

Data Bootcamp Final Project - Paleontology Database Analysis

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Backend

Installations and Imports

In []:

```
pip install geopandas
```

In []:

```
# imports
import requests
import pandas as pd
import io
import matplotlib
import matplotlib.pyplot as plt
import numpy as np
import plotly.express as px
import geopandas as gpd
import math
import seaborn as sns
from math import radians, cos, sin, asin, sqrt
from sklearn.ensemble import RandomForestRegressor as rf
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
pd.set_option("display.max_columns", 200)
pd.options.mode.chained_assignment = None
```

In []:

```
# importing data via api call (can take around 5 minutes)
url = requests.get('https://paleobiodb.org/data1.2/occs/list.csv?cc=NOA&show=attr,class,g
enus,subgenus,img,plant,abund,ecospace,taphonomy,etbasis,pres,coll,coords,loc,paleoloc,pr
ot,strat,stratext,lith,lithext,env,geo,timebins,timecompare,methods,refattr,crmod').conte
nt
occs = pd.read_csv(io.StringIO(url.decode('utf-8')))
# clean data
occs['avg_ma'] = (occs['min_ma'] + occs['max_ma']) / 2
occs.drop(columns=['reid_no', 'flags', 'record_type', 'accepted_attr', 'late_interval', 'plant
_organ', 'plant_organ2', 'reproduction', 'reproduction_basis', 'collection_subset', 'protected
', 'localbed', 'localorder', 'regionalsection', 'regionalbed', 'regionalorder', 'lithadj2', 'lit
hification2', 'minor_lithology2', 'fossilsfrom2', 'lithology2.1', 'lithadj2.1', 'lithification
2.1', 'minor_lithology2.1', 'fossilsfrom2.1', 'rock_censused', 'collectors', 'collection_dates
'], inplace=True)
```

/usr/local/lib/python3.6/dist-packages/IPython/core/interactiveshell.py:2718: DtypeWarnin
g:

Columns (3,14,26,27,28,36,37,42,43,46,47,48,65,68,71,74,76,77,78,79,80,82,87,88,89,90,91,
92,93,98,99,100,101,102,103,105,106,115,116,117,118,119,121) have mixed types.Specify dty
pe option on import or set low_memory=False.

Functions and Formulas

In []:

```
# haversine - formula used to calculate distance in between two geographic coordinates
def haversine(lat1, lng1, lat2, lng2):
    lat1, lng1, lat2, lng2, = map(np.deg2rad, [lat1, lng1, lat2, lng2])
    dlng = lng2 - lng1
    dlat = lat2 - lat1
    a = np.sin(dlat/2)**2 + np.cos(lat1) * np.cos(lat2) * np.sin(dlng/2)**2
    return 2 * np.arcsin(np.sqrt(a)) * 6371
```

In []:

```
# area of a spherical sector of the earth
def spherical_sector_area(proximity_value):
    x = 2*proximity_value/6371
    x = 6371*(1-math.cos(x/2))
    x = 2*math.pi*6371*x
    return x
```

In []:

```
# find distance in between points and every entry in df using numpy vectorization
def distances(data, lat, lng, filter_dis):
    data['dis'] = haversine(lat, lng, data['lat'].values, data['lng'].values)
    return data.loc[data['dis']<filter_dis].sort_values(by=['dis'])
```

In []:

```
# filter based on column and string, simplified .loc function
def filter(data, column, value):
    return data.loc[data[column].str.contains(value, na=False, case=False)]
```

In []:

```
# plotly heatmap
def heatmap(pdata, hov_name, hov_data, sensitivity, title):
    geo_df = gpd.read_file(gpd.datasets.get_path('naturalearth_cities'))
    return px.density_mapbox(
        pdata,
        lat=pdata.lat,
        lon=pdata.lng,
        radius=sensitivity,
        hover_name=hov_name,
        hover_data=hov_data,
        mapbox_style="stamen-terrain",
        title = title
    )
```

Data Analysis

Introduction to the data and important terms

In []:

```
print('-'*160)
print("This program allows users to learn more about the geology surrounding their locati  
on by exploring paleotological findings from the area.")
print()
print("Paleotontology involves the study of fossils, which are mineralized remains of liv  
ing things. Fossils are found everywhere.")
print()
print("Here is a scatterplot plotting the latitude and longitude of various fossils found  
in North America.")
print('-'*160)
plt.style.use('seaborn-dark')
```

```
occs.loc[occs['lat']>0].loc[occs['lng']<0].plot(kind='scatter', x='lng', y='lat', title=
'Occurences by latitude and longitude', figsize=(15, 10), s=1, alpha=0.1)
```

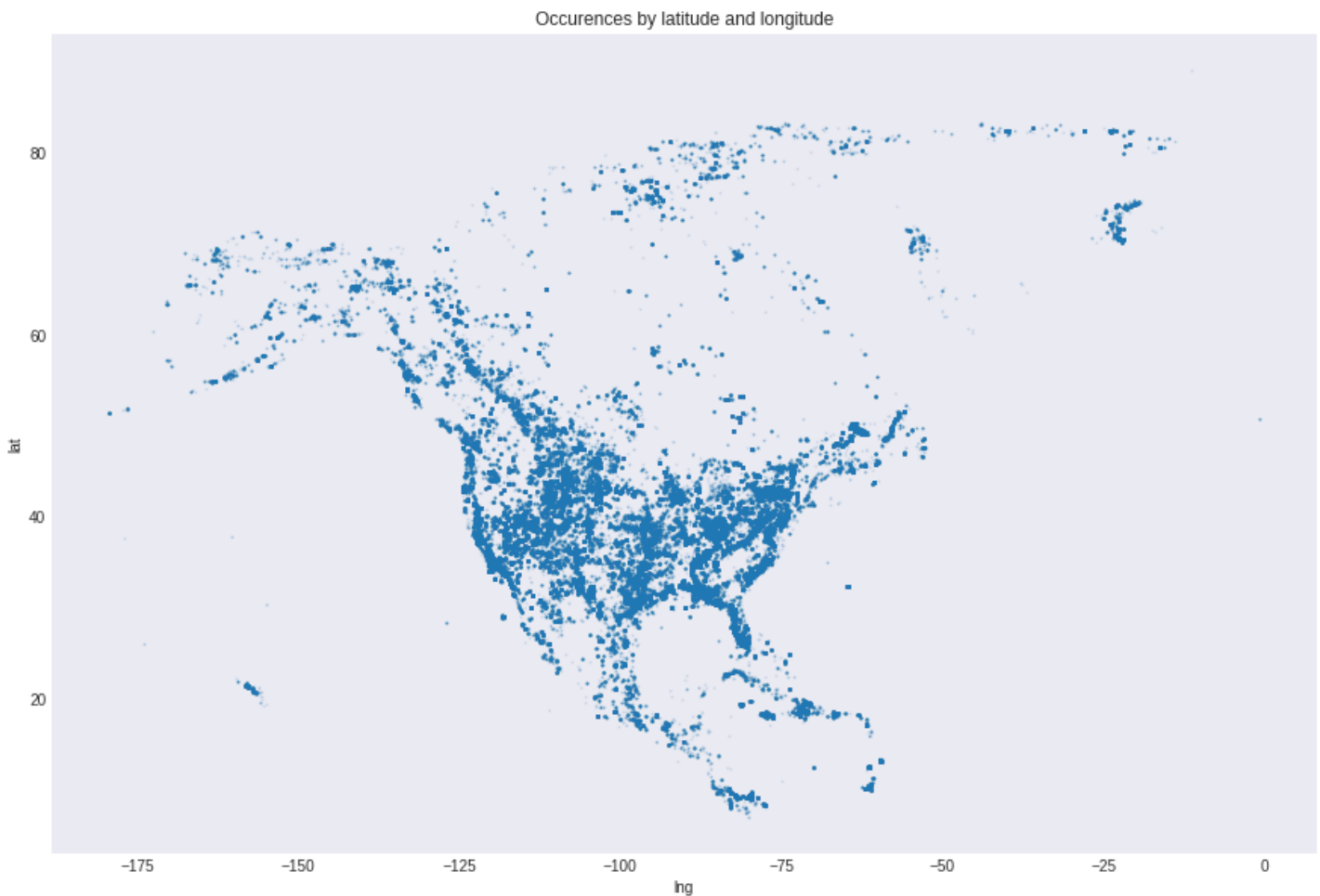
This program allows users to learn more about the geology surrounding their location by exploring paleontological findings from the area.

Paleotontology involves the study of fossils, which are mineralized remains of living things. Fossils are found everywhere.

Here is a scatterplot plotting the latitude and longitude of various fossils found in North America.

Out[]:

<matplotlib.axes._subplots.AxesSubplot at 0x7faad9c87160>



In []:

```
print('-'*160)
print("The program makes use of the Paleobiology Database, a database tracking millions o
f \"occurences\" of fossils referenced in research papers studying paleontology.", end='\
n\n')
print("When a fossil is found as part of a study, information is collected about the foss
il and the surrounding geological conditions. This information is represented" + '\n' +
"as columns within a dataframe containing data imported from the Paleobiology Database, o
r PBDB.\n")
print("Each occurrence represents a single species found at a site, and can contain multip
le specimens.")
print('-'*160)
occs.sample(5)
```

The program makes use of the Paleobiology Database, a database tracking millions of "occurences" of fossils referenced in research papers studying paleontology.

When a fossil is found as part of a study, information is collected about the fossil and

When a fossil is found as part of a study, information is collected about the fossil and the surrounding geological conditions. This information is represented as columns within a dataframe containing data imported from the Paleobiology Database, or PBDB.

Each occurrence represents a single species found at a site, and can contain multiple specimens.

Out[]:

occurrence_no	collection_no	identified_name	identified_rank	identified_no	difference	accepted_name	accepted_rank
205612	445943	43886 Fenestrellina sp.	genus	25556	NaN	Fenestrellina	genus
140337	237815	23713 Taeniocrada sp.	genus	263721	NaN	Taeniocrada	genus
88289	143151	12386 Rhipidomella sp.	genus	26974	NaN	Rhipidomella	genus
485520	1330180	179083 Phytosauridae indet.	unranked clade	38293	replaced by	Mystriosuchinae	subfamily
268010	619001	66703 Macoma balthica	species	107606	NaN	Macoma balthica	species

In []:

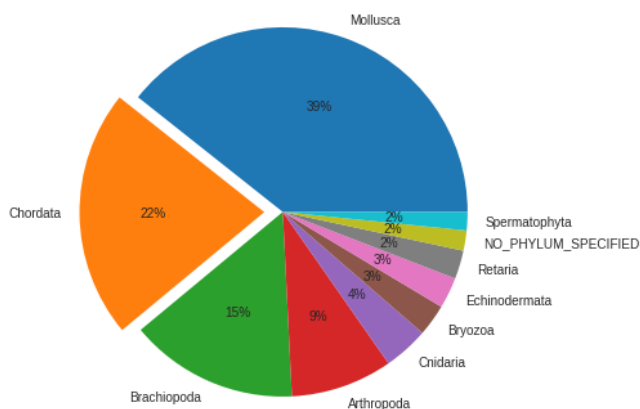
```
print('-'*160)
print("This particular dataset includes data on " + str(len(occs)) + " occurrences located in North America. The PBDB contains data on over 1.4 million occurrences in total. This may " + '\n' + "seem like a lot, but the fossils you see here are not exactly the kind of fossil you may see in a museum.", end = '\n\n')
print("A quick analysis of the different phylum (a classification rank) shows that Chordata, the phylum that mostly consists of vertebrates such as sharks and " + '\n' + "dinosaurs, makes up only 22% of all occurrences.", end = '\n\n')
print("A closer analysis of the different classes (a subset of phylums) shows that Reptilia, the class that dinosaurs fall under, make up just 3% of all occurrences." + '\n' + "Although shark teeth are some of the most commonly owned fossils, they make up less than 1% of occurrences under Chondrichthyes. A majority of occurrences" + '\n' + "are classified as what most of us recognize as just \"shells\".")
print('-'*160 + '\n')
occs_pie = occs['class'].value_counts()[:20].rename_axis('class').to_frame('count')
fig, ax = plt.subplots(1,2)
fig.set_figheight(10)
fig.set_figwidth(18)
fig.subplots_adjust(wspace=0.8)
explode1 = (0, 0.1, 0, 0, 0, 0, 0, 0, 0, 0)
explode2 = (0, 0, 0.1, 0, 0, 0, 0, 0.1, 0, 0, 0.2, 0, 0, 0, 0, 0, 0, 0.1, 0, 0)
ax[0].pie(occs['phylum'].value_counts()[:10].rename_axis('phylum').to_frame('count')['count'],labels=occs['phylum'].value_counts()[:10].rename_axis('phylum').to_frame('count').index, explode=explode1, autopct='%1.f%%')
ax[0].set_title('Phylum representation in the PBDB',size=20, fontweight = 'bold')
ax[1].pie(occs['class'].value_counts()[:20].rename_axis('class').to_frame('count')['count'],labels=occs['class'].value_counts()[:20].rename_axis('class').to_frame('count').index, explode=explode2, autopct='%1.f%%')
ax[1].set_title('Class representation in the PBDB',size=20, fontweight = 'bold')
fig.show()
```

This particular dataset includes data on 546979 occurrences located in North America. The PBDB contains data on over 1.4 million occurrences in total. This may seem like a lot, but the fossils you see here are not exactly the kind of fossil you may see in a museum.

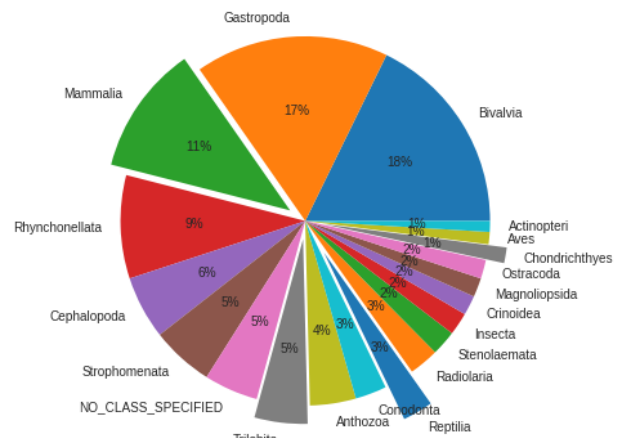
A quick analysis of the different phylum (a classification rank) shows that Chordata, the phylum that mostly consists of vertebrates such as sharks and dinosaurs, makes up only 22% of all occurrences.

A closer analysis of the different classes (a subset of phylums) shows that Reptilia, the class that dinosaurs fall under, make up just 3% of all occurrences. Although shark teeth are some of the most commonly owned fossils, they make up less than 1% of occurrences under Chondrichthyes. A majority of occurrences are classified as what most of us recognize as just "shells".

Phylum representation in the PBDB



Class representation in the PBDB



In []:

```
print('-'*160)
print("Additionally, even fossils that would be recognizable by name may not be recognizable as an occurrence. This map of T-rex occurrences shows", len(filter(occs, 'accepted_name', 'tyrannosaurus')), "total occurrences. \nAre T-rexes that common?", end = '\n\n')
print("This is because a vast majority of vertebrate fossils are found incomplete. Just a single tooth or chunk of bone would still count as an occurrence as long as it" + '\n' + "is identifiable as T-rex with reasonable confidence. Considering T-rexes existed for 2 million years and regularly regenerated teeth, it makes sense that T-rex" + '\n' + "fossils are found relatively often.\n")
print("On the other hand, only a small percentage of fossils found end up in a paper and in the PBDB. Finds made by amateur collectors make up a majority of total \nfinds for many species, but almost never get recognized as an occurrence in the PBDB.")
print('-'*160)
heatmap(filter(occs, 'accepted_name', 'tyrannosaurus'), 'accepted_name', ['occurrence_no', 'formation.1', 'min_ma'], 6, 'Tyrannosaurus Rex Occurrences').show()
```

Additionally, even fossils that would be recognizable by name may not be recognizable as an occurrence. This map of T-rex occurrences shows 79 total occurrences. Are T-rexes that common?

This is because a vast majority of vertebrate fossils are found incomplete. Just a single tooth or chunk of bone would still count as an occurrence as long as it is identifiable as T-rex with reasonable confidence. Considering T-rexes existed for 2 million years and regularly regenerated teeth, it makes sense that T-rex fossils are found relatively often.

On the other hand, only a small percentage of fossils found end up in a paper and in the PBDB. Finds made by amateur collectors make up a majority of total finds for many species, but almost never get recognized as an occurrence in the PBDB.

Location-Specific Analysis

In []:

```
# tell user about what you can find around your area

local = {
    'lat': float(input("Enter Latitude: ")),
    'prx': float(input("Enter Search Radius (km): "))
}

if local['lat'] == 0:
    local['lat'], local['lng'] = 38.954503, -77.247611
elif local['lat'] == 1:
    local['lat'], local['lng'] = 40.729009, -73.995959
elif local['lat'] == 2:
    local['lat'], local['lng'] = 43.058888, -76.031289
else:
    local['lng'] = float(input("Enter Longitude: "))

proximity = distances(occs, local['lat'], local['lng'], local['prx'])

print('-'*120)
print('Search Report Summary')
print('The search returned ' + str(len(proximity)) + ' occurrences within ' + str(local['prx']) + ' kilometers of ' + str(local['lat']) + ', ' + str(local['lng']) + '.')
usa_occ_score, y_occ_score = round(100*409217/3797000,2), round(100*len(proximity)/spherical_sector_area(local['prx']),2)
print('Your search radius contains ' + str(y_occ_score) + ' occurrences per square km, which is ' + str(abs(round(100*y_occ_score / usa_occ_score) - 100)) + "% " + ('higher' if 100*y_occ_score / usa_occ_score > 100 else 'lower') + ' than the national average of ' + str(usa_occ_score) + '.')
print('The average age of occurrences within your search is',round(proximity['avg_ma'].mean(),2), 'million years.')
print('-'*120)
heatmap(proximity, 'accepted_name', ['occurrence_no', 'formation.1', 'min_ma'], 6, 'Nearby Fossil Occurences').show()
```

Enter Latitude: 0
Enter Search Radius (km): 100

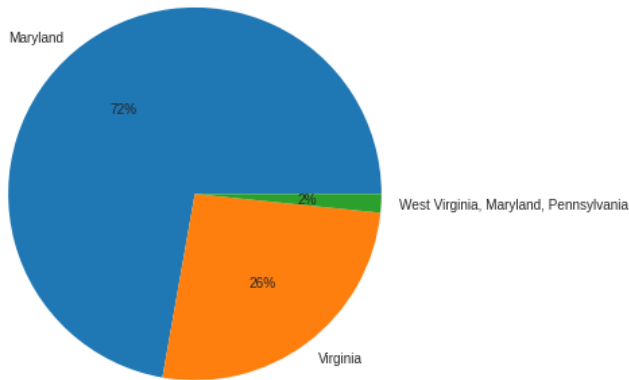
Search Report Summary

The search returned 5084 occurrences within 100.0 kilometers of 38.954503, -77.247611.
Your search radius contains 16.18 occurrences per square km, which is 50% higher than the national average of 10.78.
The average age of occurrences within your search is 89.09 million years.

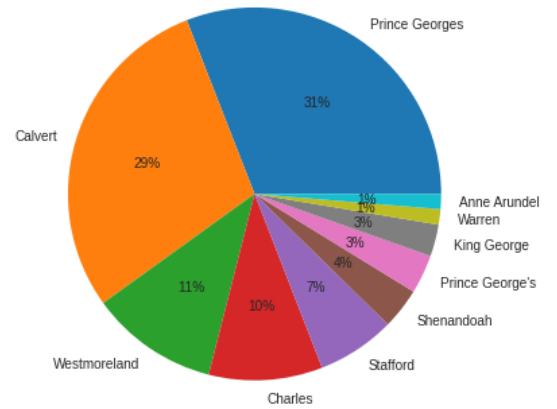
In []:

```
fig, ax = plt.subplots(2,2)
fig.set_figheight(14)
fig.set_figwidth(18)
fig.subplots_adjust(wspace=0.2)
ax[0,0].pie(proximity['state'].value_counts()[:3].rename_axis('state').to_frame('count')
['count'],labels=proximity['state'].value_counts()[:3].rename_axis('state').to_frame('count').index, autopct='%1.f%%')
ax[0,0].set_title('States with the most occurrences',size=20, fontweight = 'bold')
ax[0,1].pie(proximity['county'].value_counts()[:10].rename_axis('county').to_frame('count')
['count'],labels=proximity['county'].value_counts()[:10].rename_axis('county').to_frame('count').index, autopct='%1.f%%')
ax[0,1].set_title('Counties with the most occurrences',size=20, fontweight = 'bold')
ax[1,0].bar(proximity['accepted_name'].value_counts()[:10].rename_axis('accepted_name').to_frame('count').index, height=proximity['county'].value_counts()[:10].rename_axis('accepted_name').to_frame('count')['count'],)
ax[1,0].set_title('Commonly found species',size=20, fontweight = 'bold')
ax[1,0].set_xticklabels(proximity['accepted_name'].value_counts()[:10].rename_axis('accepted_name').to_frame('count').index, Rotation='60', ha="right")
ax[1,0].set_xlabel("Species",size=15, fontweight = 'bold')
ax[1,0].set_ylabel("No. of occurrences",size=15, fontweight = 'bold')
ax[1,1].hist(proximity['avg_ma'],bins=50)
ax[1,1].set_title('Distribution of average age of occurrences',size=20, fontweight = 'bold')
ax[1,1].set_xlabel("Age (in millions of years)",size=15, fontweight = 'bold')
ax[1,1].set_ylabel("No. of occurrences",size=15, fontweight = 'bold')
fig.show()
```

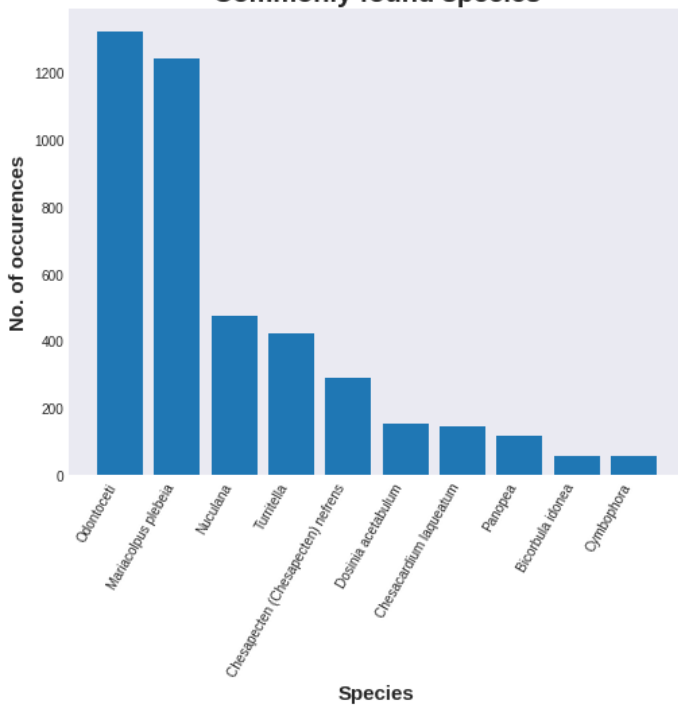
States with the most occurrences



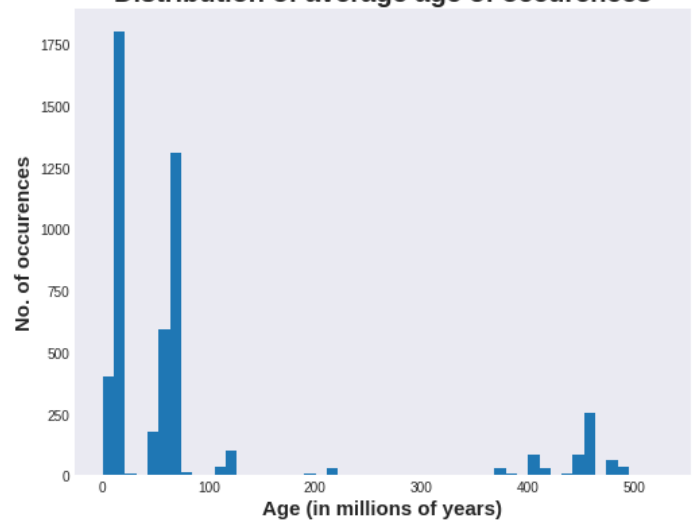
Counties with the most occurrences



Commonly found species



Distribution of average age of occurrences



In []:

```
# group, formation, member
group_age = proximity.groupby('stratgroup.1')['avg_ma'].mean().sort_values()
formation_age = proximity.groupby('formation.1')['avg_ma'].mean().sort_values()
member_age = proximity.groupby('member.1')['avg_ma'].mean().sort_values()
gmf = proximity.groupby(['stratgroup.1', 'formation.1', 'member.1', 'avg_ma']).mean()
gmf.drop(gmf.columns.difference(['lng', 'lat']), 1, inplace=True)
gmf_r = gmf.reset_index()
heatmap(gmf_r, 'member.1', ['avg_ma', 'formation.1', 'stratgroup.1'], 10, 'Estimated Location
of Members, Formations, and Groups').show()
gmf
```


Out[]:

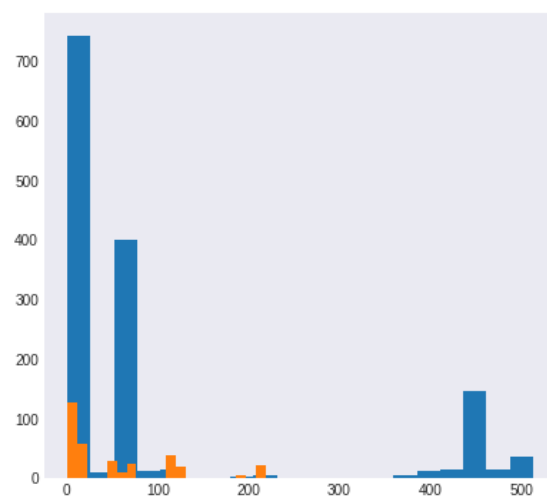
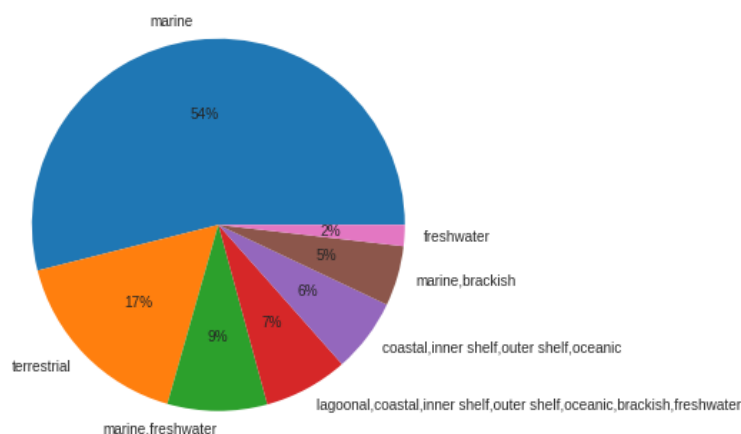
				lng	lat
stratgroup.1	formation.1	member.1	avg_ma		
Chatham	Bull Run	Balls Bluff	218.2500	-77.481913	38.883427
		Groveton	216.7500	-77.915054	38.439735
	Manassas Sandstone	Poolesville	218.2500	-77.455517	38.778140
Chesapeake	Calvert	Boston Cliffs	12.7200	-76.461945	38.450279
		Calvert Beach	12.7200	-76.513611	38.517502
			13.7890	-76.966942	38.180279
			14.8950	-76.710510	38.473481
		Conoy	12.7200	-76.461945	38.450279
		Drumcliff	12.7200	-76.471466	38.461135
		Fairhaven	18.2050	-76.782070	38.633863
		Little Cove Point	9.4330	-76.461945	38.450279
		Plum Point	12.7200	-76.500000	38.400002
			13.7890	-76.522408	38.638704
			14.8950	-76.686371	38.373145
			18.2050	-76.522915	38.627697
		Plum Point Marl	13.7890	-76.525722	38.645944
		Popes Creek Sand	18.2050	-76.726461	38.700186
	Choptank	Boston Cliffs	12.7200	-76.551573	38.411286
			13.7890	-76.505445	38.508456
		Conoy	12.7200	-76.478615	38.357224
		Drumcliff	12.7200	-76.508268	38.435260
			13.7890	-76.491818	38.396405
		St. Leonard	12.7200	-76.482498	38.471668
	Eastover	Claremont Manor	6.2895	-76.831112	38.163496
	St Mary's	Little Cove Point	8.4705	-76.387497	38.361389
	St Marys	Little Cove Point	9.4330	-76.387497	38.362778
Pamunkey	Aquia	Paspotansa	57.2500	-77.272084	38.318055
		Piscataway	57.2500	-77.299446	38.372780
			57.6000	-77.010399	38.743500
	Nanjemoy	Potapaco	52.2000	-77.265160	38.242618
		Woodstock	44.5500	-76.991669	38.407223

51.9000 -77.0152 38.3825

stratigraphic formation Bells Landing formation 51.9000 -76.54889 38.953056

In []:

```
fig, ax = plt.subplots(1,2)
fig.set_figheight(6)
fig.set_figwidth(18)
fig.subplots_adjust(wspace=0.8)
taxon_ages = proximity[['taxon_environment', 'avg_ma']].dropna()
ax[0].pie(proximity['taxon_environment'].value_counts()[7].rename_axis('taxon_environment').to_frame('count')['count'], labels=proximity['taxon_environment'].value_counts()[7].rename_axis('taxon_environment').to_frame('count').index, autopct='%1.f%%')
ax[1].hist(taxon_ages.loc[taxon_ages['taxon_environment'].str.contains('marine', na=False)]['avg_ma'], bins=20)
ax[1].hist(taxon_ages.loc[taxon_ages['taxon_environment'].str.contains('terr', na=False)]['avg_ma'], bins=20)
fig.show()
```



In []:

```
# track paleological location over time
paleopr = distances(occs, local['lat'], local['lng'], local['prx'] if input("Scale up search radius to increase accuracy? (Y/N) ") == 'N' else 300)
paleoloc = paleopr[['avg_ma', 'paleolat', 'paleolng']]
paleoloc['avg_ma'] = paleoloc['avg_ma'].round(0)
empty = pd.DataFrame(index=np.arange(528), columns=np.arange(0))
empty.reset_index(inplace=True)
empty.rename(columns={'index': 'avg_ma'}, inplace=True)
locs = pd.merge(paleoloc.groupby('avg_ma')['paleolat'].mean().sort_values(), paleoloc.groupby('avg_ma')['paleolng'].mean().sort_values(), how='inner', on='avg_ma')
paleoloc_ = pd.merge(empty, locs, how='left', on='avg_ma')
paleoloc_.sort_values('avg_ma', inplace=True)
paleoloc_['paleolat'] = paleoloc_['paleolat'].interpolate(method='spline', order=2)
paleoloc_['paleolng'] = paleoloc_['paleolng'].interpolate(method='spline', order=2)
heatmap(paleoloc_.rename(columns={'paleolat': 'lat', 'paleolng': 'lng'}), 'avg_ma', ['lat', 'lng'], 10, 'Track Your Geology Over Time').show()
```

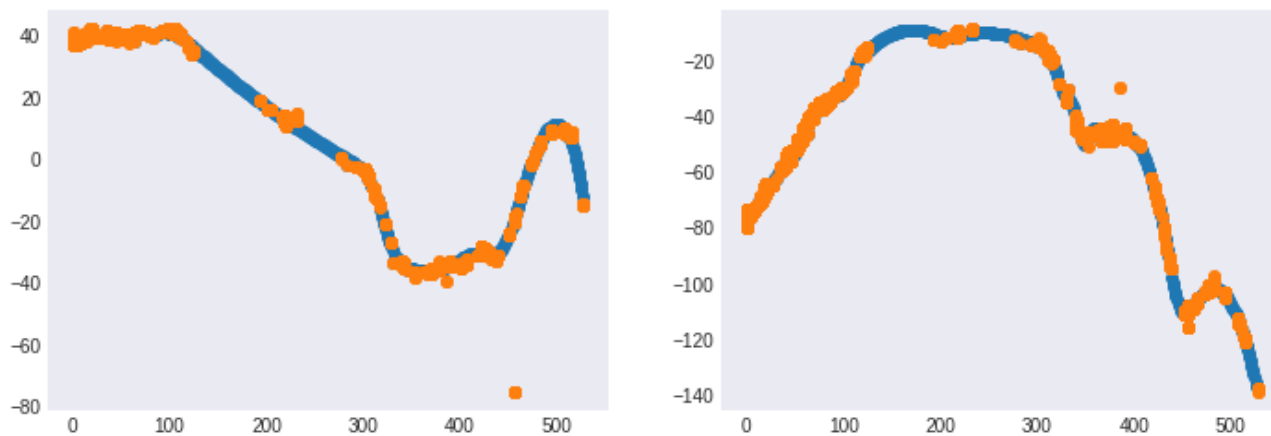
Scale up search radius to increase accuracy? (Y/N) Y

Tests

In []:

```
# Tests
print("Actual interpolation")
fig, ax = plt.subplots(1,2)
fig.set_figheight(4)
fig.set_figwidth(12)
ax[0].scatter(paleoloc_['avg_ma'], paleoloc_['paleolat'])
ax[0].scatter(paleoloc['avg_ma'], paleoloc['paleolat'])
ax[1].scatter(paleoloc_['avg_ma'], paleoloc_['paleolng'])
ax[1].scatter(paleoloc['avg_ma'], paleoloc['paleolng'])
fig.show()
```

Actual interpolation



In []:

```
# Heatmap using data before interpolation
heatmap(paleoloc.rename(columns={'paleolat': "lat", 'paleolng': "lng"}), 'avg_ma', ['lat', 'lng'], 10, 'Track Your Geology Over Time').show()
```

Occurence Search Tools

Search by species

In []:

```
heatmap(filter(occs, 'accepted_name', input('Enter specimen name: ')), 'accepted_name',  
         ['occurrence_no', 'formation.1', 'min_ma'], 6, 'Specimens Map').show()
```

Enter specimen name: trilobit

Search by state

In []:

```
heatmap(filter(occs, 'state', input('Enter state: ')), 'state', ['occurrence_no', 'formation.1', 'min_ma'], 6, 'Specimens Map').show()
```

Enter state: New York

Search by county

Visualizations

In []:

```
import requests
import io
import seaborn as sns
import matplotlib
import matplotlib.pyplot as plt
from math import radians, cos, sin, asin, sqrt
pd.options.mode.chained_assignment = None
```

In []:

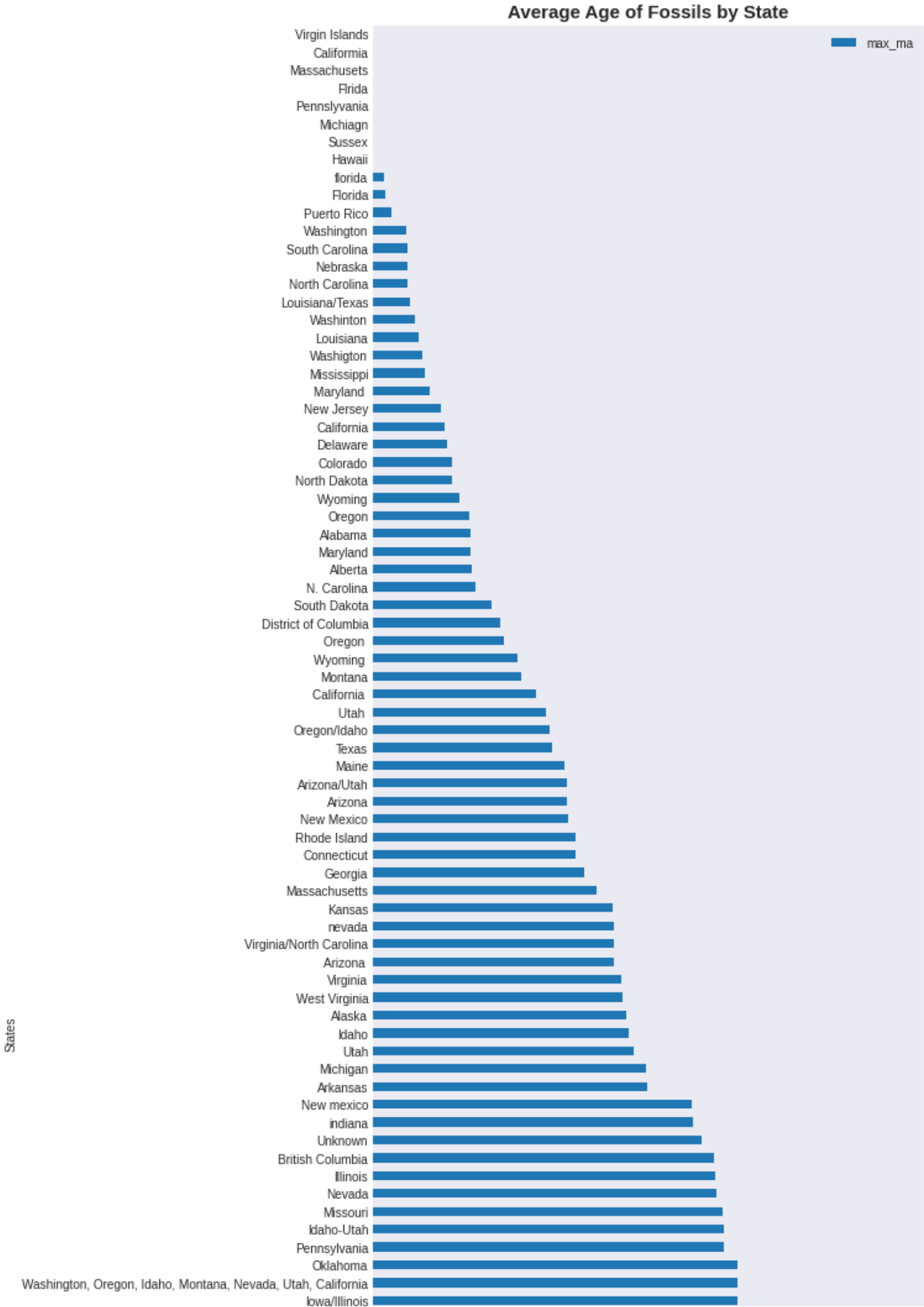
```
states = occs.loc[occs['cc'] == 'US']
states = states.groupby(['state'])['max_ma'].mean()
#We would like to see what states the oldest fossils would be located and where the young est are
#This could give us insights into the previous environments of the current states
states = pd.DataFrame(states)
states = states.sort_values(by='max_ma', ascending=False)
states = states.reset_index()
states = states[states.state != ('California', 'Flrida', 'Sussex', 'Michiagn', 'florida', 'Unknown', '')]
states = states.sort_values(by = 'max_ma', ascending = False)
states = states.set_index('state')
```

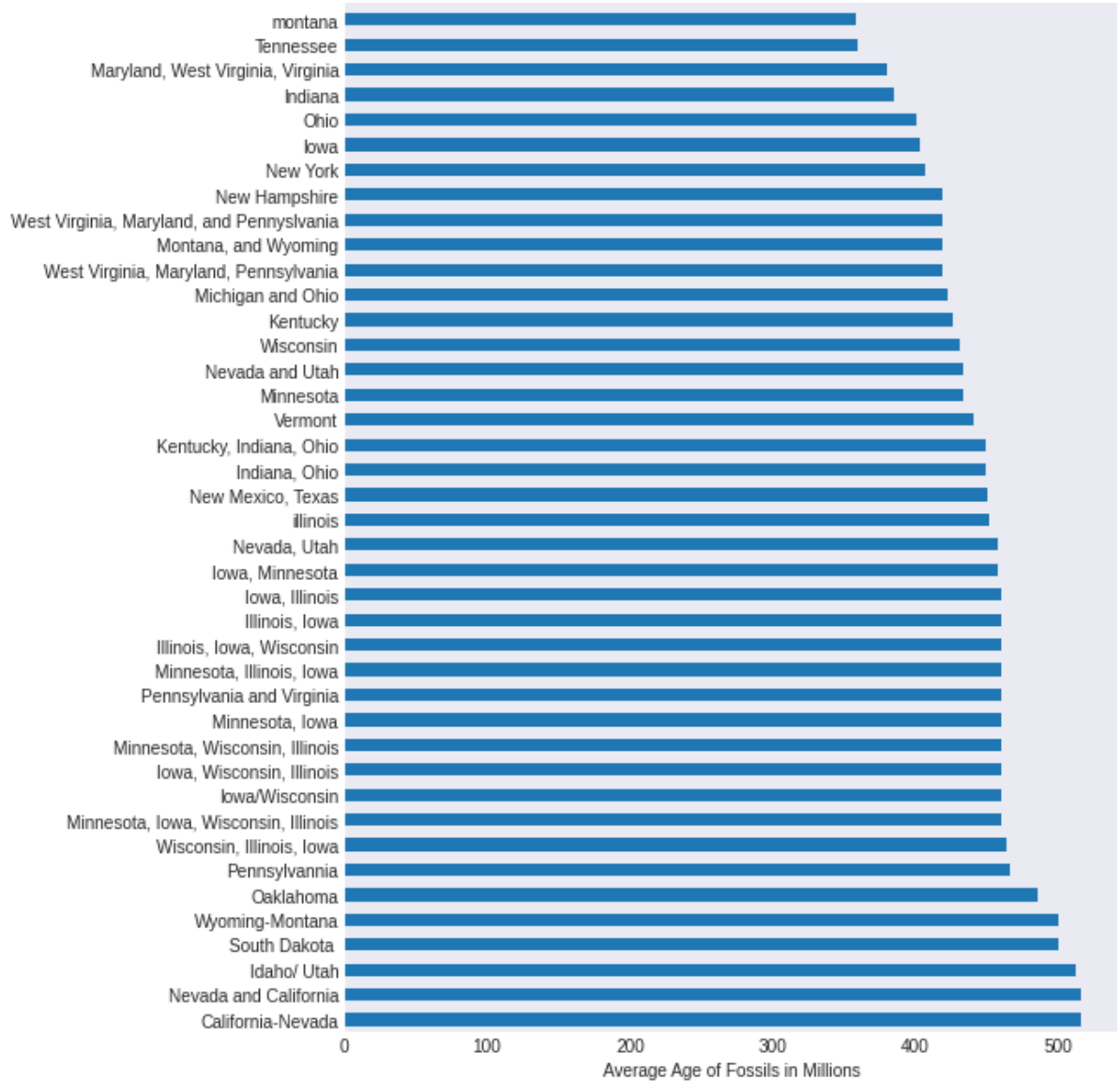
In []:

```
fig, ax = plt.subplots()
```

```
states.plot.barh(figsize = (8,30), ax=ax)
ax.set_title('Average Age of Fossils by State',size=15, fontweight = 'bold')
ax.set_ylabel('States')
ax.set_xlabel('Average Age of Fossils in Millions')
```

```
Out[ ]:
Text(0.5, 0, 'Average Age of Fossils in Millions')
```





In []:

```
rank = occs.groupby('identified_rank')['max_ma'].mean()
rank = pd.DataFrame(rank)
rank = rank.reset_index()
rank = rank.loc[(rank['identified_rank']).isin(['kingdom','phylum','class','order','family','genus','species'])]
rank = rank.reindex([6,8,0,7,1,2,9])
rank
```

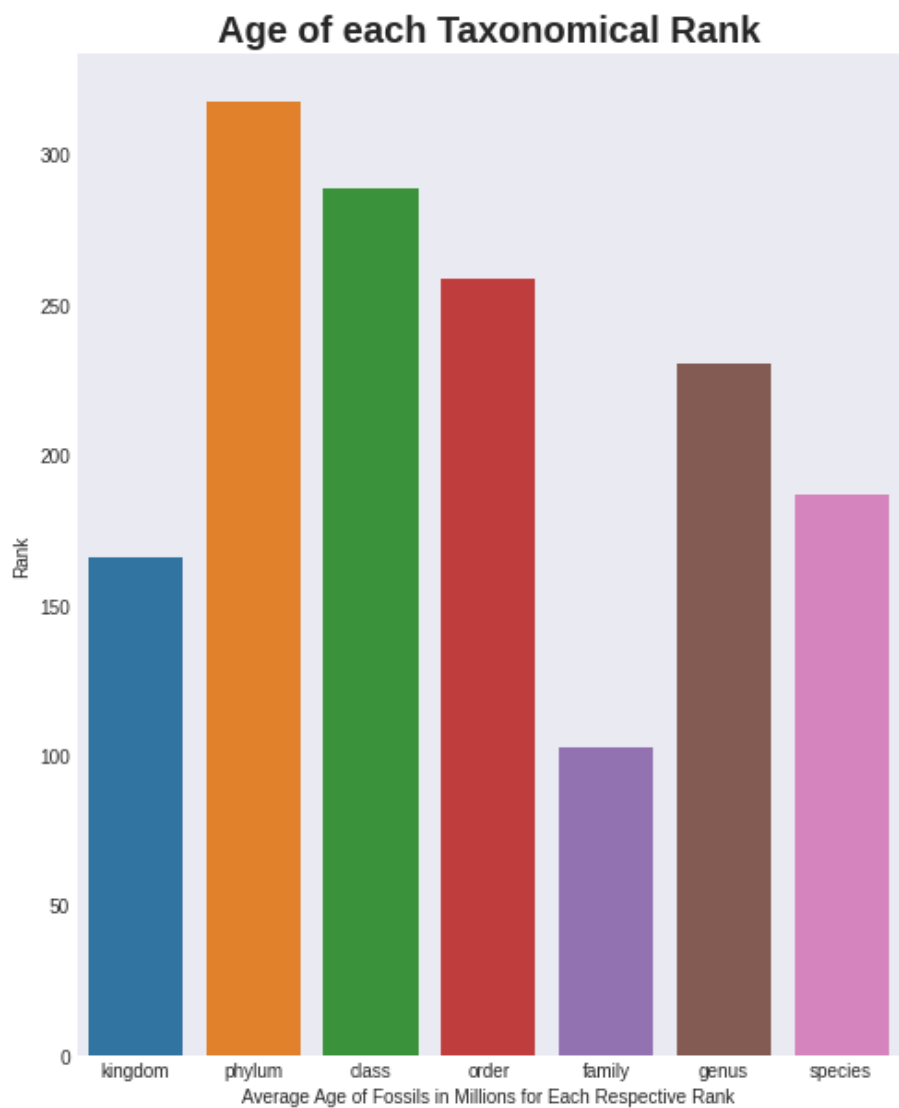
Out []:

	identified_rank	max_ma
6	kingdom	166.153996
8	phylum	318.027774
0	class	288.973864
7	order	258.718479
1	family	102.719258
2	genus	230.715823
9	species	187.043246

In []:

```
fig = plt.figure(figsize=(8,10))
sns.barplot(x='identified_rank', y='max_ma', data=rank)
plt.title('Age of each Taxonomical Rank', fontsize=20, fontweight= 'bold')
plt.ylabel('Rank')
plt.xlabel('Average Age of Fossils in Millions for Each Respective Rank')
```

```
Out[ ]:
Text(0.5, 0, 'Average Age of Fossils in Millions for Each Respective Rank')
```



```
In [ ]:
```