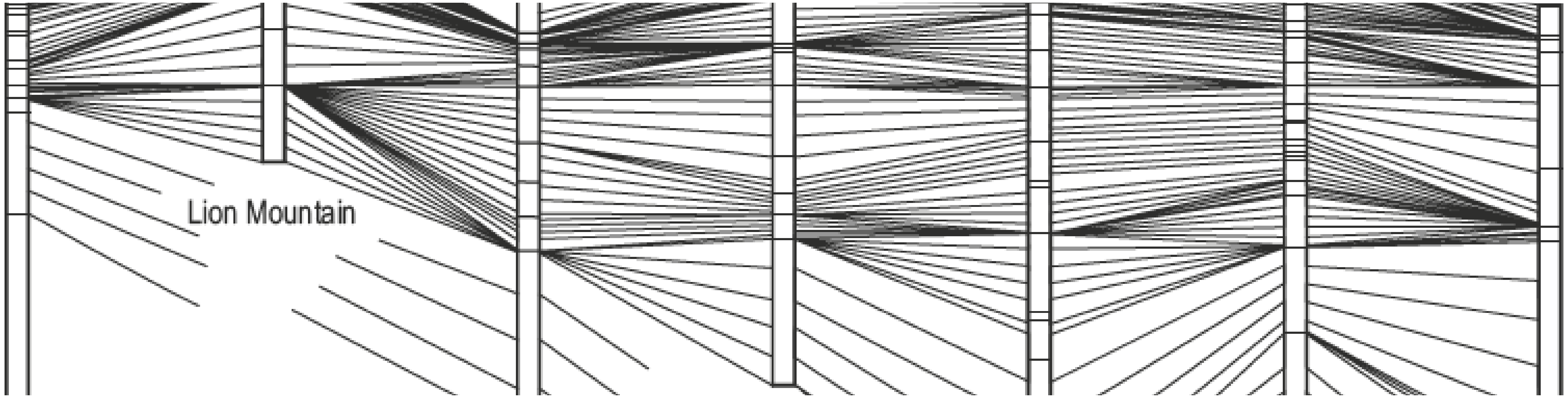
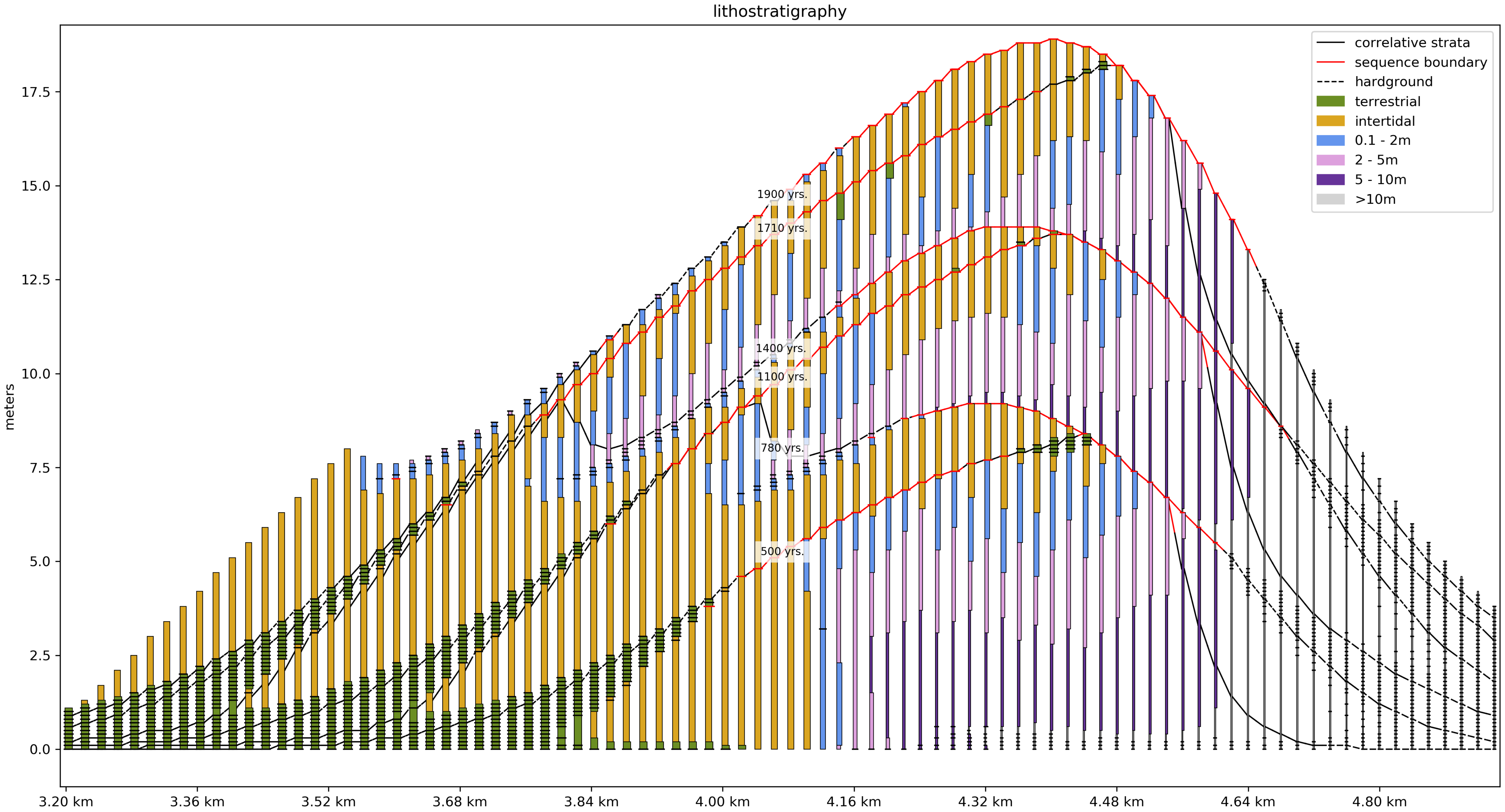


Lecture 14: Introduction to Age Models

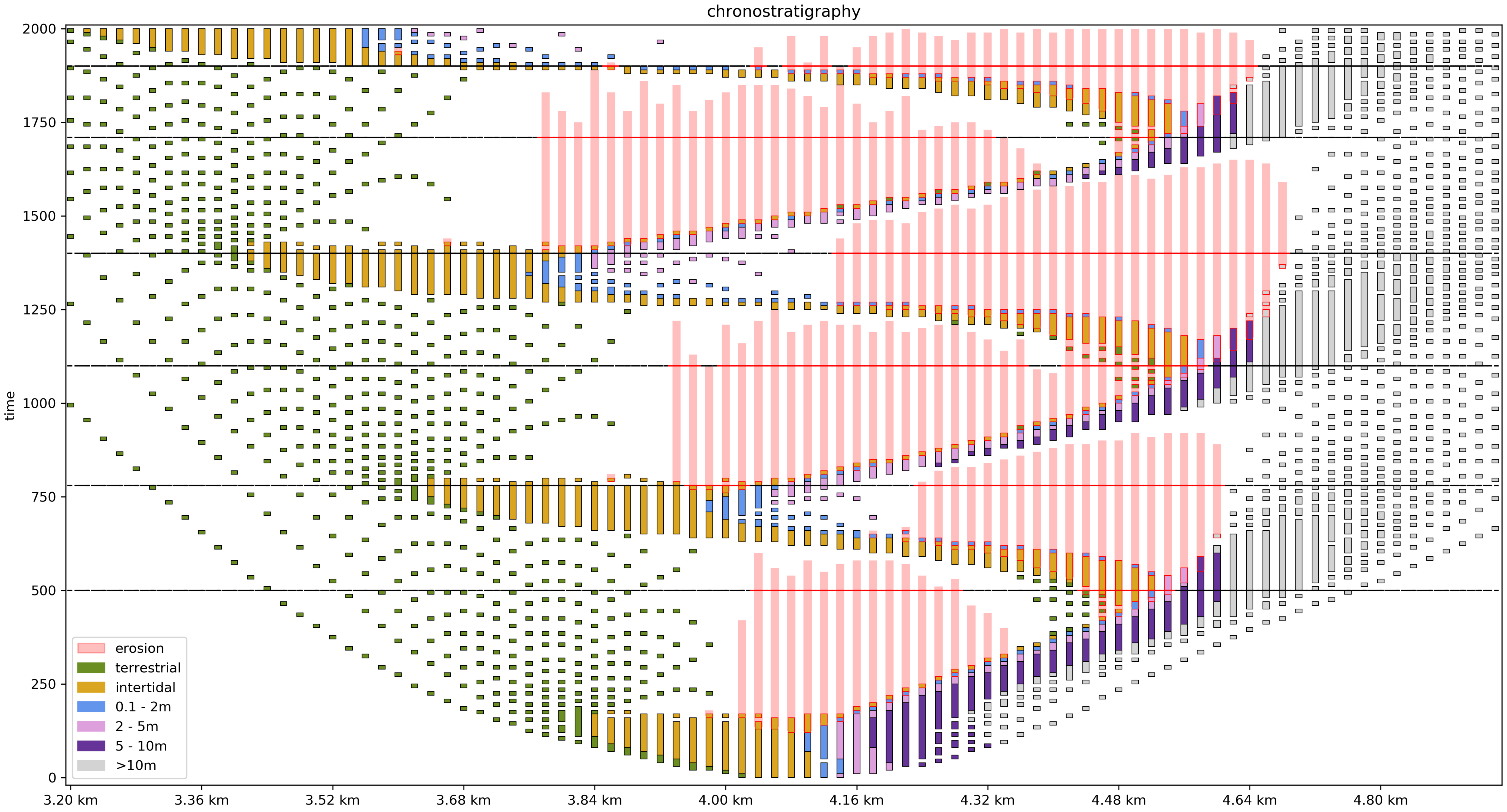
1. The importance of knowing time
2. Building an age model
    - Markov chain Monte Carlo approaches
    - constant sedimentation rates
    - varying sedimentation rates

We acknowledge and respect the lək̓ʷəŋən peoples on whose traditional territory the university stands and the Songhees, Esquimalt and W̱SÁNEĆ peoples whose historical relationships with the land continue to this day.

Importance of knowing time



Importance of knowing time

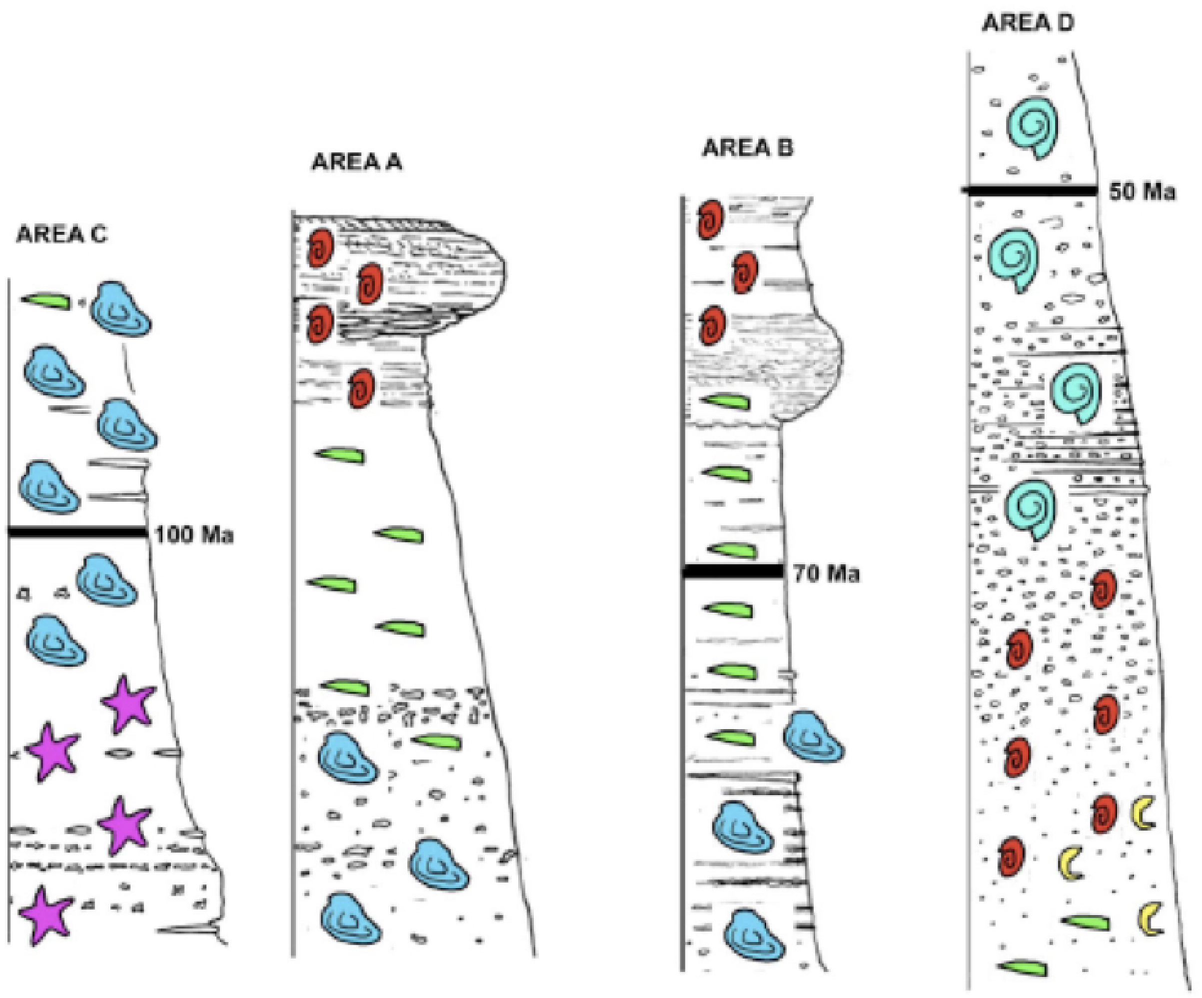


Age models are important: how do we get them?

1. Cyclostratigraphy
2. Biostratigraphy
3. Absolute ages
    - U-Pb (volcanics), Ar-Ar (volcanics), Re-Os (sediments)
4. Signal matching
    - magnetostratigraphy
    - chemostratigraphy

Biostratigraphy

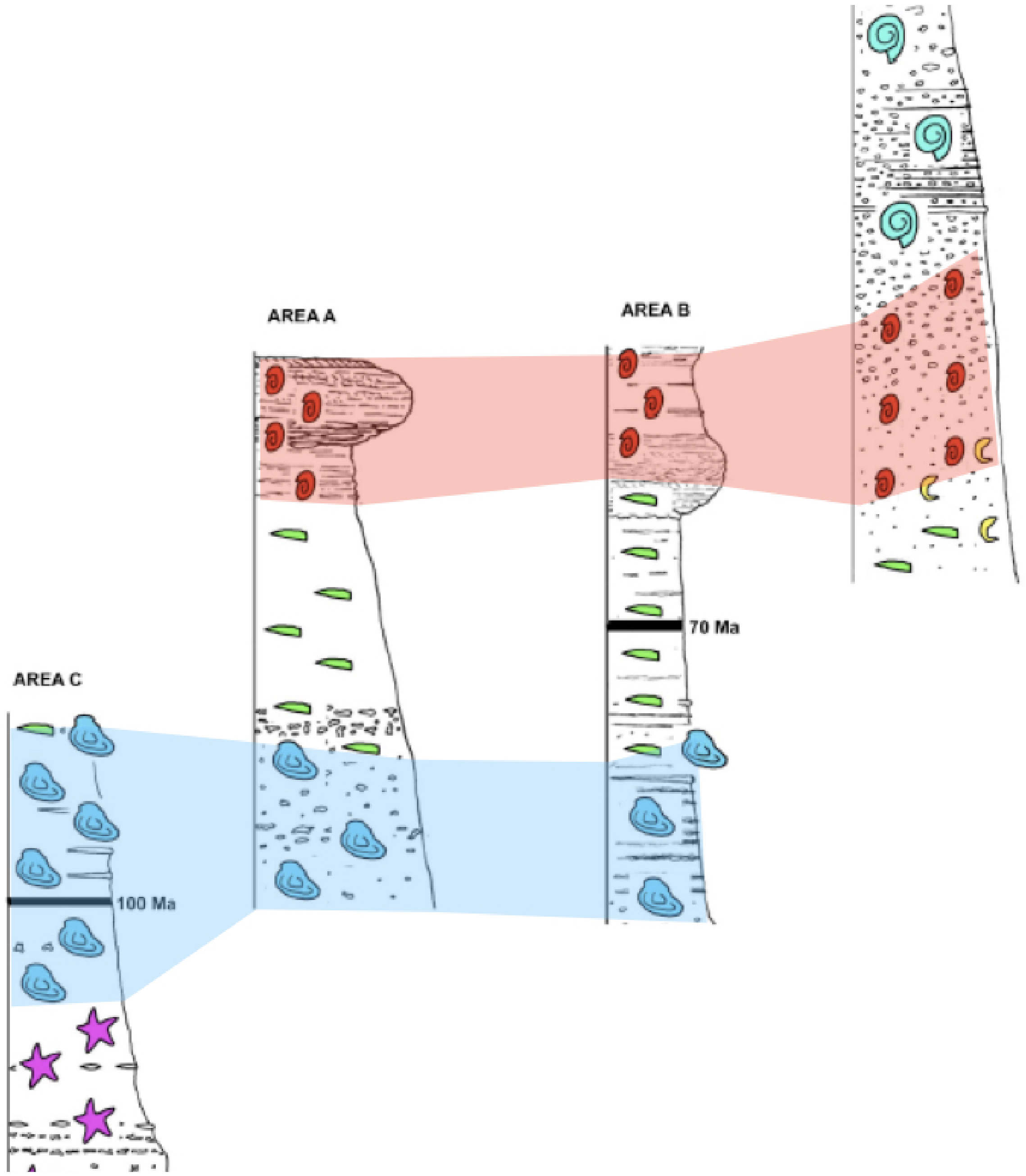
- based on the unique, sequential, nonrepeating appearance of fossils through time



http://www.labspaces.net/pictures/blog/4d497dd38d7031296661971_blog.jpg

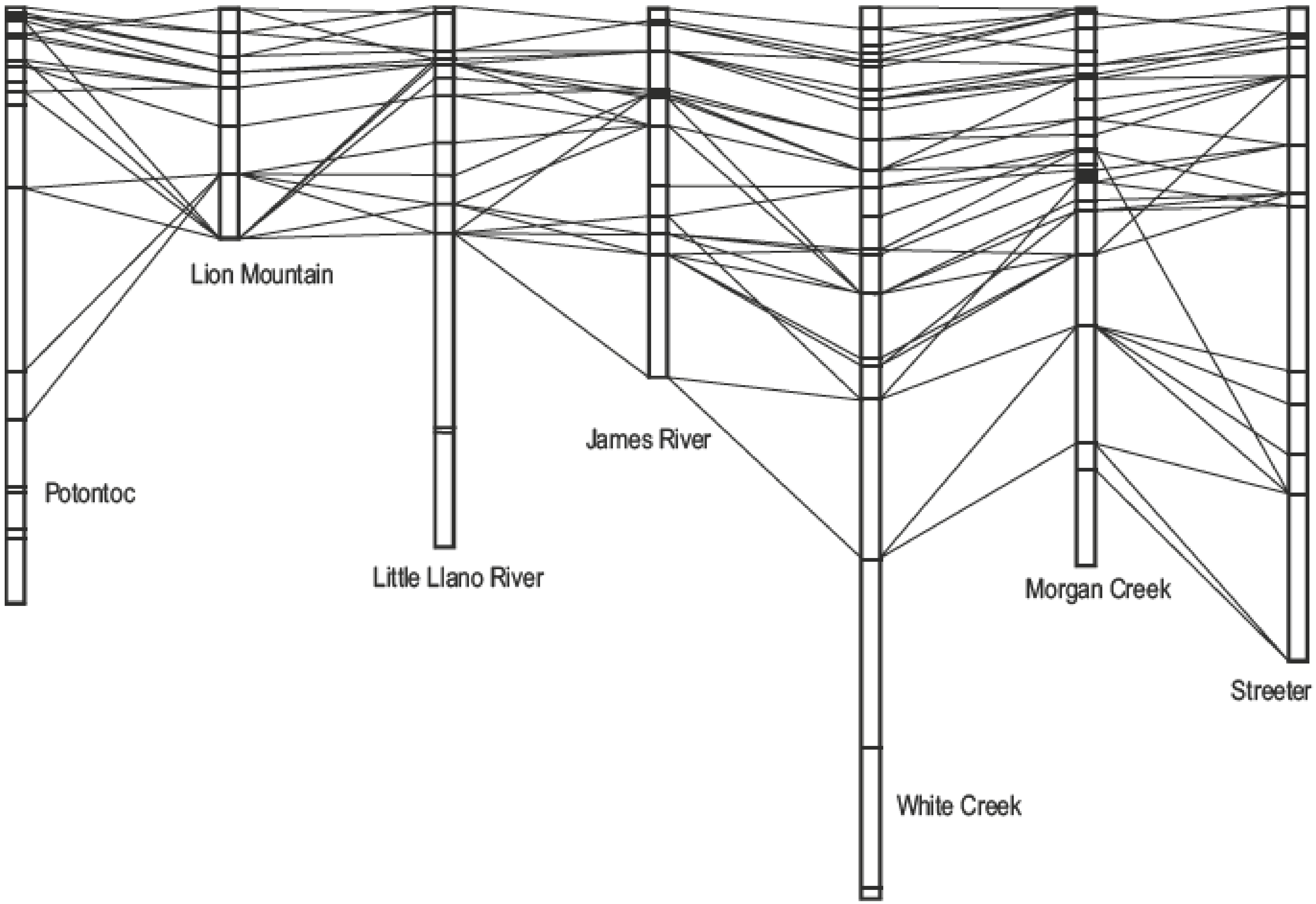
Biostratigraphy

- based on the unique, sequential, nonrepeating appearance of fossils through time



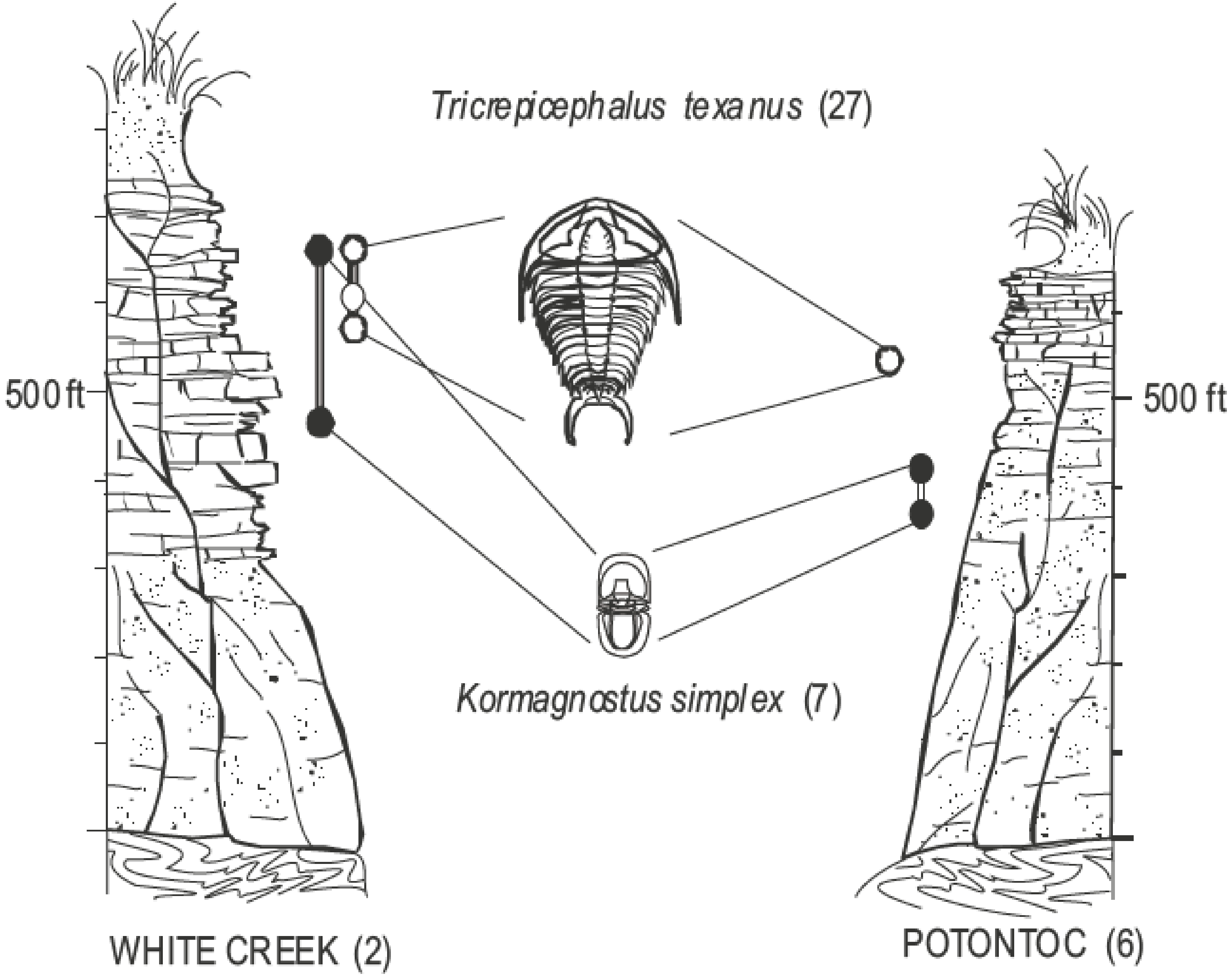
Biostratigraphy

- what is wrong with this picture?



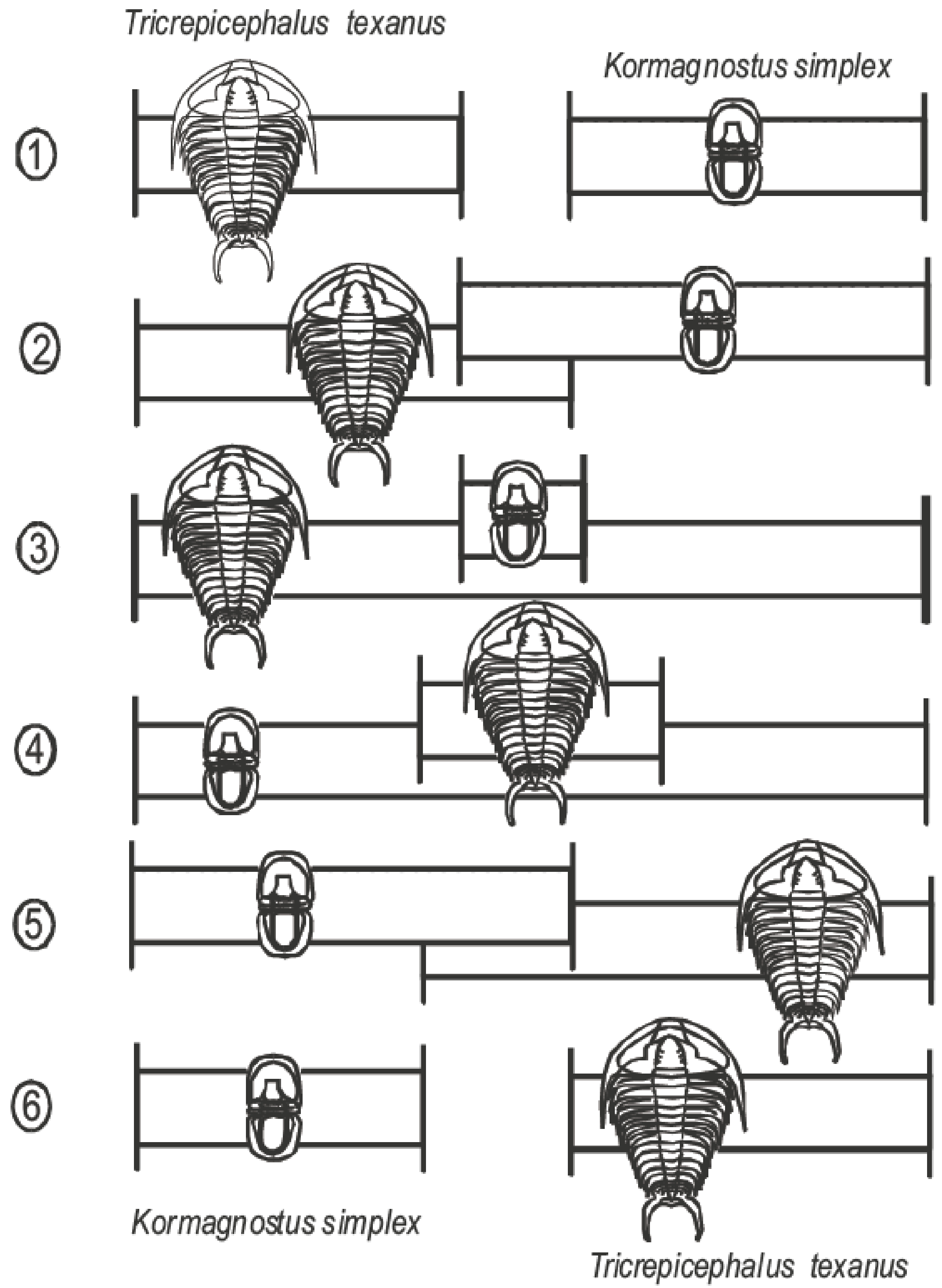
Contradictory ranges

- what could be causing this?



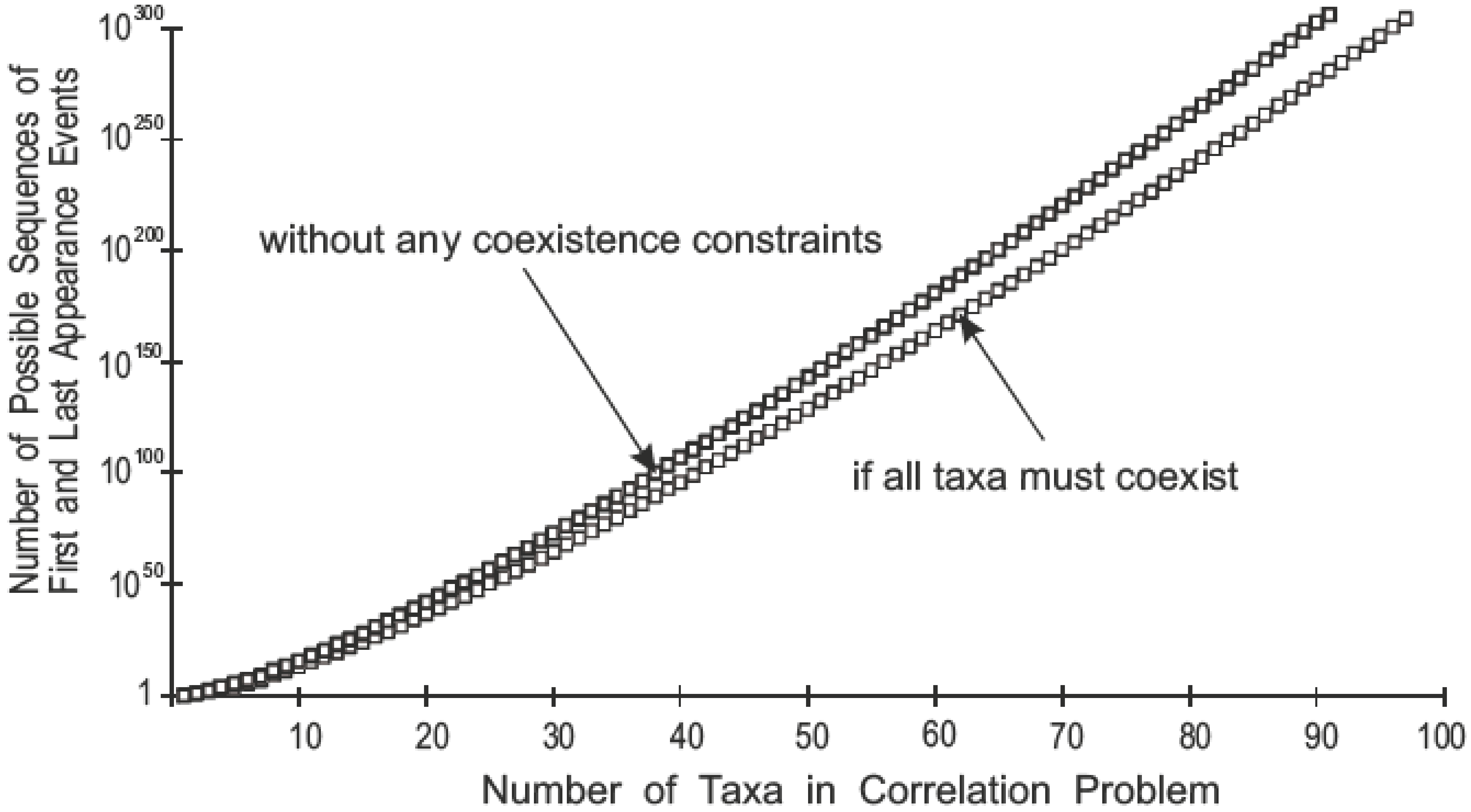
Resolving contradictory ranges

- ranges of original data need modifcation



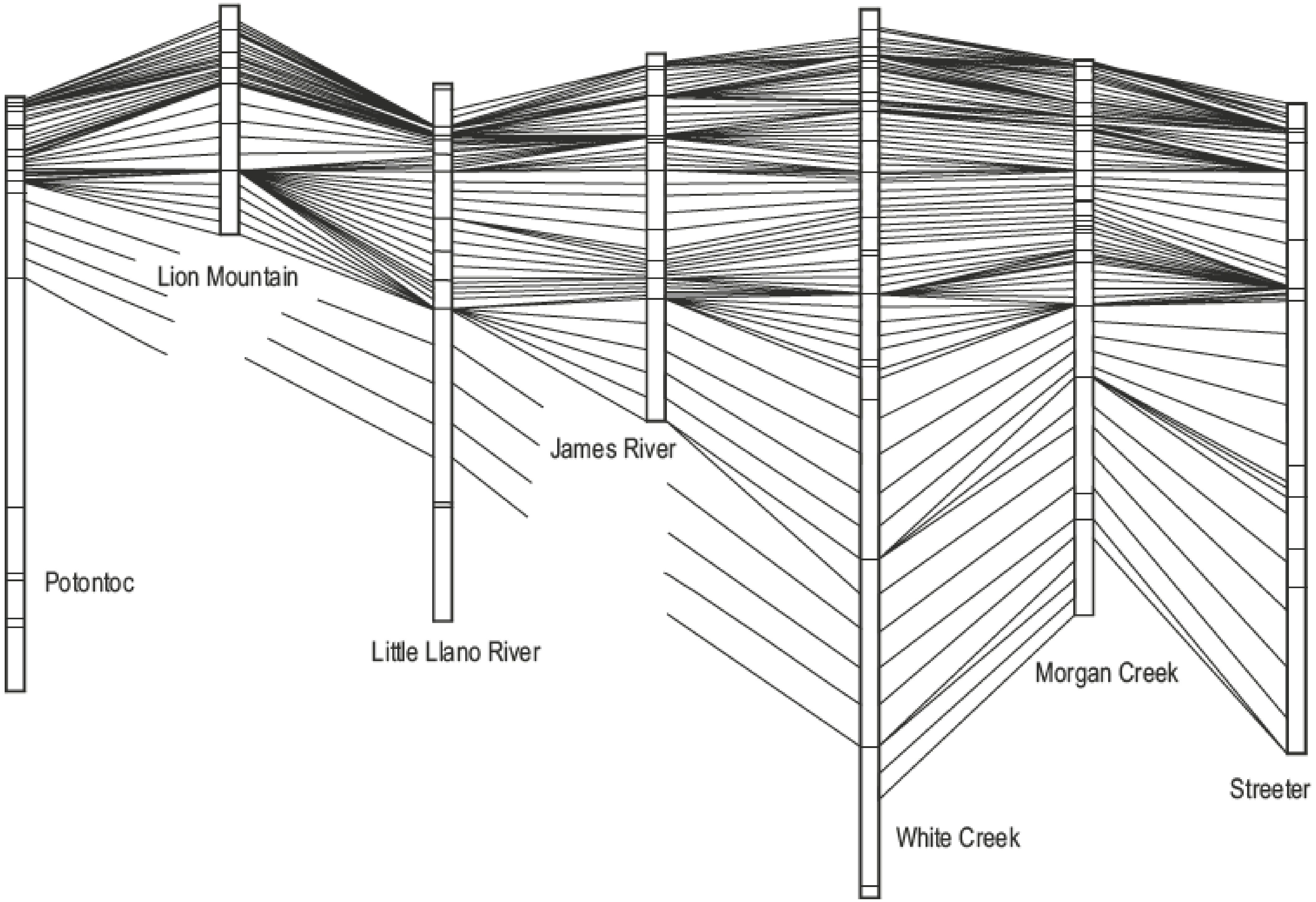
Number of possible sequences

- requires constrained optimization (CONOP9; Sadler and Cooper, 2008)



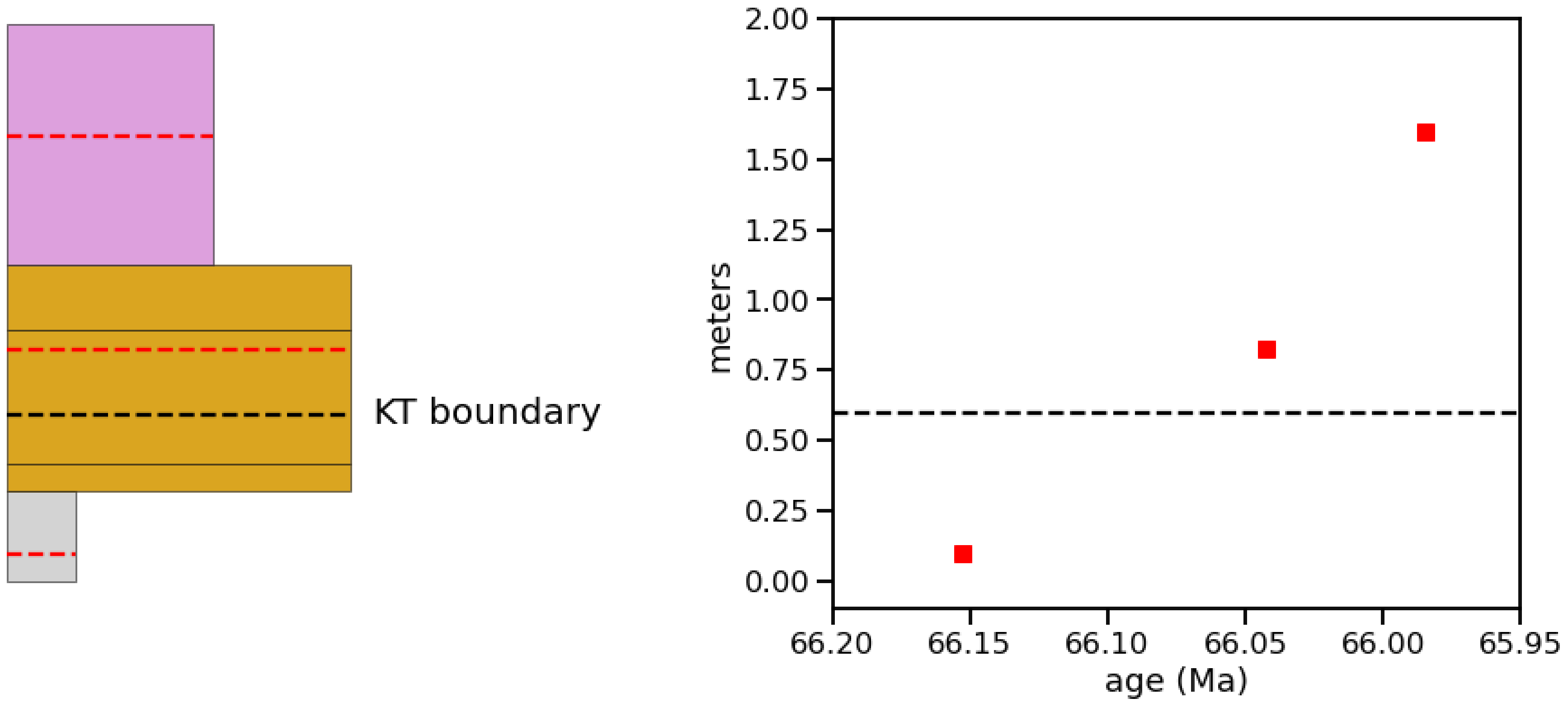
Best-fit solution

- what are some features of this that look familiar to our model outputs?

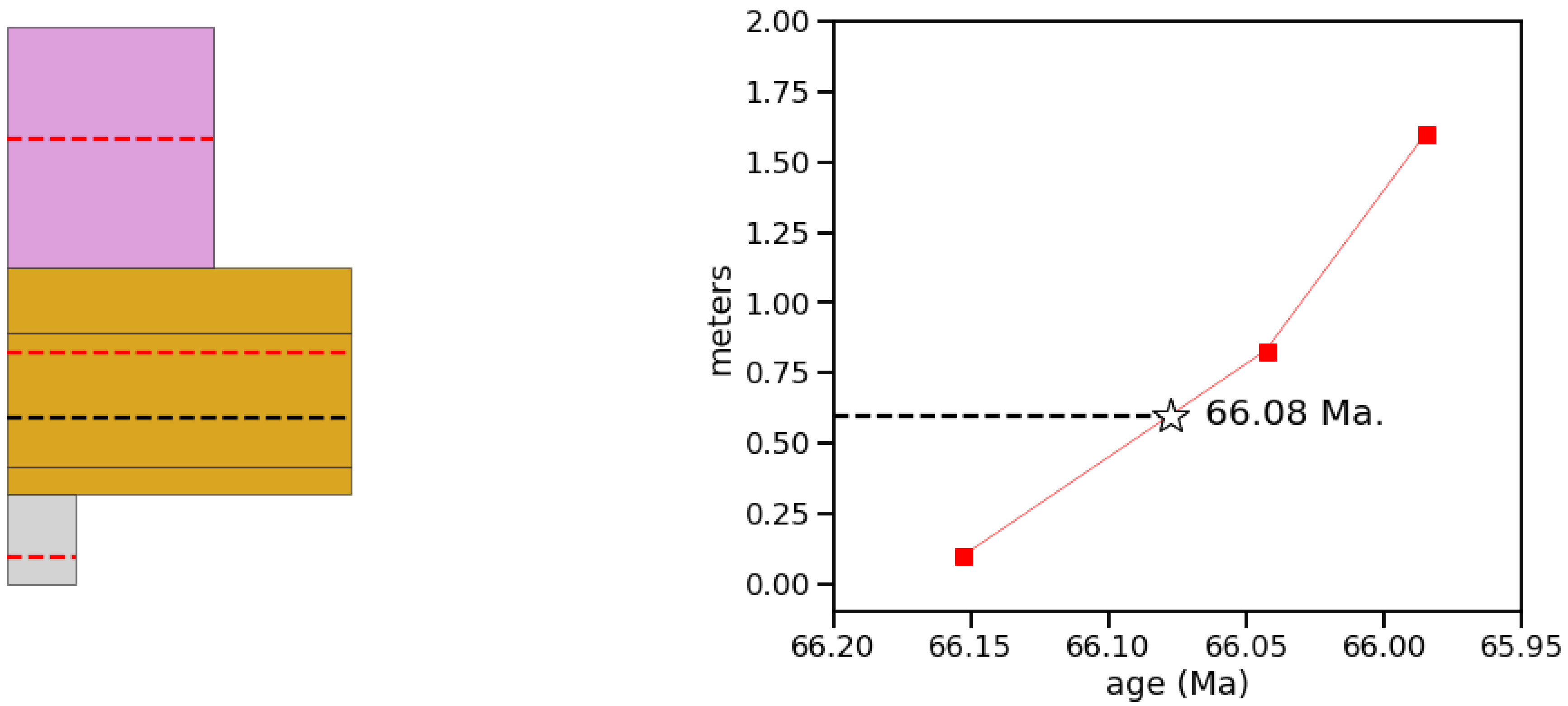


Building an age model

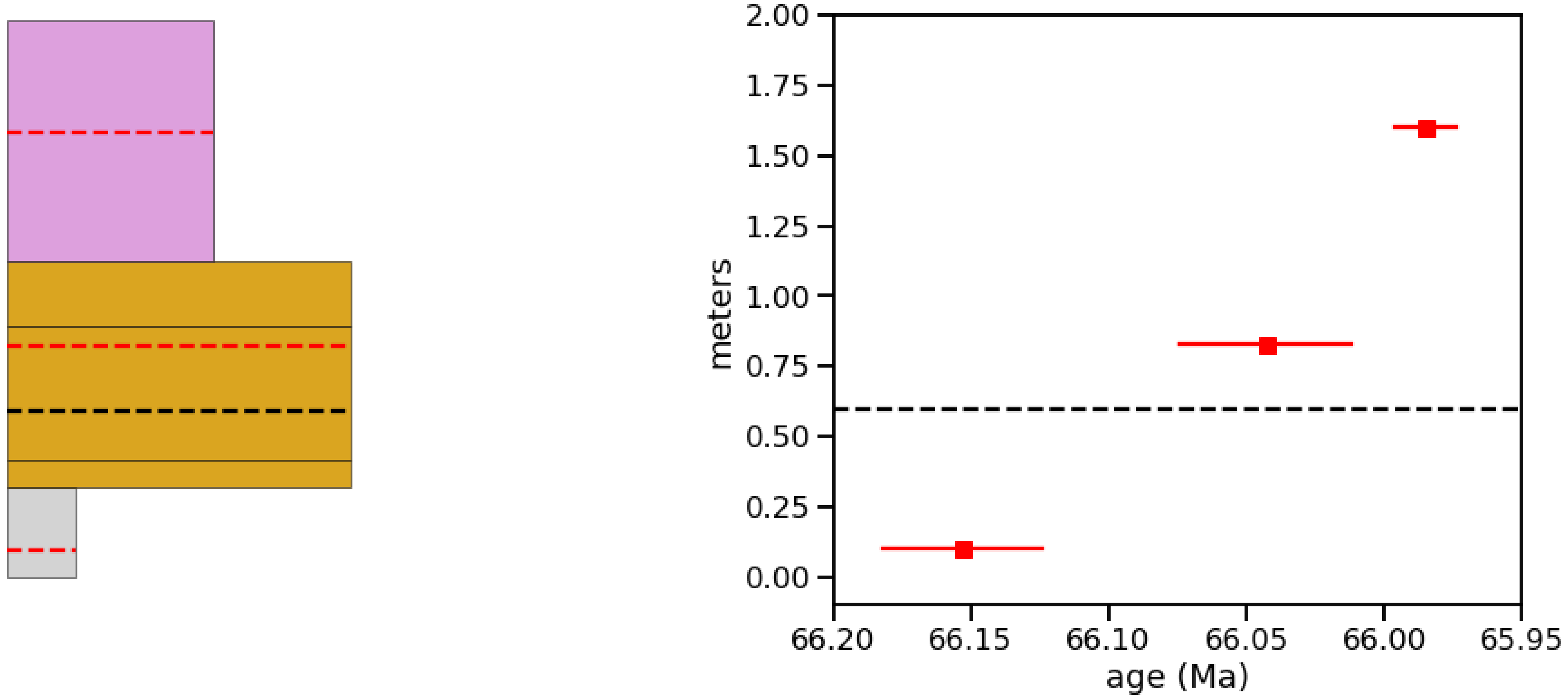
Building an age model



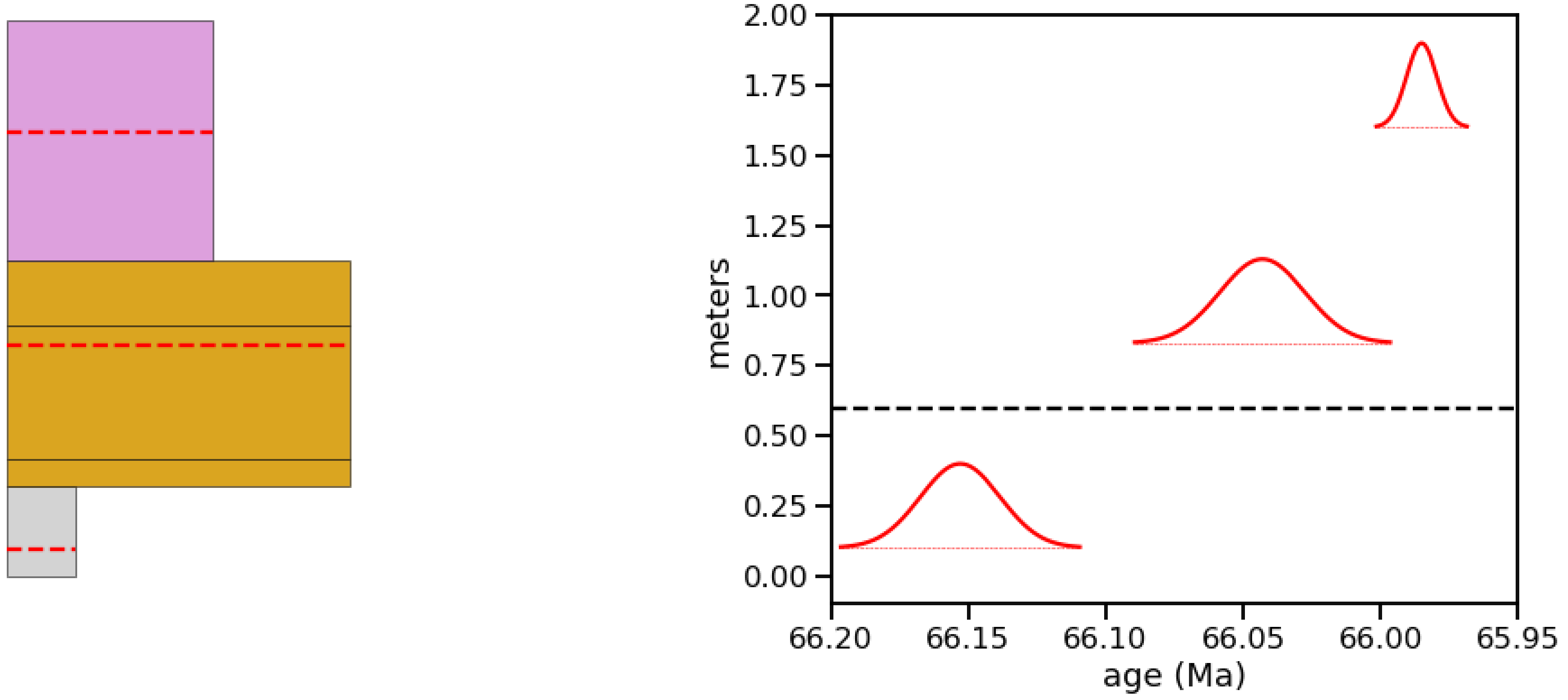
Building an age model



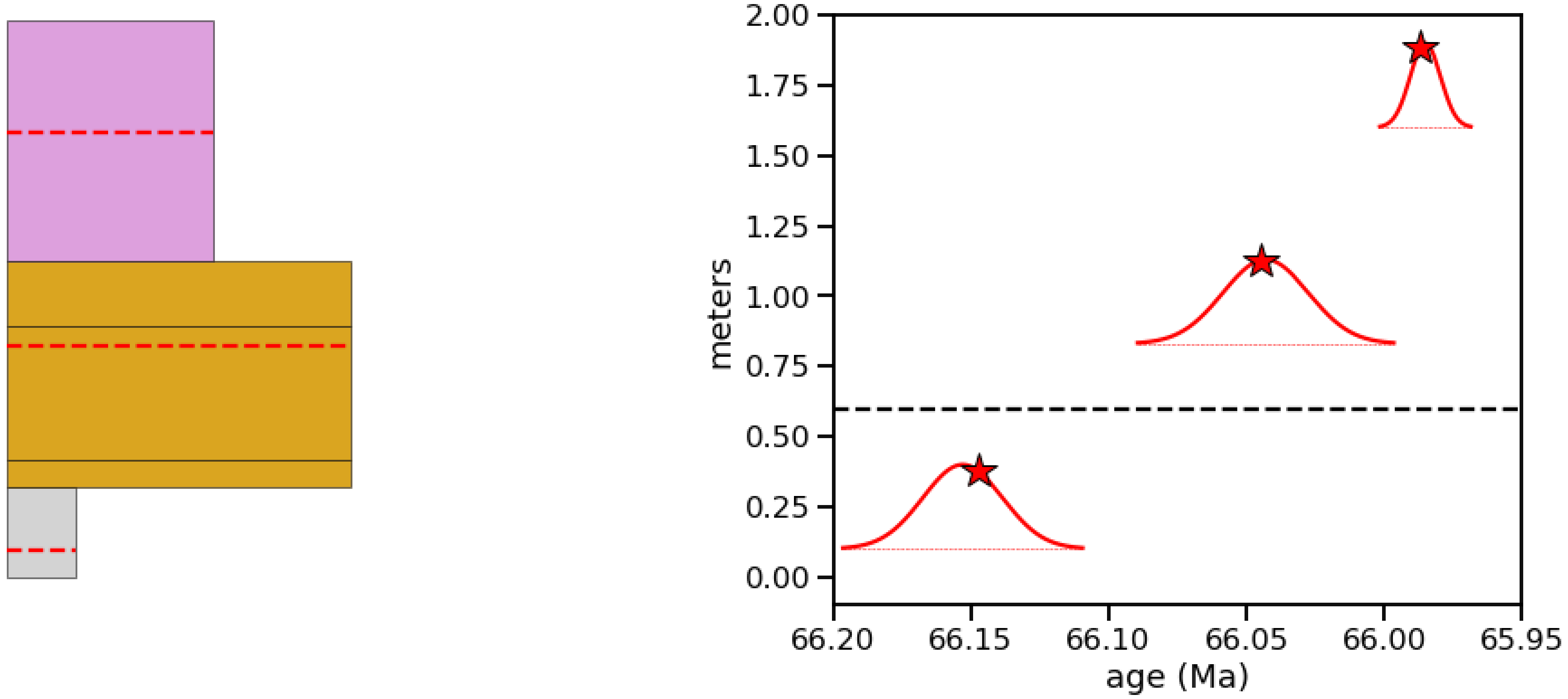
Building an age model



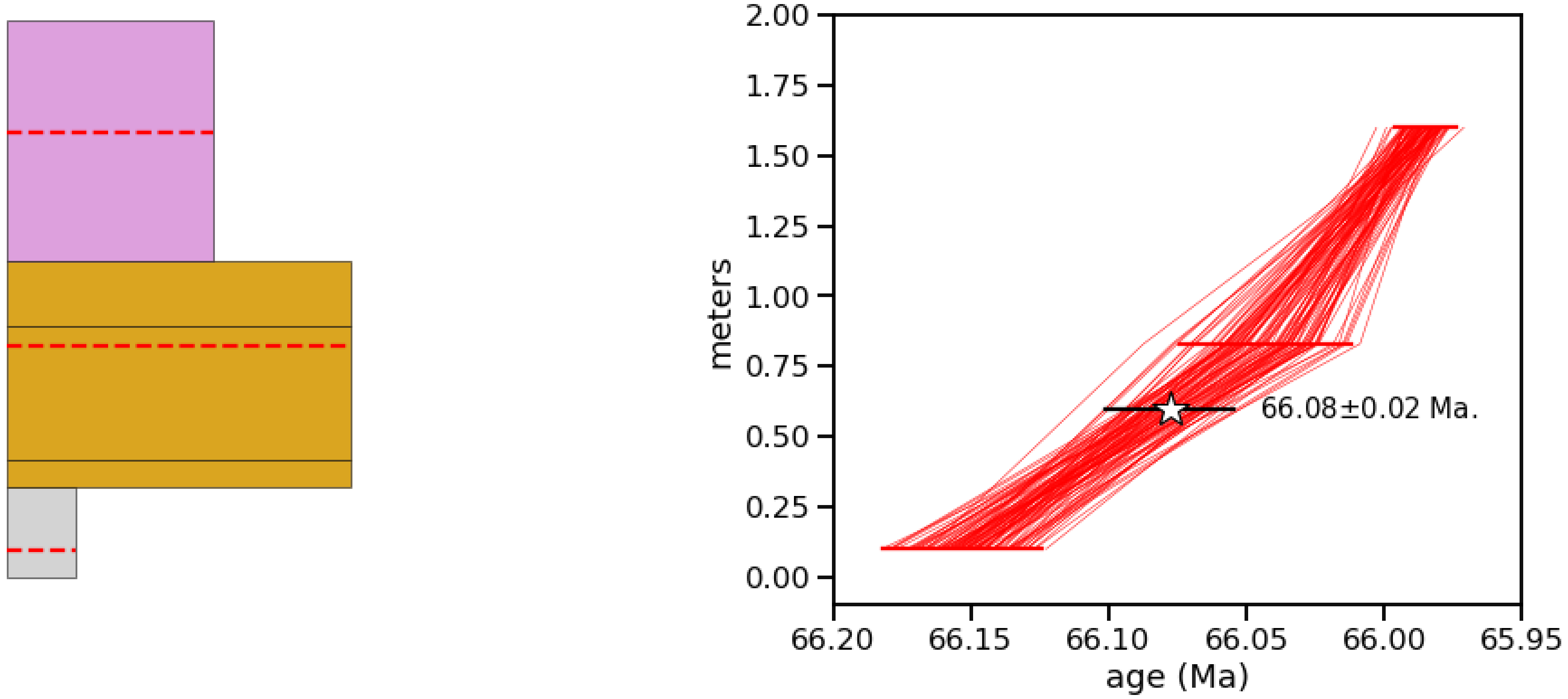
Building an age model



Building an age model

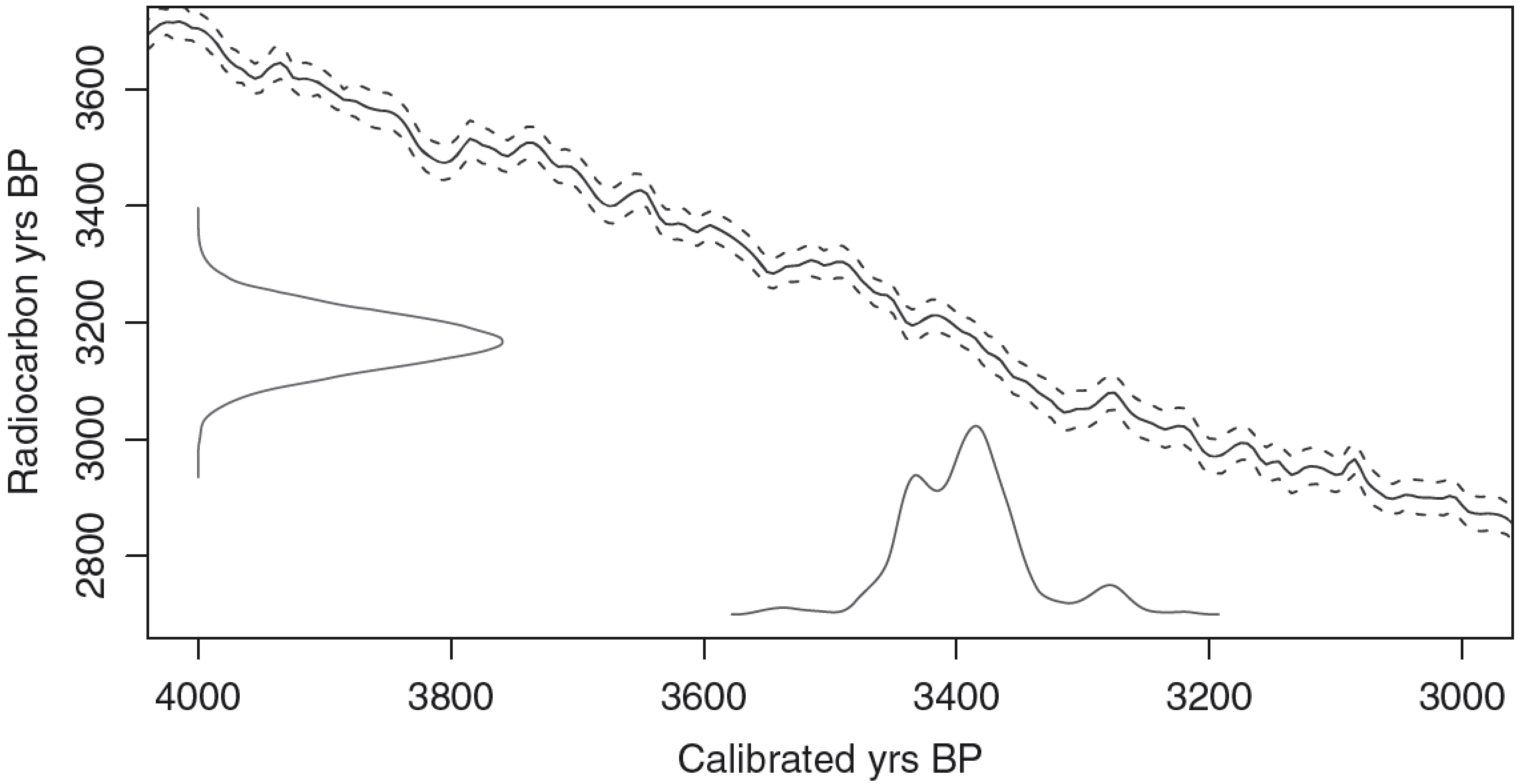


Building an age model



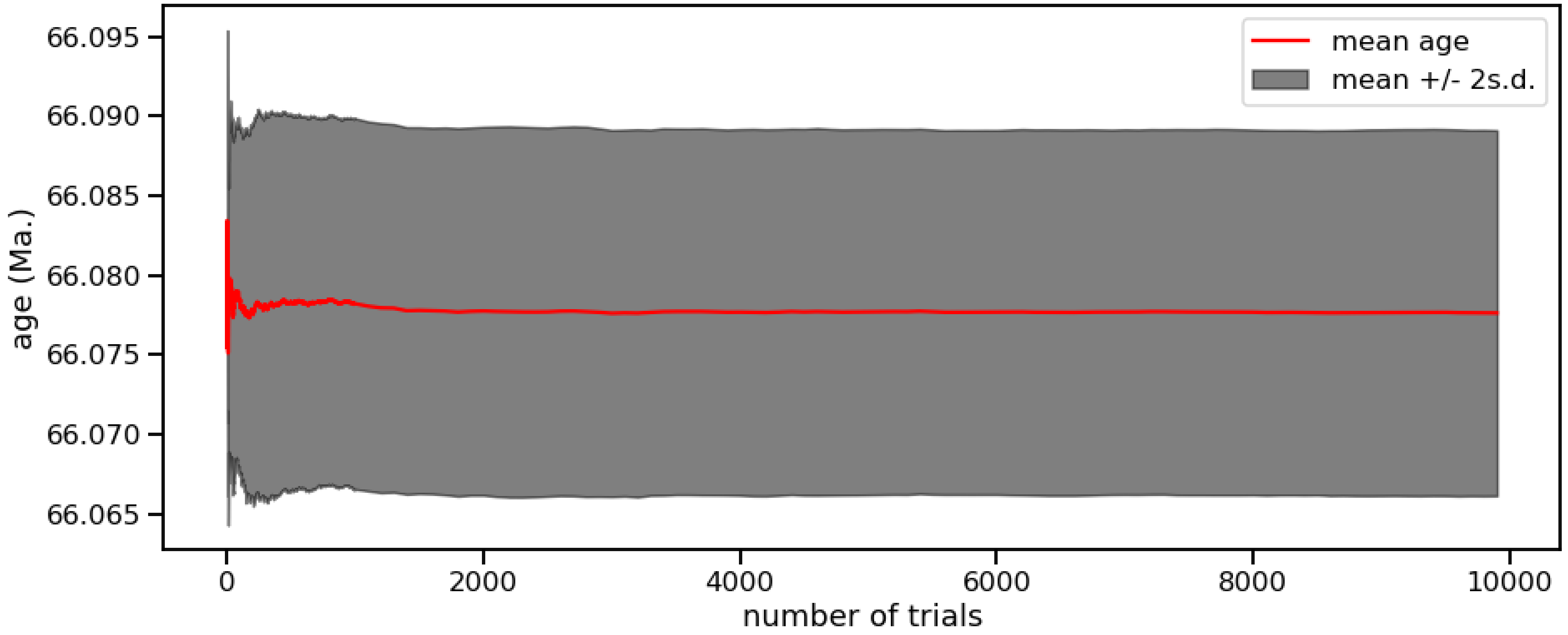
Power of Markov Chain Monte Carlo approaches

- prior distributions need not be Gaussian (figure from Haslett and Parnell, 2008)

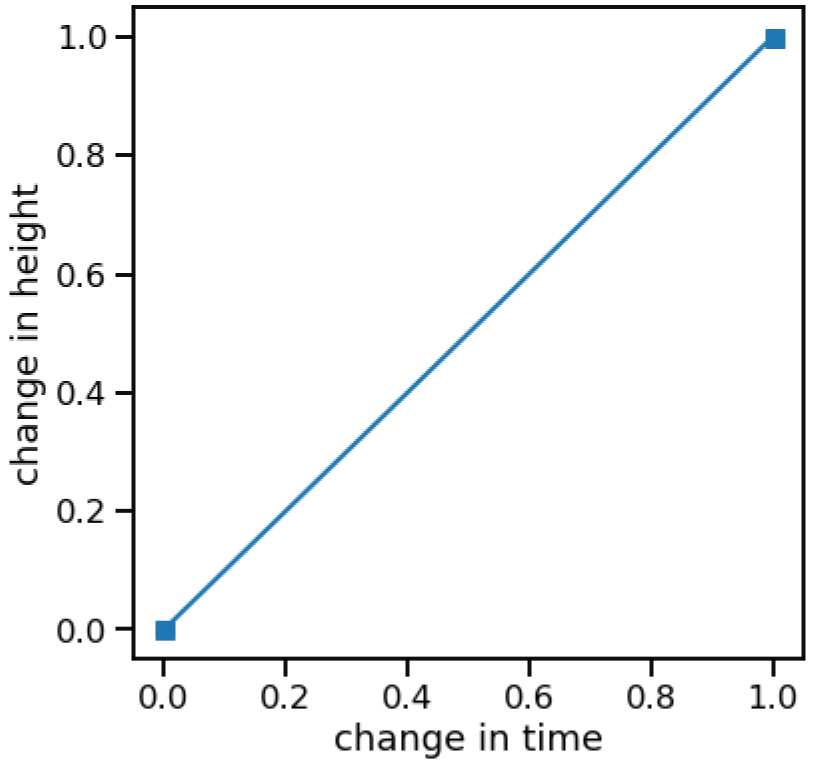


How many samples is enough?

How many samples is enough?



Constant sedimentation rate assumption



Constant sedimentation rate assumption

In [103]:

```
fig=plt.figure(1,figsize=(6,6)); ax=fig.add_subplot(111);
ax.set_xlabel('change in time'); _=ax.set_ylabel('change in height')
num_paths=200 #add knots to the path
for i in range(num_paths):
    pts=np.random.poisson(5, 1)[0] #discrete integer
    t_path=make_path(pts,1,1,1) #age change between knots
    h_path=make_path(pts,1,1,1) #position change between knots
    ax.plot([0]+list(np.cumsum([1/pts]*pts)),[0]+list(np.cumsum([1/pts]*pts)),'-s')
#     ax.plot(t_path,h_path,'-s') #plot the path
    #plot many paths
    ax.plot(t_path,h_path,'k-',lw=0.5,alpha=0.25)
```

Constant sedimentation rate assumption

In [ ]:

```
...
for i in range(num_paths):
    pts=np.random.poisson(5, 1)[0] #discrete integer
    ...
```

Constant sedimentation rate assumption

```
...
for i in range(num_paths):
    pts=np.random.poisson(5, 1)[0] #discrete integer
    ...
```

Poisson distribution is a discrete probability distribution that expresses the probability of a given number of events occurring in a fixed interval of time or space if these events occur with a known constant mean rate and independently of the time since the last event.

Constant sedimentation rate assumption

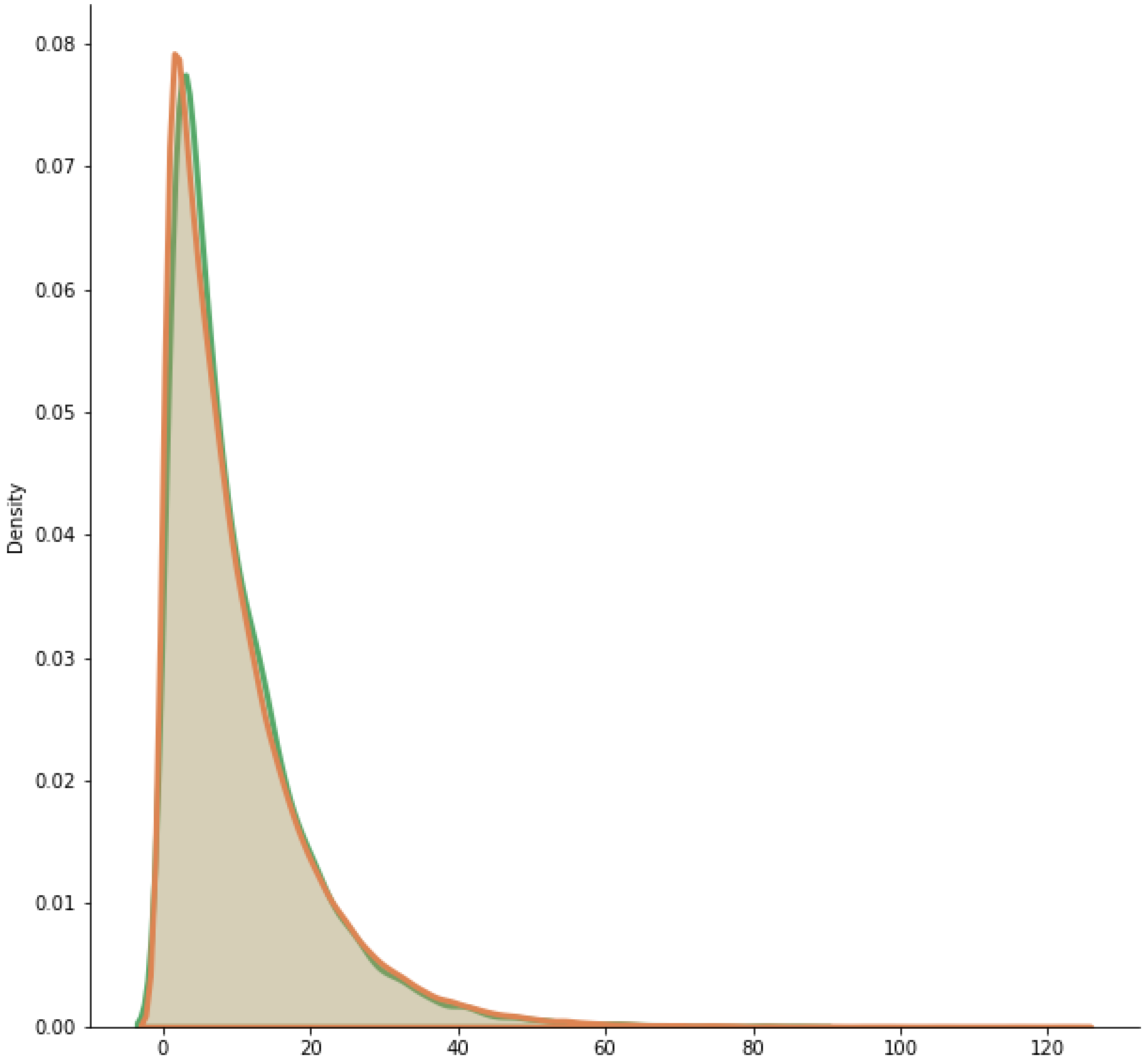
```
...
for i in range(num_paths):
    pts=np.random.poisson(5, 1)[0] #discrete integer
    ...
```

Poisson distribution is a discrete probability distribution that expresses the probability of a given number of events occurring in a fixed interval of time or space if these events occur with a known constant mean rate and independently of the time since the last event.

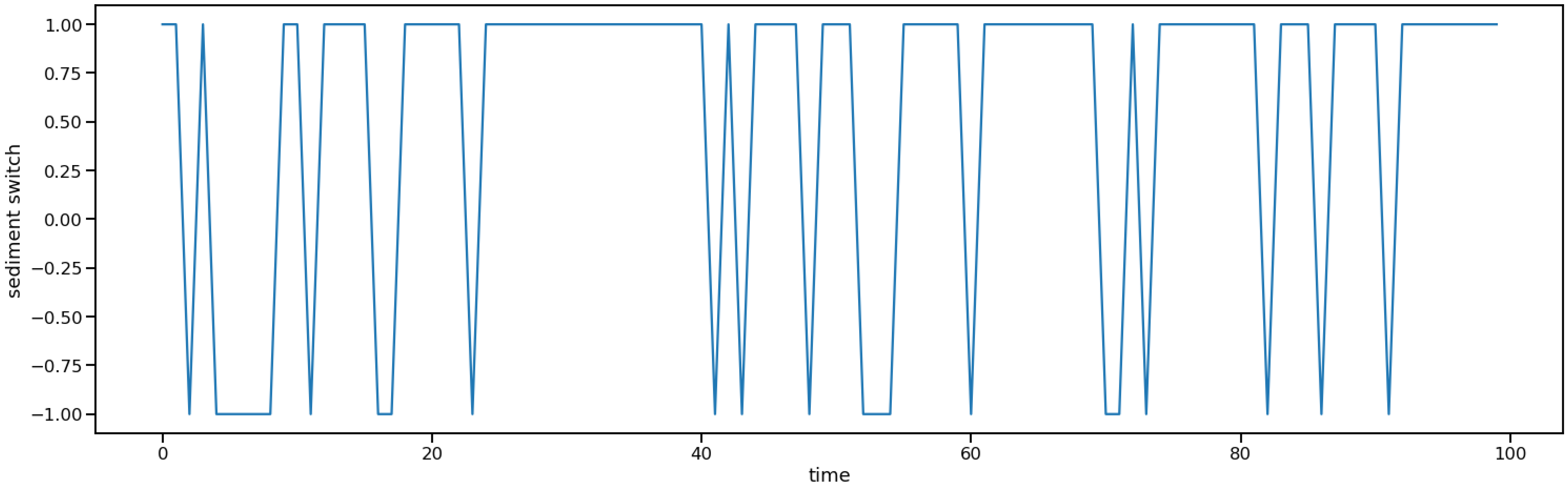
Exponential distribution is the probability distribution of the time between events in a *Poisson point process*

In [22]:

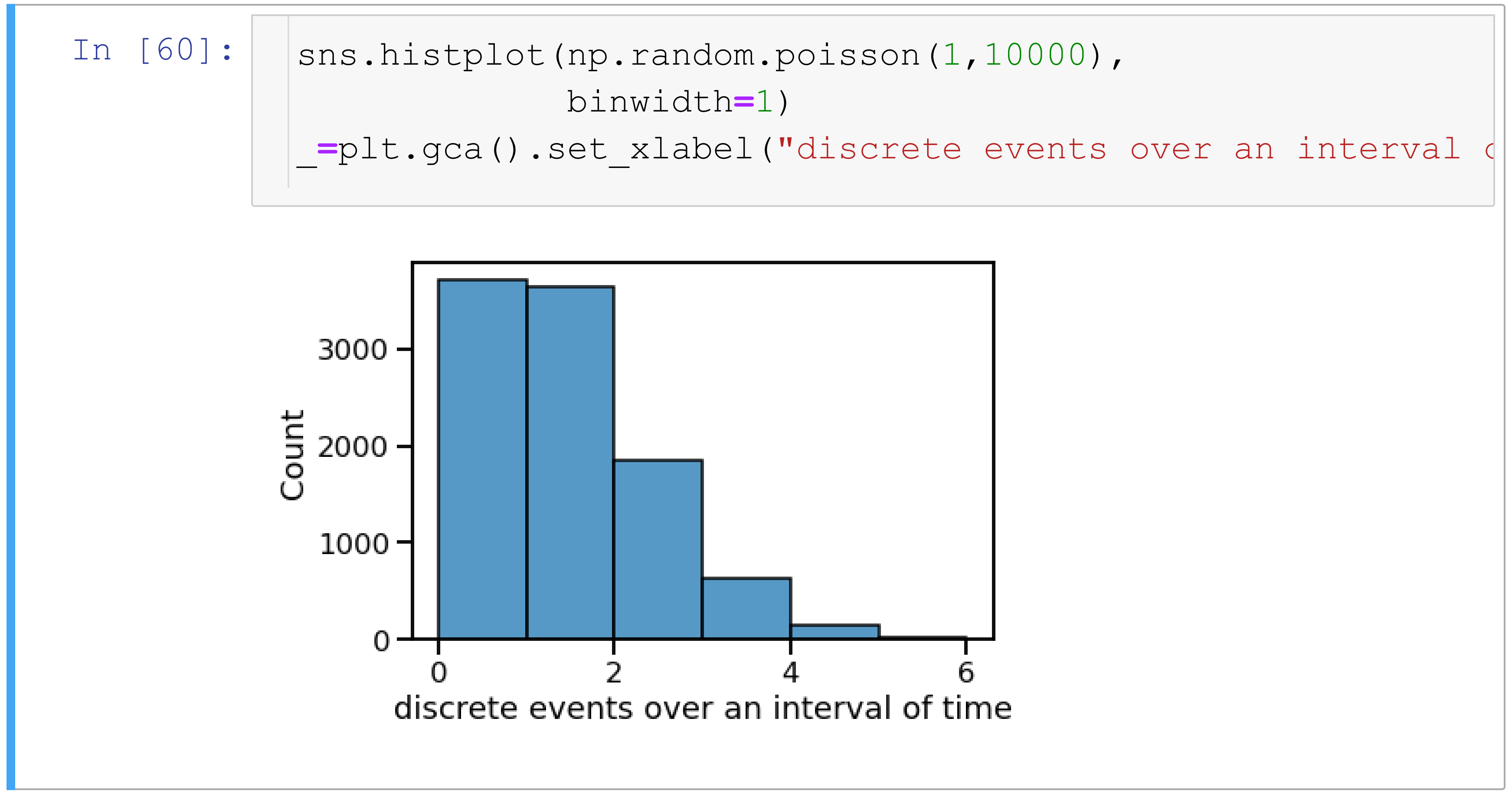
```python
import numpy as np
from matplotlib import pyplot as plt
import seaborn as sns
fig=plt.figure(figsize=(10,10))
a = np.random.uniform(0,1,100000)
b = a<0.1
sns.kdeplot(np.diff(np.where(b)[0]),color=sns.color_palette('deep')[2],fill=True,lw=3)
c = np.random.exponential(10,100000)
sns.kdeplot(c,color=sns.color_palette('deep')[1],fill=True,lw=3)
sns.despine()
```



Deciding on number of sedimentation rate changes



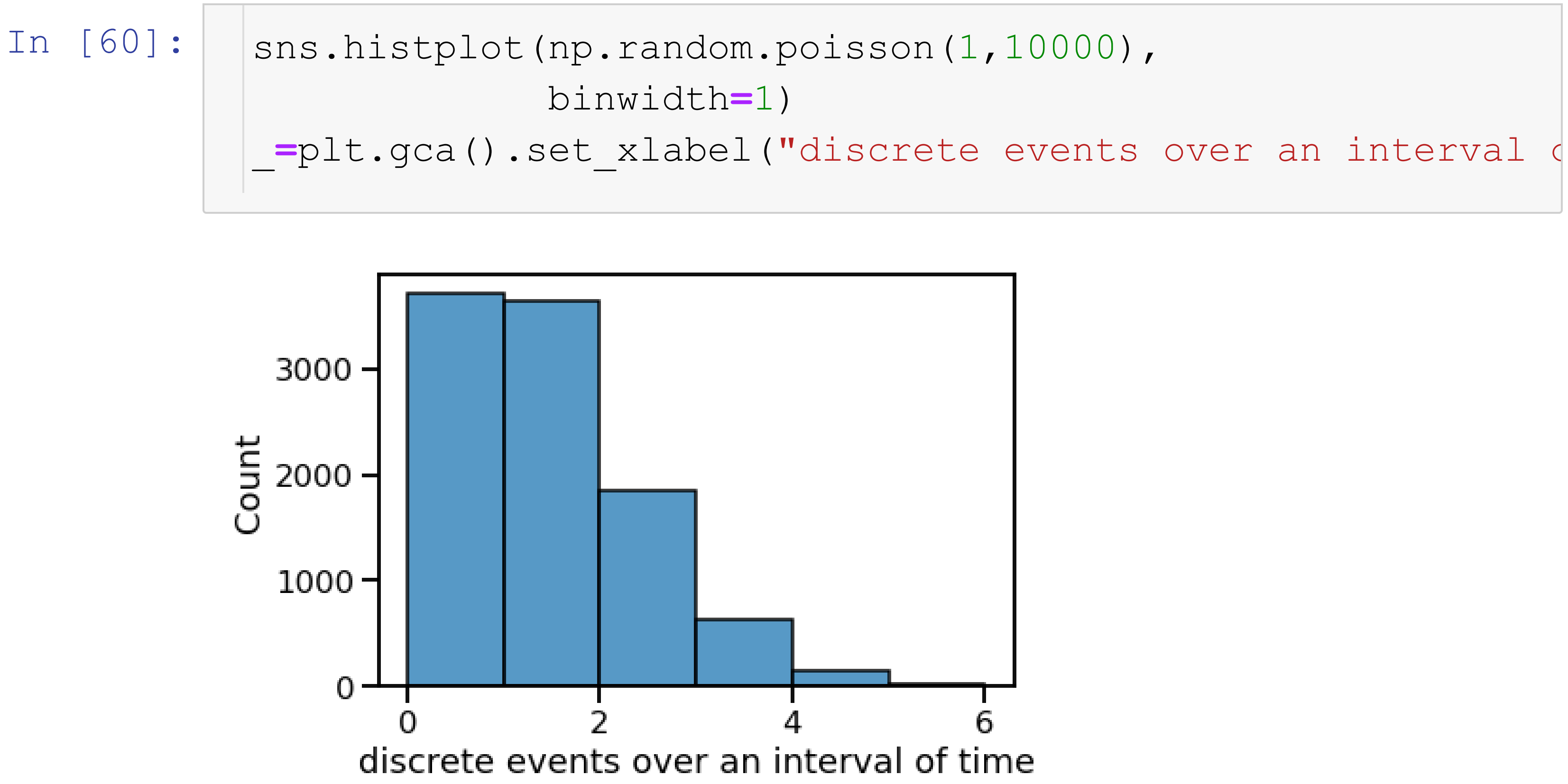
Deciding on number of sedimentation rate changes



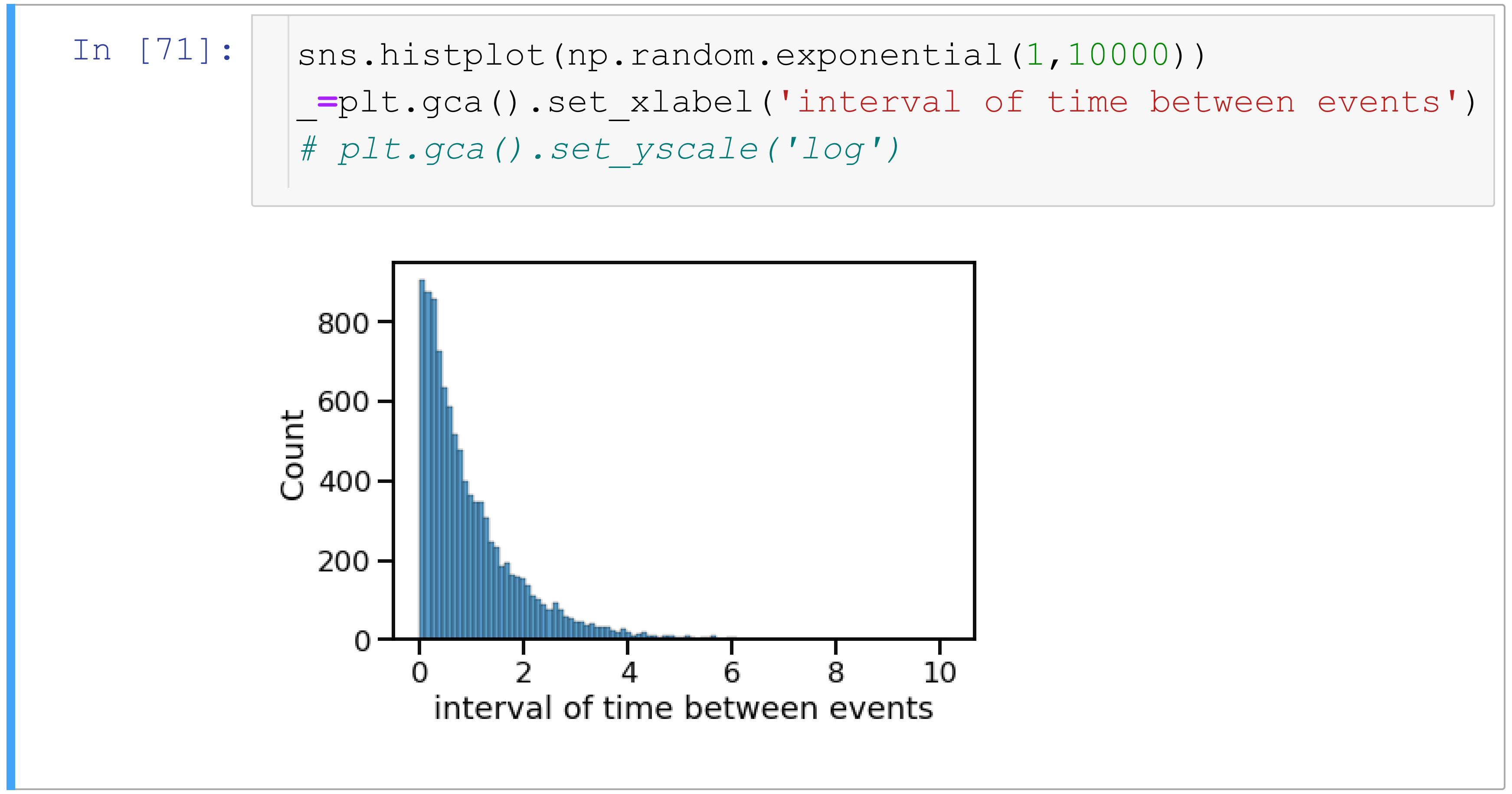
In [60]:

```
sns.histplot(np.random.poisson(1,10000),
             binwidth=1)
_=plt.gca().set_xlabel("discrete events over an interval 
```

Deciding on number of sedimentation rate changes

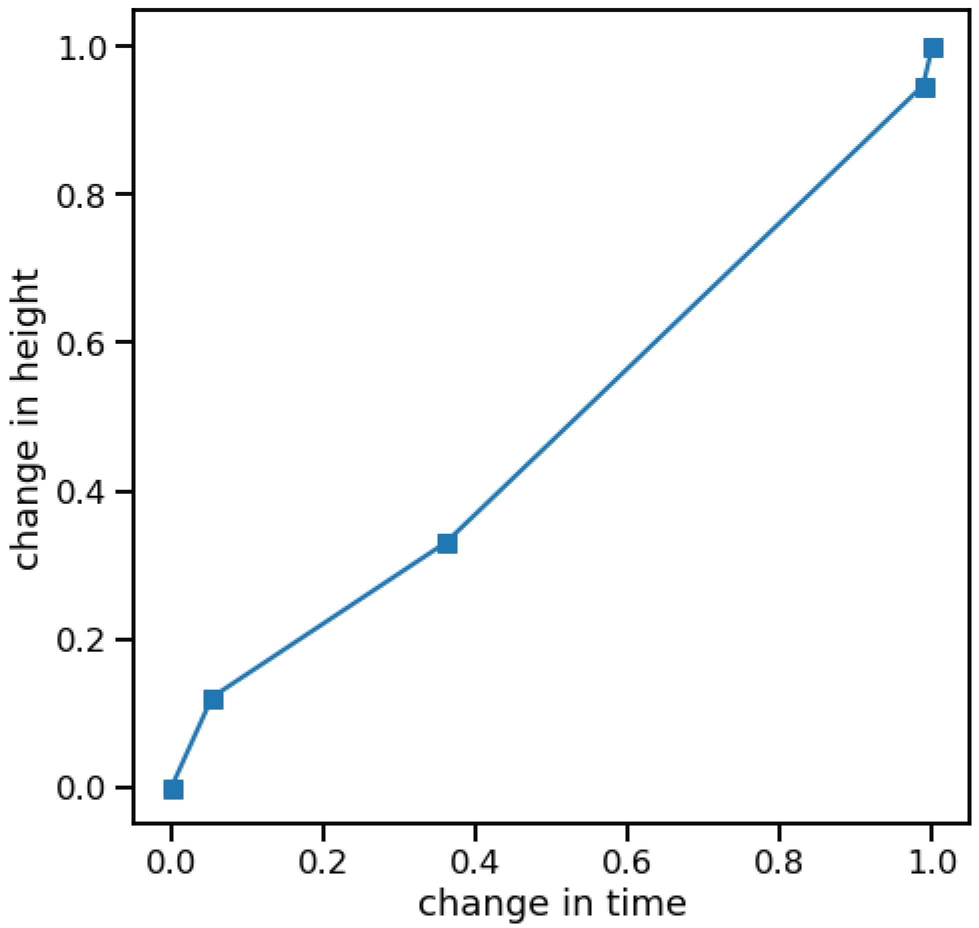


```
In [60]:  sns.histplot(np.random.poisson(1,10000),
                       binwidth=1)
          _=plt.gca().set_xlabel("discrete events over an interval 
```

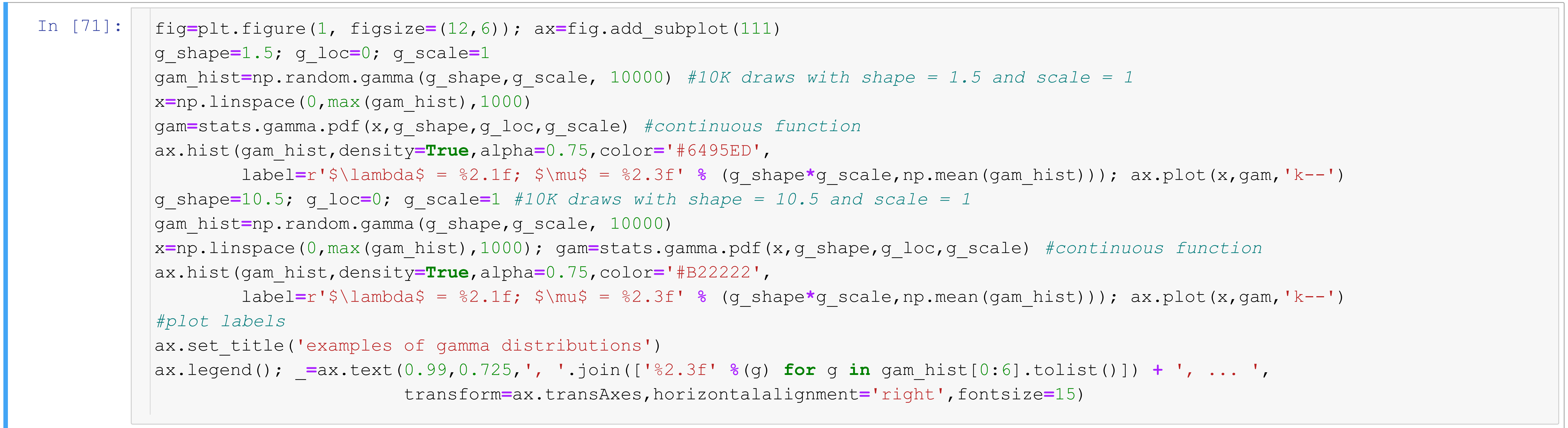


```
In [71]:  sns.histplot(np.random.exponential(1,10000))
          _=plt.gca().set_xlabel('interval of time between events')
          # plt.gca().set_yscale('log')
```

Deciding on number of sedimentation rate changes

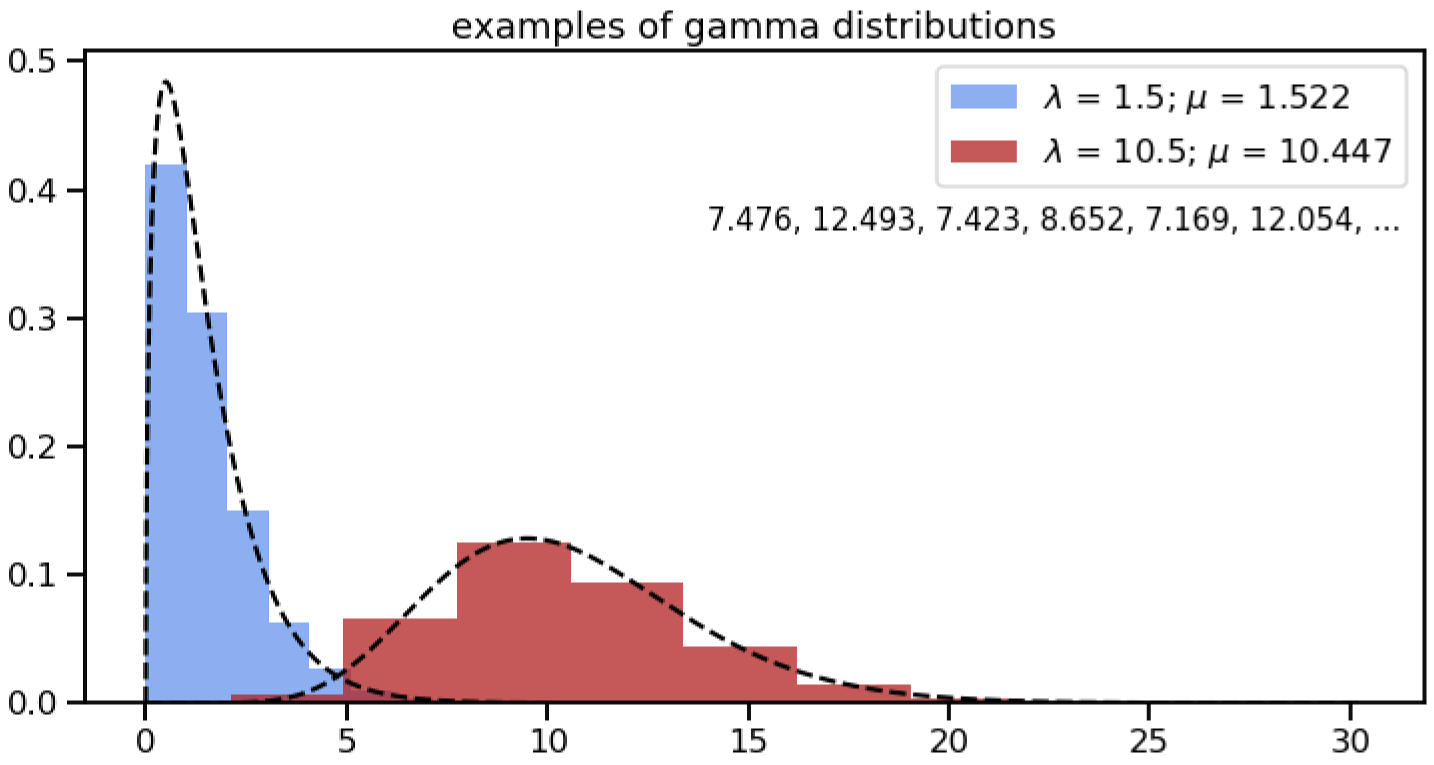


Picking sedimentation rates

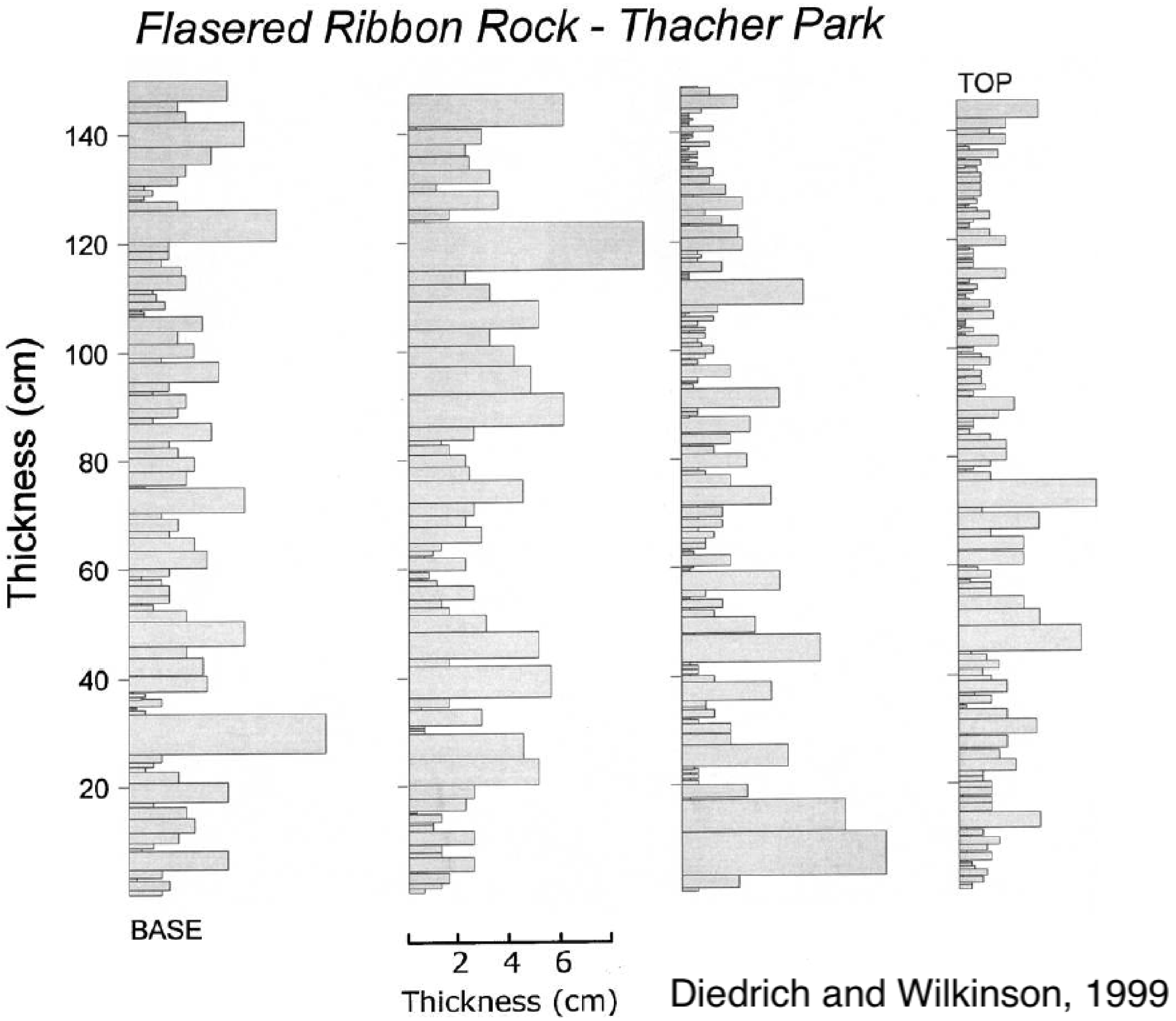


In [71]:

```
fig=plt.figure(1, figsize=(12,6)); ax=fig.add_subplot(111)
g_shape=1.5; g_loc=0; g_scale=1
gam_hist=np.random.gamma(g_shape,g_scale, 10000) #10K draws with shape = 1.5 and scale = 1
x=np.linspace(0,max(gam_hist),1000)
gam=stats.gamma.pdf(x,g_shape,g_loc,g_scale) #continuous function
ax.hist(gam_hist,density=True,alpha=0.75,color='#6495ED',
        label=r'$\lambda$ = %2.1f; $\mu$ = %2.3f' % (g_shape*g_scale,np.mean(gam_hist))); ax.plot(x,gam,'k--')
g_shape=10.5; g_loc=0; g_scale=1 #10K draws with shape = 10.5 and scale = 1
gam_hist=np.random.gamma(g_shape,g_scale, 10000)
x=np.linspace(0,max(gam_hist),1000); gam=stats.gamma.pdf(x,g_shape,g_loc,g_scale) #continuous function
ax.hist(gam_hist,density=True,alpha=0.75,color='#B22222',
        label=r'$\lambda$ = %2.1f; $\mu$ = %2.3f' % (g_shape*g_scale,np.mean(gam_hist))); ax.plot(x,gam,'k--')
#plot labels
ax.set_title('examples of gamma distributions')
ax.legend(); _=ax.text(0.99,0.725,', '.join(['%2.3f' %(g) for g in gam_hist[0:6].tolist()]) + ', ... ',
                       transform=ax.transAxes,horizontalalignment='right',fontsize=15)
```

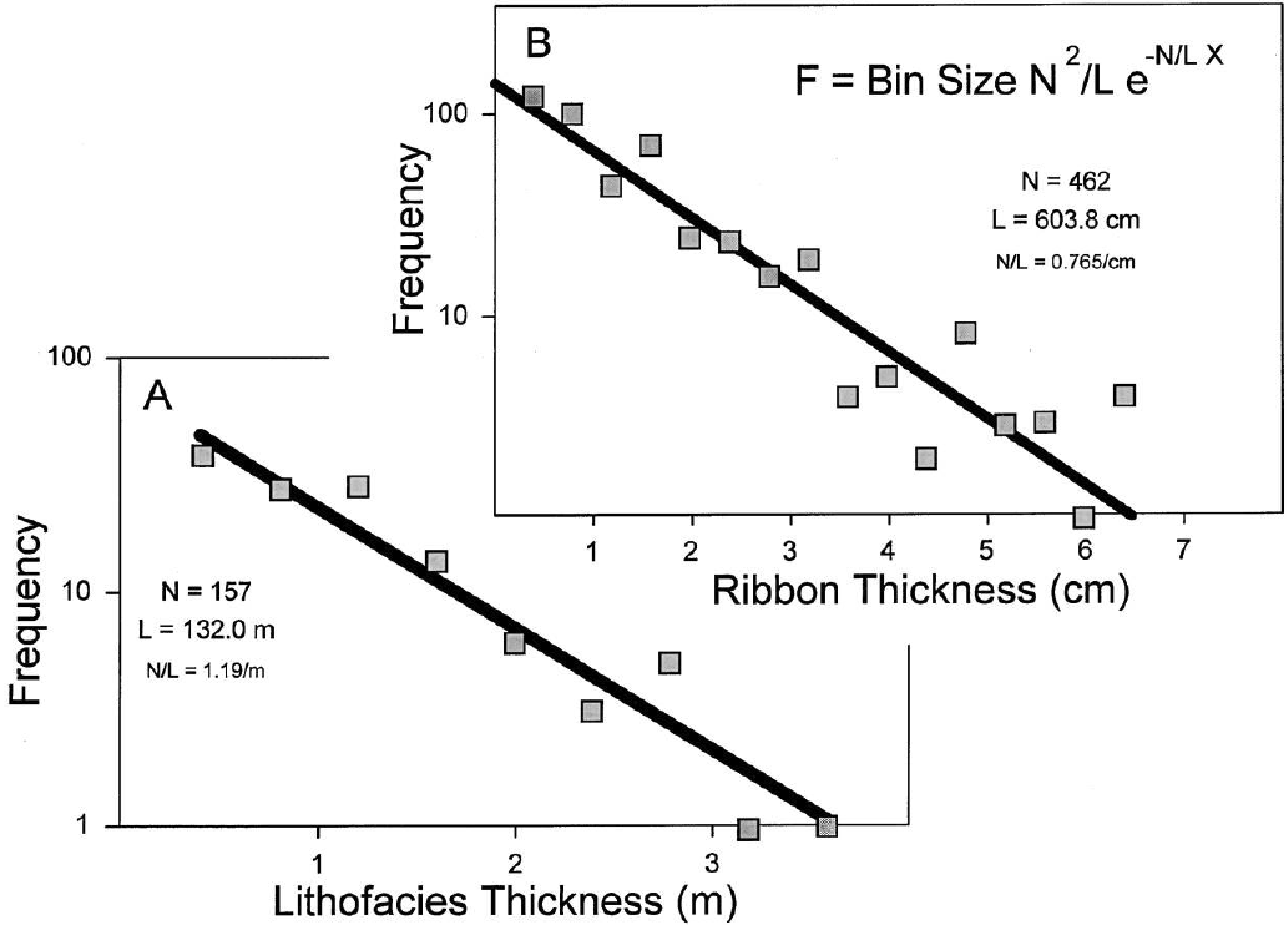


gamma distributions in sedimentology

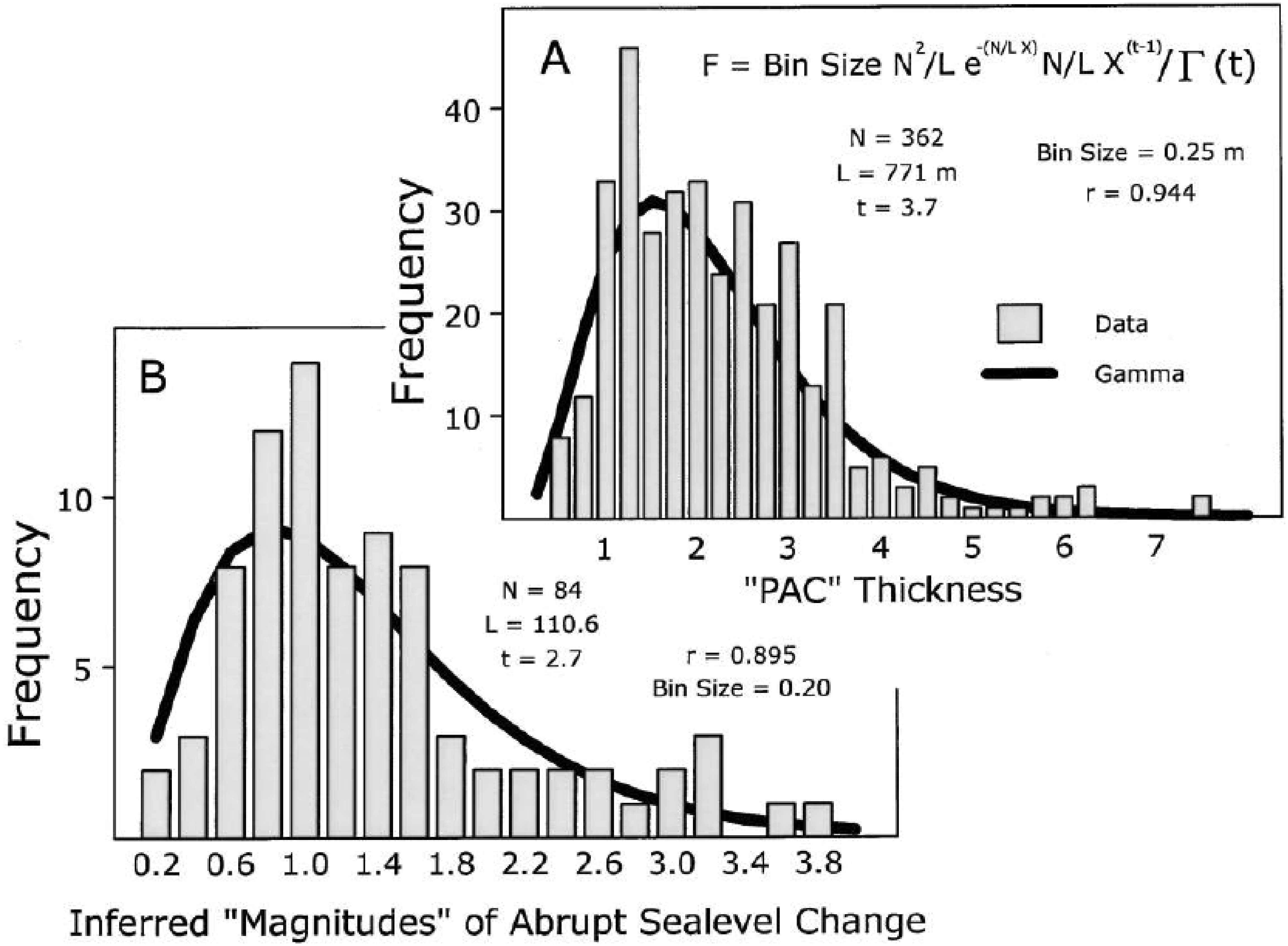


Diedrich and Wilkinson, 1999

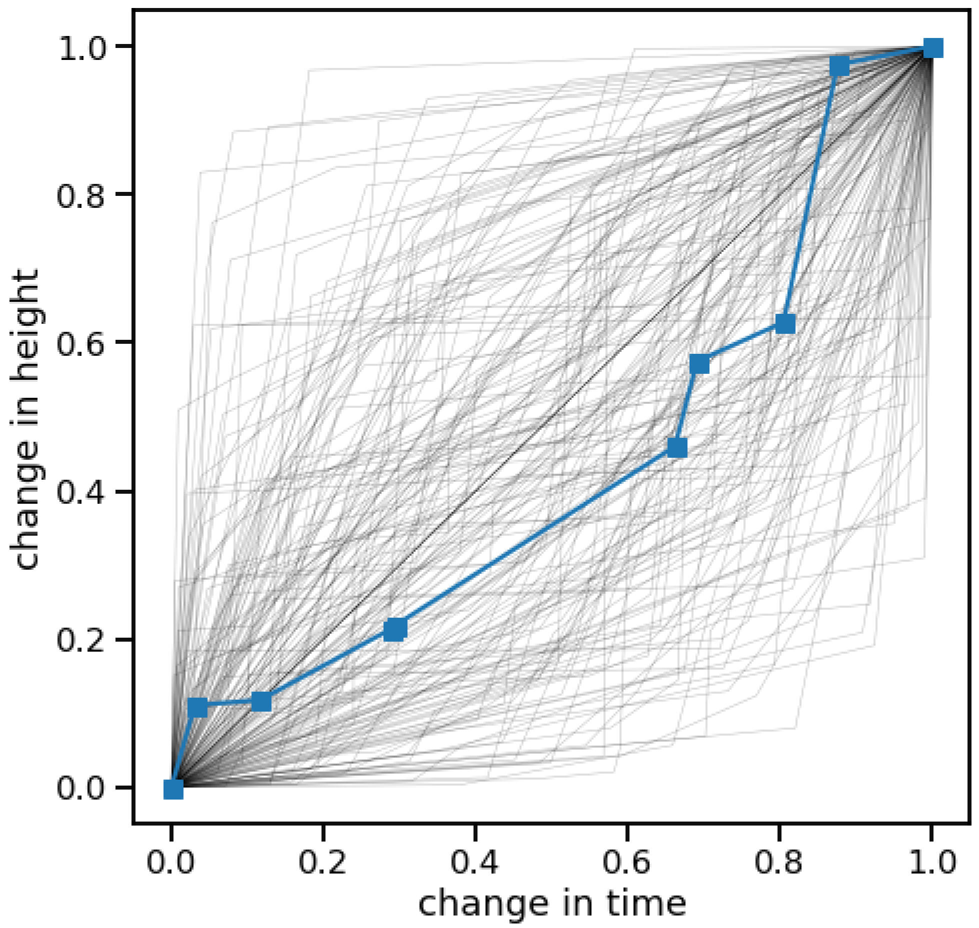
gamma distributions in sedimentology



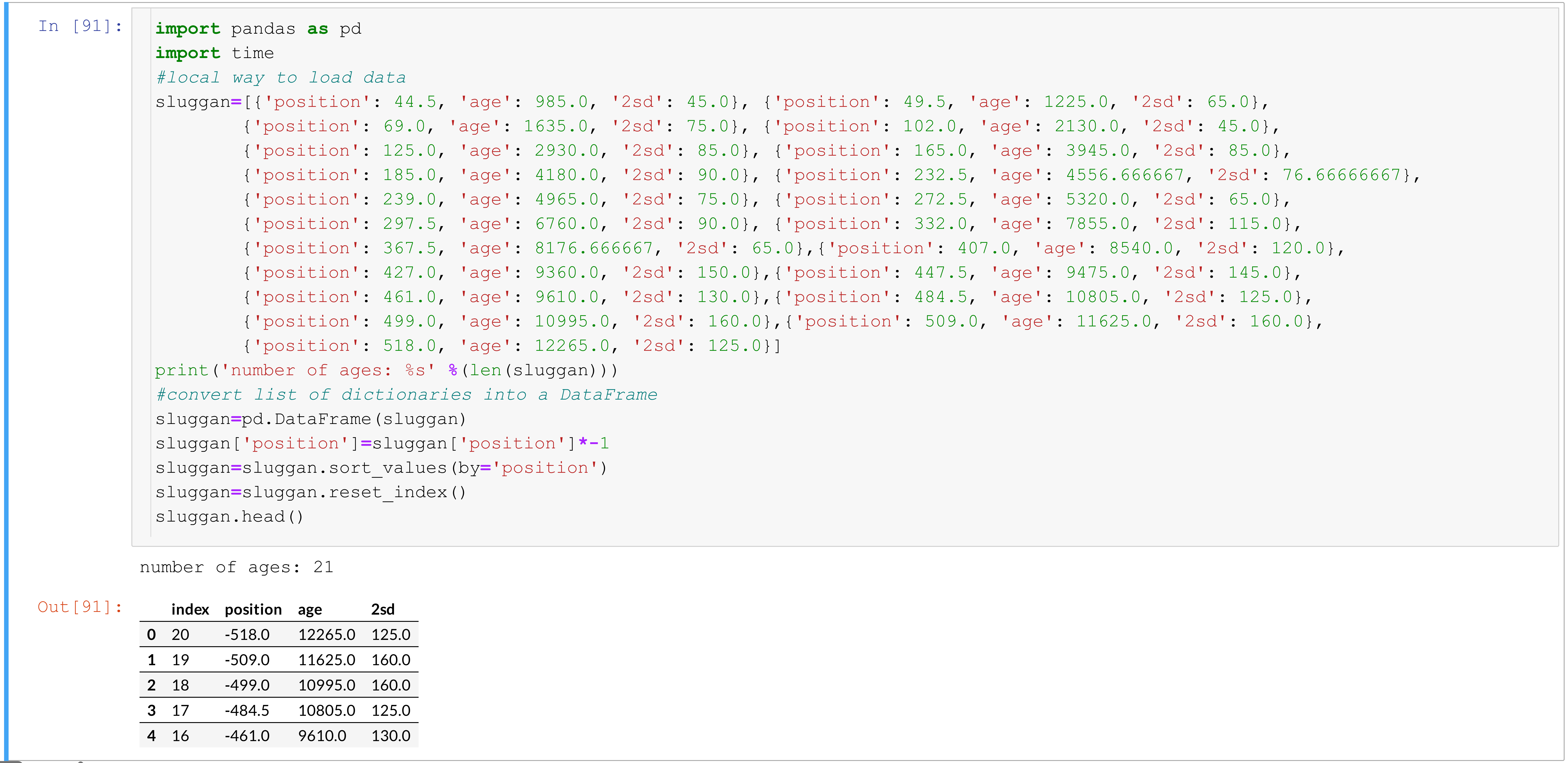
gamma distributions in sedimentology



compound Poisson gamma age models



compound Poisson gamma age models



In [91]:

```
import pandas as pd
import time
#local way to load data
sluggan=[{'position': 44.5, 'age': 985.0, '2sd': 45.0}, {'position': 49.5, 'age': 1225.0, '2sd': 65.0},
        {'position': 69.0, 'age': 1635.0, '2sd': 75.0}, {'position': 102.0, 'age': 2130.0, '2sd': 45.0},
        {'position': 125.0, 'age': 2930.0, '2sd': 85.0}, {'position': 165.0, 'age': 3945.0, '2sd': 85.0},
        {'position': 185.0, 'age': 4180.0, '2sd': 90.0}, {'position': 232.5, 'age': 4556.666667, '2sd': 76.66666667},
        {'position': 239.0, 'age': 4965.0, '2sd': 75.0}, {'position': 272.5, 'age': 5320.0, '2sd': 65.0},
        {'position': 297.5, 'age': 6760.0, '2sd': 90.0}, {'position': 332.0, 'age': 7855.0, '2sd': 115.0},
        {'position': 367.5, 'age': 8176.666667, '2sd': 65.0},{'position': 407.0, 'age': 8540.0, '2sd': 120.0},
        {'position': 427.0, 'age': 9360.0, '2sd': 150.0},{'position': 447.5, 'age': 9475.0, '2sd': 145.0},
        {'position': 461.0, 'age': 9610.0, '2sd': 130.0},{'position': 484.5, 'age': 10805.0, '2sd': 125.0},
        {'position': 499.0, 'age': 10995.0, '2sd': 160.0},{'position': 509.0, 'age': 11625.0, '2sd': 160.0},
        {'position': 518.0, 'age': 12265.0, '2sd': 125.0}]
print('number of ages: %s' %(len(sluggan)))
#convert list of dictionaries into a DataFrame
sluggan=pd.DataFrame(sluggan)
sluggan['position']=sluggan['position']*-1
sluggan=sluggan.sort_values(by='position')
sluggan=sluggan.reset_index()
sluggan.head()
```

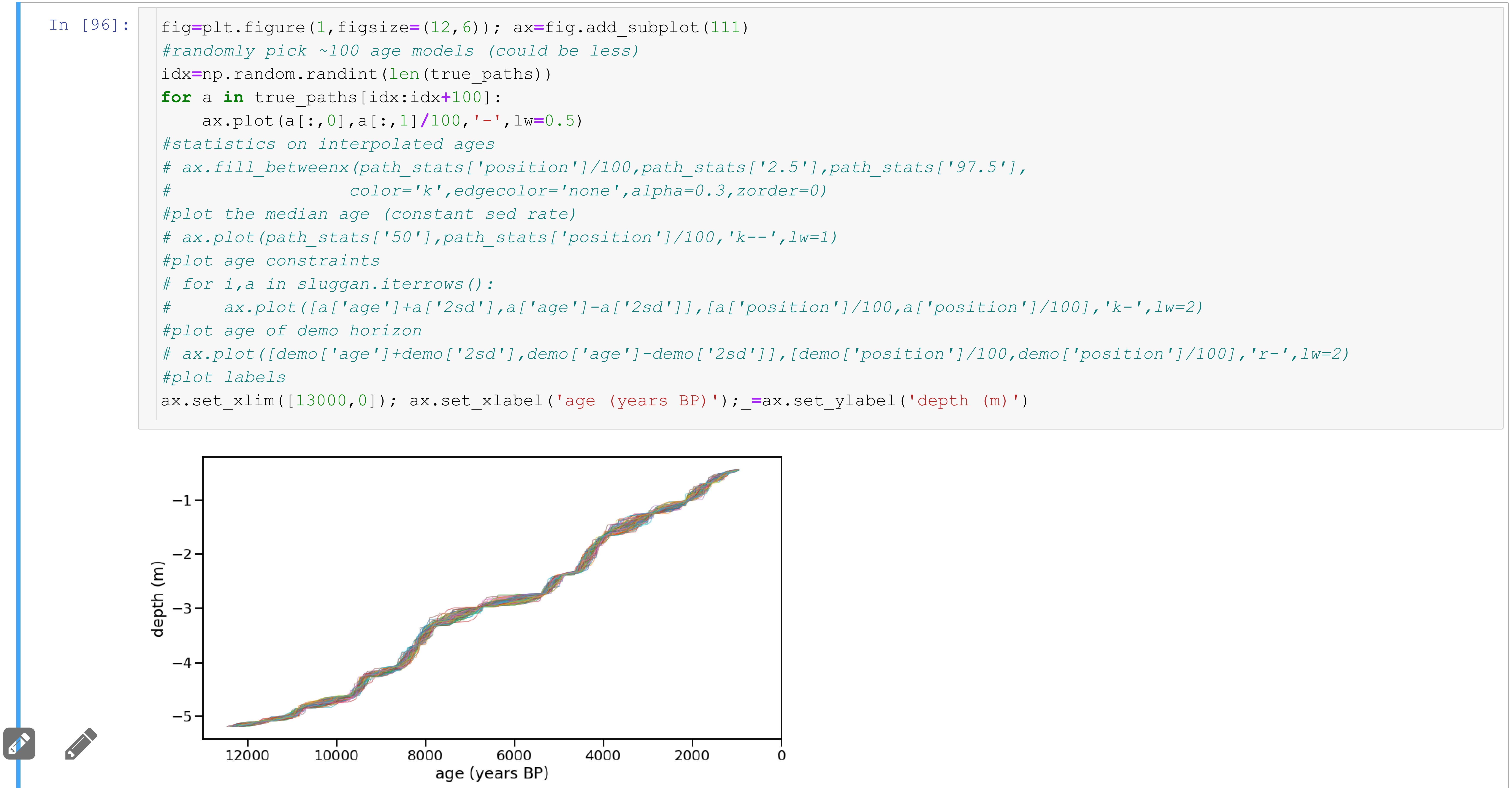
```
number of ages: 21
```

Out[91]:

	index	position	age	2sd
0	20	-518.0	12265.0	125.0
1	19	-509.0	11625.0	160.0
2	18	-499.0	10995.0	160.0
3	17	-484.5	10805.0	125.0
4	16	-461.0	9610.0	130.0

compound Poisson gamma age models

compound Poisson gamma age models



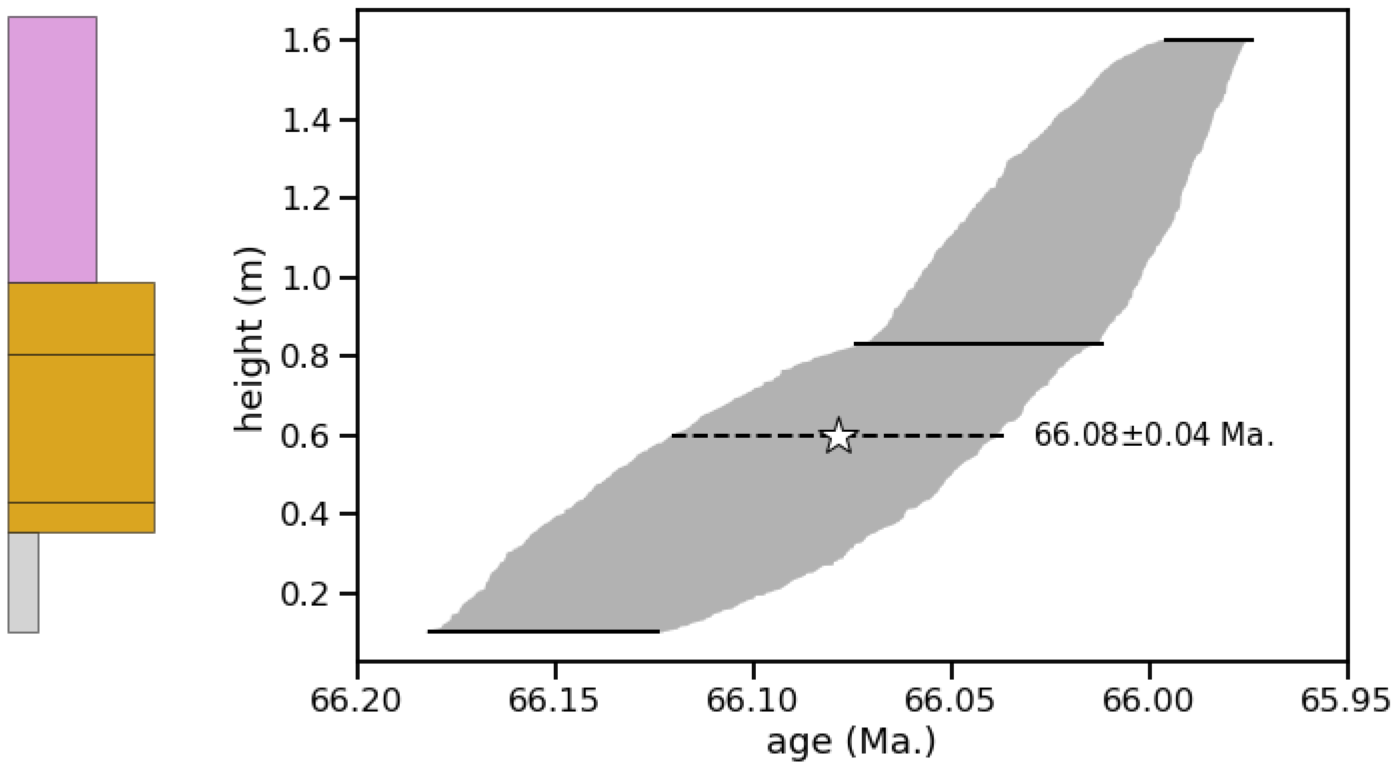
```
fig=plt.figure(1,figsize=(12,6)); ax=fig.add_subplot(111)
#randomly pick ~100 age models (could be less)
idx=np.random.randint(len(true_paths))
for a in true_paths[idx:idx+100]:
    ax.plot(a[:,0],a[:,1]/100,'-',lw=0.5)
#statistics on interpolated ages
# ax.fill_betweenx(path_stats['position']/100,path_stats['2.5'],path_stats['97.5'],
#                  color='k',edgecolor='none',alpha=0.3,zorder=0)
#plot the median age (constant sed rate)
# ax.plot(path_stats['50'],path_stats['position']/100,'k--',lw=1)
#plot age constraints
# for i,a in sluggan.iterrows():
#     ax.plot([a['age']+a['2sd'],a['age']-a['2sd']],[a['position']/100,a['position']/100],'k-',lw=2)
#plot age of demo horizon
# ax.plot([demo['age']+demo['2sd'],demo['age']-demo['2sd']],[demo['position']/100,demo['position']/100],'r-',lw=2)
#plot labels
ax.set_xlim([13000,0]); ax.set_xlabel('age (years BP)');_=ax.set_ylabel('depth (m)')
```

compound Poisson gamma age models

```python
#RUN AGE MODEL FOR KT U-Pb DATA
tic=time.time()
#pick self-consistent ages (based on Markov Chain Monte Carlo)
num_trials=1000
KT_picks=age_pick(KTashes,num_trials)
#define lambda for poisson draws
#NB: if lambda=0, "constant sed rate model" is result
p_lam=0
p_lam=10.5
#define shape and scale for gamma draws
#NB: age model only sensitive to shape
g_shape=1.5
g_scale=1\
#number of interpolation points per age anchor
num_interp=1000
#run compound Poission-Gamma age model
true_paths,interp_paths,path_stats,age_models = make_age_model(KTashes,KT_picks,p_lam,g_shape,g_scale,num_interp)
#age of KT Boundary
KT={'position':0.6,
       'age': np.mean([a(0.6) for a in age_models]),
        '2sd': 2*np.std([a(0.6) for a in age_models])}
toc=time.time()
print(r'number of trials: %s' %(num_trials))
print(r'model run time: %2.2f seconds' % (toc-tic))
print(r'age of KT boundary produce by model: %2.2f +/- %2.2f Ma.' %(KT['age'],KT['2sd']))
```

```
number of trials: 1000
model run time: 0.47 seconds
age of KT boundary produce by model: 66.08 +/- 0.04 Ma.
```

compound Poisson gamma age models



compound Poisson gamma age models

Appendix: more on gamma distributions in sedimentology

In [80]:

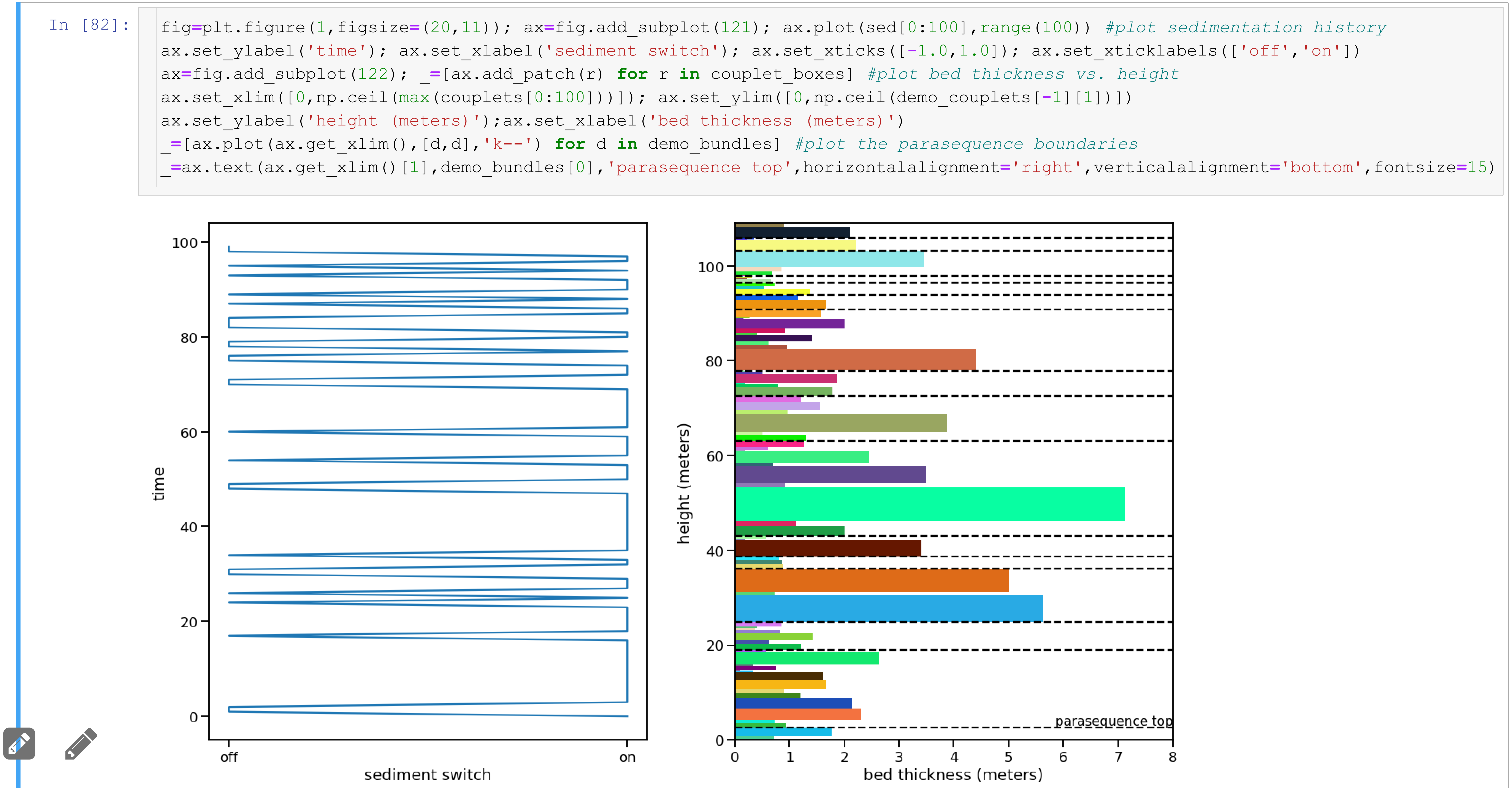
```
#timesteps; probability of change; starting state
t=20000; prob=0.25; state=1
#minimum beds in a parasequence
min_couplet_num=3

#switch state
sed=np.array([state*-1 if np.random.random()<prob else state for i in range(t)])
#find the "on" periods
on=np.where(sed==1)[0]

#find indices of consecutive "on" periods
on_breaks=list(np.where(np.diff(on)!=1)[0]+1)

#group into pairs
on_breaks=[0]+on_breaks+[len(on)]
on_breaks=list(zip(on_breaks[0:-1],on_breaks[1:]))

#calculate lengths of "sediment on" period
on_time=[]
for o in on_breaks:
    on_time.append(len(on[o[0]:o[1]]))

#here, the "on" periods are used to bundle couplets
#--> value = number of couplets
on_time=np.cumsum(np.array(on_time)+min_couplet_num-1)
couplet_idx=list(zip(list(on_time[0:-1]),list(on_time[1:])))
couplet_idx=[tuple((0, couplet_idx[0][0]))]+couplet_idx
#generate thickess of those couplets
couplets=np.random.gamma(1,1, couplet_idx[-1][1])
#package them up
bundles=[np.sum(couplets[i[0]:i[1]]) for i in couplet_idx]
```

Appendix: more on gamma distributions in sedimentology

In [81]:

```
#first hundred couplets for plotting
demo_couplets=list(np.cumsum(couplets)[0:100])
demo_couplets=[0]+demo_couplets
demo_couplets=list(zip(demo_couplets[0:-1],demo_couplets[1:]))
#make thickness vs. height boxes
couplet_boxes=[]
for d in demo_couplets:
    xy=np.array([(0,d[0]),(d[1]-d[0],d[0]),(d[1]-d[0],d[1]),(0,d[1])])
    rect = Polygon(xy,closed=True,facecolor="#"+''.join([np.random.choice([a for a in '0123456789ABCDEF']) for j in range(6)]))
    couplet_boxes.append(rect)
#bundles of couplets
demo_bundles=np.cumsum(bundles)[0:100]
demo_bundles=demo_bundles[demo_bundles<demo_couplets[-1][1]]
```

Appendix: more on gamma distributions in sedimentology



```
fig=plt.figure(1,figsize=(20,11)); ax=fig.add_subplot(121); ax.plot(sed[0:100],range(100)) #plot sedimentation history
ax.set_ylabel('time'); ax.set_xlabel('sediment switch'); ax.set_xticks([-1.0,1.0]); ax.set_xticklabels(['off','on'])
ax=fig.add_subplot(122); _=[ax.add_patch(r) for r in couplet_boxes] #plot bed thickness vs. height
ax.set_xlim([0,np.ceil(max(couplets[0:100]))]); ax.set_ylim([0,np.ceil(demo_couplets[-1][1])])
ax.set_ylabel('height (meters)');ax.set_xlabel('bed thickness (meters)')
_=[ax.plot(ax.get_xlim(),[d,d],'k--') for d in demo_bundles] #plot the parasequence boundaries
_=ax.text(ax.get_xlim()[1],demo_bundles[0],'parasequence top',horizontalalignment='right',verticalalignment='bottom',fontsize=15)
```

Appendix: more on gamma distributions in sedimentology

In [83]:

```
#histogram of bed thickness
fig=plt.figure(1,figsize=(20,11)); ax=fig.add_subplot(221)
ax.hist(couplets,bins=30,density=True); ax.set_xlabel('bed thickness (meters)')
#histogram of number of beds in a parasequence
ax=fig.add_subplot(222); ax.hist([i[1]-i[0] for i in couplet_idx],bins=30,density=True); ax.set_xlabel('beds per parasequence')
#histogram of parasequence thickness
ax=fig.add_subplot(212); ax.hist(bundles,bins=30,density=True);_=ax.set_xlabel('parasequence thickness (meters)')
```