

Ultimate-final-project

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1 Final Project: Did the Domestic Dog Descend from the Grey Wolf?

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```
In [2]: from IPython.display import Image  
        Image(filename = '/home/eeb177-student/Desktop/eeb-177/eeb177-final-project')
```

Out [2]:



2 Abstract

The origin of the domestic dog has been a heated topic of controversy. Even though there is no doubt that the grey wolf and the domestic dog are closely related species, there is no definite

evidence to support the belief that the ancestor of dogs is a wolf. In this project, the genus *Canis* of the family *Canidae* will be studied in order to determine whether dogs (*Canis familiaris*) are truly descendants from the grey wolf (*Canis lupus*). Various graphs will be created using a dataset downloaded from the PaleoBiology Database to observe evolutionary trends and to ultimately determine whether the domestic dog may possibly be nested within the wolf species.

3 Introduction

The genus *Canis* consists of various extant species, including dogs, coyotes, and wolves. Characteristic of these species are their large, well-developed skulls, short ears and tails, long legs, and moderate to large size. Within the *Canis* genus, there is an ongoing debate between those who believe that the derivation of dogs from the grey wolf is primarily based on morphological and behavioral similarities, and those who claim that not enough evidence is present to clarify the lineage (Koler-Matznick 2002). In fact, it has also been suggested that domestic dogs may have descended from an ancestral pariah-like form that is distinct from wolves. Moreover, wolves may be too behaviorally aggressive and difficult to train, which calls for the unlikeliness for them to have evolved into a more domesticated species (Jhala & Sharma 2004). For this project, the *Canis familiaris* and *Canis lupus* species will be analyzed within the dataset from the PaleoBiology Database using the graphs generated to determine whether domestic dogs have truly evolved from grey wolves or if they are merely separate lineages within the *Canis* genus.

4 Methods and Figures

Different methods of visualizing the data will be utilized in order to conclude what type of evolutionary relationship is evident between the domestic dog and the grey wolf.

4.0.1 1. Explore the *Canis* dataset: list the unique species in the dataset.

There are a total of 87 unique species as seen from the output of this function. We also see that in this list, there are *Canis lupus* and *Canis familiaris*, the two species of interest, which confirms their presence in the dataset we are working with.

```
In [4]: #output name of species along with the rank "species."
def species_list(filename): #function species_list
    dog_species = {}
    ff = open(filename, "r", encoding = "ISO-8859-15")
    ss = ff.readlines()[3:] #read file from line 2
    for line in ss:
        line = line.split(",")
        name = line[5] #read 5th column
        rank = line[6] #read 6th column
        if rank == 'species':
            dog_species[name] = rank #matching name to rank
    return dog_species
species_list("my-final-formatted-dog.csv")

#87 unique species
```

```
Out[4]: {'Aenocyon ayersi': 'species',
'Aenocyon ayersi ?': 'species',
'Aenocyon cf. ayersi': 'species',
'Aenocyon cf. dirus': 'species',
'Aenocyon dirus': 'species',
'Canis (Xenocyon) falconeri': 'species',
'Canis ? latrans': 'species',
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'Canis edwardii': 'species',
'Canis etruscus': 'species',
'Canis ex gr. etruscus': 'species',
'Canis falconeri': 'species',
'Canis familiaris': 'species',
```

```

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'Canis kuruksaensis': 'species',
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'Pseudalopex gymnocercus': 'species',
'aff. Canis brevirostris': 'species',
'cf. Canis brevirostris': 'species',
'cf. Canis mesomelas': 'species',
'n. gen. Pachycyon n. sp. robustus': 'species'}

```

4.0.2 2. Making a dictionary that lists the number of occurrences

The output of this code presents a dictionary consisting of a list of occurrences and time periods for the different species in this dataset. We are interested in first having a broad view of the entire dataset and the occurrences of different species over time before we narrow down to work with only the two species of interest: *Canis lupus* and *Canis familiaris*.

```
In [10]: def makeCanisDict(filename): # creates a makeCanisDict function
        CanisDict = {} # empty CanisDict dictionary
        fobj = open(filename, "r", encoding = "ISO-8859-15") # opening the file
        all_records = fobj.readlines()[1:] # starting reading from line #1
        for line in all_records:
            line = line.strip().strip('\n') # skip empty lines
            record_elements = line.split(",") # split the lines
            occurrence = record_elements[0] # list the # of occurrences under
            species = record_elements[5] # list the different species under co
            time = record_elements[12] # list the different time periods under
            CanisDict[occurrence, time] = species # list occurrences, time per
        return CanisDict
makeCanisDict("my-final-formatted-dog.csv")
```

```
Out[10]: {('1003082', 'Holocene'): 'Canis familiaris',
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( '970676', 'Late Pleistocene'): 'cf. Canis mesomelas',
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( '970808', 'Pleistocene'): 'Canis cf. mesomelas',
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( 'occurrence_no', 'early_interval'): 'identified_name'}
```

4.0.3 3. Grepping out Canis familiaris species.

We are now narrowing down to Canis familiaris, grepping out only this species from the dataset to list its occurrences and time periods.

```
In [13]: Canis = makeCanisDict("my-final-formatted-dog.csv") # use dictionary from
occurrence = list(Canis.keys()) # list occurrences
Canis
{k:v for k,v in Canis.items() if 'familiaris' in v} # list names of species

Out[13]: {('1003082', 'Holocene'): 'Canis familiaris',
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('1310800', 'Holocene'): 'Canis familiaris',
('1314668', 'Holocene'): 'Canis familiaris',
('220528', 'Holocene'): 'Canis familiaris',
('382572', 'Quaternary'): 'Canis familiaris',
('662059', 'Holocene'): 'Canis familiaris',
('662312', 'Holocene'): 'Canis familiaris',
('834584', 'Holocene'): 'Canis familiaris',
('835238', 'Holocene'): 'Canis familiaris',
('919450', 'Holocene'): 'Canis familiaris'}
```

4.0.4 4. Grepping out Canis lupus species.

We are now narrowing down to Canis lupus, grepping out only this species from the dataset to list its occurrences and time periods.

```
In [14]: Canis = makeCanisDict("my-final-formatted-dog.csv") # use dictionary from
occurrence = list(Canis.keys()) # list occurrences
Canis
{k:v for k,v in Canis.items() if 'lupus' in v} # list names of species from

Out[14]: {('1196539', 'Late Pleistocene'): 'Canis cf. lupus',
('1197870', 'Late Pleistocene'): 'Canis lupus',
('1201222', 'Late Pleistocene'): 'Canis lupus',
('1230888', 'Holocene'): 'Canis lupus',
('1310775', 'Holocene'): 'Canis lupus',
('1350564', 'Pleistocene'): 'Canis lupus',
('1356828', 'Late Pleistocene'): 'Canis lupus',
('196953', 'Irvingtonian'): 'Canis lupus',
('197489', 'Irvingtonian'): 'Canis lupus',
('198253', 'Irvingtonian'): 'Canis cf. lupus',
('199069', 'Irvingtonian'): 'Canis lupus',
('199393', 'Late Pleistocene'): 'Canis cf. lupus',
('199487', 'Late Pleistocene'): 'Canis lupus',
('199643', 'Late Pleistocene'): 'Canis lupus',
('199750', 'Late Pleistocene'): 'Canis lupus',
('358468', 'Pleistocene'): 'Canis lupus',
('358553', 'Pleistocene'): 'Canis lupus',
('367573', 'Early Pleistocene'): 'Canis lupus',
('367963', 'Early Pleistocene'): 'Canis lupus',
('369203', 'Middle Pleistocene'): 'Canis lupus',
('369226', 'Middle Pleistocene'): 'Canis lupus',
('374162', 'Villanyian'): 'Canis lupus',
('375514', 'Early Pleistocene'): 'Canis lupus',
('379666', 'Early Pleistocene'): 'Canis lupus',
('380822', 'Middle Pleistocene'): 'Canis cf. lupus',
('381189', 'Middle Pleistocene'): 'Canis lupus',
('381231', 'Pleistocene'): 'Canis lupus',
('381395', 'Middle Pleistocene'): 'Canis lupus',
('381462', 'Middle Pleistocene'): 'Canis lupus',
('381496', 'Middle Pleistocene'): 'Canis lupus',
('398243', 'Pleistocene'): 'Canis cf. lupus',
('408440', 'Pleistocene'): 'Canis lupus',
('417541', 'Middle Pleistocene'): 'Canis lupus',
('420015', 'Middle Pleistocene'): 'Canis lupus',
('440026', 'Middle Pleistocene'): 'Canis lupus',
('442555', 'Middle Pleistocene'): 'Canis lupus',
('442574', 'Late Pleistocene'): 'Canis lupus',
('442635', 'Late Pleistocene'): 'Canis lupus',
('442664', 'Late Pleistocene'): 'Canis lupus',
```

('442682', 'Late Pleistocene'): 'Canis lupus',
 ('442712', 'Late Pleistocene'): 'Canis lupus',
 ('442908', 'Early Pleistocene'): 'Canis lupus',
 ('443152', 'Middle Pleistocene'): 'Canis lupus',
 ('443180', 'Middle Pleistocene'): 'Canis lupus',
 ('443190', 'Middle Pleistocene'): 'Canis lupus',
 ('443238', 'Middle Pleistocene'): 'Canis lupus',
 ('443254', 'Middle Pleistocene'): 'Canis lupus',
 ('443315', 'Pleistocene'): 'Canis lupus',
 ('443400', 'Middle Pleistocene'): 'Canis lupus',
 ('443582', 'Late Pleistocene'): 'Canis lupus',
 ('443685', 'Middle Pleistocene'): 'Canis cf. lupus',
 ('443733', 'Middle Pleistocene'): 'Canis lupus',
 ('447654', 'Middle Pleistocene'): 'Canis cf. lupus',
 ('447692', 'Pleistocene'): 'Canis lupus',
 ('485282', 'Late Pleistocene'): 'Canis lupus',
 ('488520', 'Middle Pleistocene'): 'Canis lupus',
 ('493158', 'Middle Pleistocene'): 'Canis lupus',
 ('493203', 'Middle Pleistocene'): 'Canis lupus',
 ('494704', 'Middle Pleistocene'): 'Canis lupus',
 ('497012', 'Middle Pleistocene'): 'Canis lupus',
 ('497081', 'Middle Pleistocene'): 'Canis lupus',
 ('497120', 'Middle Pleistocene'): 'Canis lupus',
 ('497444', 'Pleistocene'): 'Canis lupus',
 ('497510', 'Middle Pleistocene'): 'Canis lupus',
 ('497635', 'Middle Pleistocene'): 'Canis lupus',
 ('497675', 'Middle Pleistocene'): 'Canis lupus',
 ('498812', 'Early Pleistocene'): 'Canis lupus',
 ('502572', 'Middle Pleistocene'): 'Canis lupus',
 ('536650', 'Holocene'): 'Canis lupus',
 ('565629', 'Holocene'): 'Canis lupus',
 ('684223', 'Middle Pleistocene'): 'Canis lupus',
 ('713685', 'Late Pliocene'): 'Canis aff. lupus',
 ('740001', 'Late Pleistocene'): 'Canis lupus',
 ('819173', 'Late Pleistocene'): 'Canis lupus',
 ('839054', 'Late Pleistocene'): 'Canis cf. lupus',
 ('839986', 'Late Pleistocene'): 'Canis lupus',
 ('840115', 'Late Pleistocene'): 'Canis lupus',
 ('841539', 'Late Pleistocene'): 'Canis lupus',
 ('841710', 'Late Pleistocene'): 'Canis cf. lupus',
 ('841734', 'Late Pleistocene'): 'Canis lupus',
 ('841749', 'Late Pleistocene'): 'Canis lupus',
 ('841978', 'Late Pleistocene'): 'Canis cf. lupus',
 ('847926', 'Early Pleistocene'): 'Canis lupus',
 ('906500', 'Late Pleistocene'): 'Canis lupus',
 ('906526', 'Late Pleistocene'): 'Canis lupus',
 ('906585', 'Late Pleistocene'): 'Canis lupus',
 ('919540', 'Late Pleistocene'): 'Canis lupus',

```

('934378', 'Late Pleistocene'): 'Canis cf. lupus',
('935492', 'Late Pleistocene'): 'Canis lupus',
('938097', 'Late Pleistocene'): 'Canis lupus',
('973715', 'Late Pleistocene'): 'Canis cf. lupus'}

```

4.0.5 5. Create a bar chart that visualizes the number of occurrences of *Canis lupus* and *Canis familiaris* for the different time periods for easier comparison.

```

In [32]: import numpy as np
import matplotlib.pyplot as plt

N = 5
ind = np.arange(N)
width = 0.27
fig = plt.figure()
ax = fig.add_subplot(111)

familiaris = [12851036, 1196938, 382572, 0, 0]
rects1 = ax.bar(ind, familiaris, width, color='yellow')
lupus = [3643942, 24952241, 17148387, 3280362, 1879611]

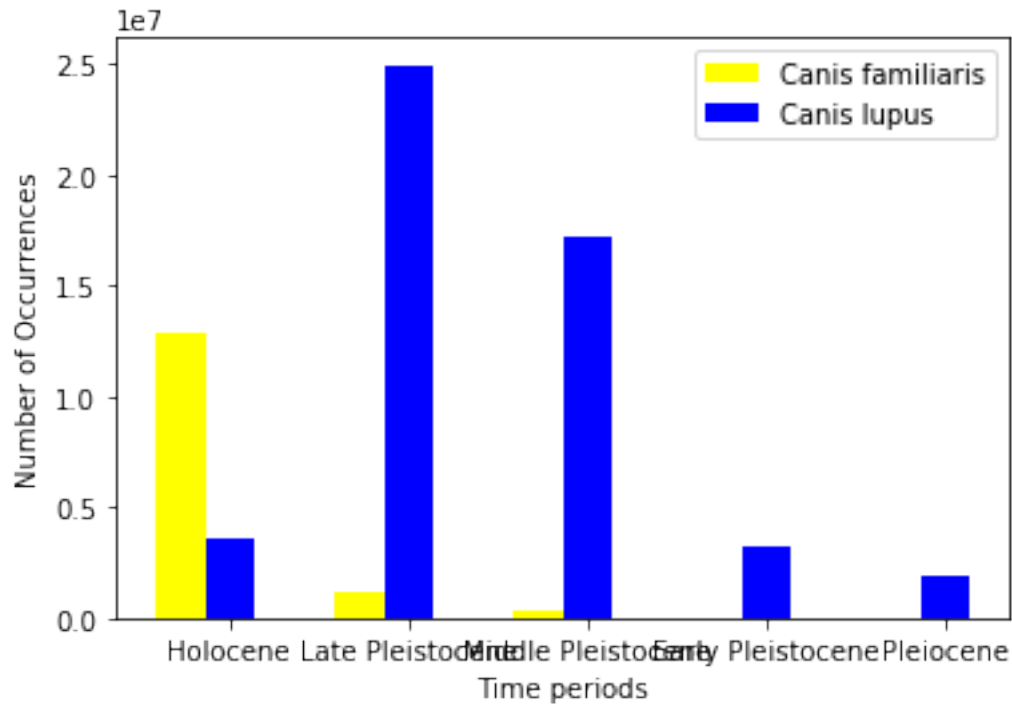
rects2 = ax.bar(ind+width, lupus, width, color='blue')

ax.set_ylabel('Number of Occurrences')
ax.set_xticks(ind+width)
ax.set_xticklabels( ('Holocene', 'Late Pleistocene', 'Middle Pleistocene',
ax.set_xlabel('Time periods')
ax.legend( ('Canis familiaris', 'Canis lupus') )

plt.show()

<matplotlib.figure.Figure at 0x7f4ec2f84c88>

```



This outputted bar graph presents the number of occurrences for the geographic time scale from most recent (Holocene) to oldest (Pleiocene). *Canis lupus* is clearly the older species when comparing *Canis familiaris* and *Canis lupus*, which may hint towards *Canis familiaris* being a descendant of *Canis lupus*. *Canis lupus* is most prominent during the Late Pleistocene era before it drops in the Holocene era. On the other hand, *Canis familiaris* is first seen in the Late Pleistocene period and is more prominent in the more recent period (Holocene period).

4.0.6 6. Make a list of time periods along with their first and last occurrences.

The function outputs a list of first and last occurrences using the min and max ages for the various species. This will be useful in creating the R plot later on for the various species in this genus. We can use this data to get a general idea of what the species occurrences are over the different geologic time periods.

```
In [2]: def Min_ma(filename):
        minage_dict = {}
        species_data = open(filename, "r", encoding = "ISO-8859-15")
        minage_records = species_data.readlines()[3:]
        for line in minage_records:
            line = line.replace('\\"', '')
            minage_elements = line.split(",")
            time = minage_elements[12] #read column 5
            starting_period = float(minage_elements[14]) #read column 14
            minage_dict[time] = starting_period
        return minage_dict
```



```
fo_dict = Min_ma("my-final-formatted-dog.csv") #list species names with fil
fo_dict
```

```
Out[2]: {'Blancan': 4.9,
        'Calabrian': 1.806,
        'Early Pleistocene': 2.588,
        'Early Pliocene': 5.333,
        'Gelasian': 2.588,
        'Hemphillian': 10.3,
        'Holocene': 0.0117,
        'Irvingtonian': 1.8,
        'Late Hemphillian': 10.3,
        'Late Miocene': 11.608,
        'Late Pleistocene': 0.126,
        'Late Pliocene': 3.6,
        'Lujanian': 0.781,
        'MN 14': 4.9,
        'MN 15': 4.2,
        'MN 16': 3.2,
        'MN 17': 2.588,
        'Messinian': 7.246,
        'Middle Pleistocene': 0.781,
        'Miocene': 23.03,
        'Neogene': 23.03,
        'Piacenzian': 3.6,
        'Pleistocene': 2.588,
        'Pliocene': 5.333,
        'Quaternary': 2.588,
        'Rancholabrean': 0.3,
        'Ruscinian': 5.333,
        'Turolian': 8.7,
        'Villanyian': 3.2,
        'Zanclean': 5.333}
```

```
In [3]: def Min_ma(filename):
        minage_dict = {}
        species_data = open(filename, "r", encoding = "ISO-8859-15")
        minage_records = species_data.readlines()[3:]
        for line in minage_records:
            line = line.replace('\\"', '')
            minage_elements = line.split(",")
            time = minage_elements[12] #read column 5
            starting_period = float(minage_elements[15]) #read column 14
            minage_dict[time] = starting_period
        return minage_dict
```

```
lo_dict = Min_ma("my-final-formatted-dog.csv") #list species names with fil
lo_dict
```

```

Out[3]: {'Blancan': 1.8,
        'Calabrian': 0.781,
        'Early Pleistocene': 0.781,
        'Early Pliocene': 3.6,
        'Gelasian': 0.781,
        'Hemphillian': 4.9,
        'Holocene': 0.0,
        'Irvingtonian': 0.3,
        'Late Hemphillian': 4.9,
        'Late Miocene': 0.781,
        'Late Pleistocene': 0.0117,
        'Late Pliocene': 2.588,
        'Lujanian': 0.012,
        'MN 14': 4.2,
        'MN 15': 2.588,
        'MN 16': 2.588,
        'MN 17': 1.806,
        'Messinian': 2.588,
        'Middle Pleistocene': 0.126,
        'Miocene': 5.333,
        'Neogene': 2.588,
        'Piacenzian': 2.588,
        'Pleistocene': 0.0117,
        'Pliocene': 2.588,
        'Quaternary': 0.0,
        'Rancholabrean': 0.012,
        'Ruscinian': 3.2,
        'Turolian': 5.333,
        'Villanyian': 2.588,
        'Zanclean': 3.6}

```

```

In [4]: # Combine the first and last occurrences of the species into one dictionary
from collections import defaultdict

firstandlast_dict = defaultdict(list) # Make a list for the items in the dict

for d in (fo_dict, lo_dict):
    for key, value in d.items():
        firstandlast_dict[key].append(value) # Add both first and last values

firstandlast_dict # Output combined dictionary

```

```

Out[4]: defaultdict(list,
                    {'Blancan': [4.9, 1.8],
                     'Calabrian': [1.806, 0.781],
                     'Early Pleistocene': [2.588, 0.781],
                     'Early Pliocene': [5.333, 3.6],
                     'Gelasian': [2.588, 0.781],

```

```

'Hemphillian': [10.3, 4.9],
'Holocene': [0.0117, 0.0],
'Irvingtonian': [1.8, 0.3],
'Late Hemphillian': [10.3, 4.9],
'Late Miocene': [11.608, 0.781],
'Late Pleistocene': [0.126, 0.0117],
'Late Pliocene': [3.6, 2.588],
'Lujanian': [0.781, 0.012],
'MN 14': [4.9, 4.2],
'MN 15': [4.2, 2.588],
'MN 16': [3.2, 2.588],
'MN 17': [2.588, 1.806],
'Messinian': [7.246, 2.588],
'Middle Pleistocene': [0.781, 0.126],
'Miocene': [23.03, 5.333],
'Neogene': [23.03, 2.588],
'Piacenzian': [3.6, 2.588],
'Pleistocene': [2.588, 0.0117],
'Pliocene': [5.333, 2.588],
'Quaternary': [2.588, 0.0],
'Rancholabrean': [0.3, 0.012],
'Ruscinian': [5.333, 3.2],
'Turolian': [8.7, 5.333],
'Villanyian': [3.2, 2.588],
'Zanclean': [5.333, 3.6]})

```

4.0.7 7. Generate a graph using Rstudio to present a broad view of all fossil occurrences of species within the Canis genus.

```

In [33]: #library(ggplot2)
         #setwd("/home/eeb177-student/Desktop/eeb-177/eeb177-final-project/")
         #canis <- read.csv("/home/eeb177-student/Desktop/eeb-177/eeb177-final-project/canis.csv")
         #names(canis) <- c("genus", "species", "minage", "maxage")
         #head(canis)

         #canis_occ <- ggplot(canis, aes(species, ymin =maxage, ymax=minage), color=genus)
         #canis_occ <- canis_occ + geom_linerange()
         #canis_occ <- canis_occ + theme(legend.position = "none")
         #canis_occ <- canis_occ + coord_flip()
         #canis_occ <- canis_occ + theme(axis.text.y = element_text(size=4.5))
         #canis_occ <- canis_occ + theme(axis.ticks.y=element_blank())
         #canis_occ <- canis_occ + scale_y_continuous(limits=c(0,10),expand=c(0,0))
         #canis_occ <- canis_occ + labs(title="Canis Fossil Occurrences",x="Species")
         #canis_occ

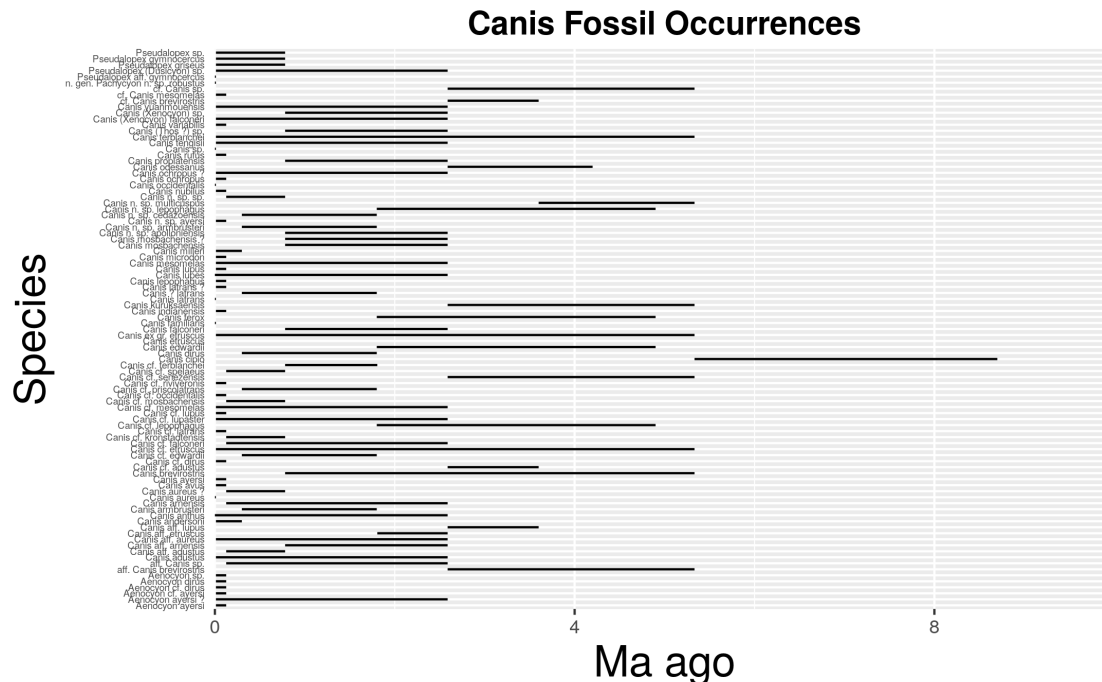
```

```

In [1]: from IPython.display import Image
        Image(filename = '/home/eeb177-student/Desktop/eeb-177/eeb177-final-project/canis_occ.png')

```

Out[1]:



This R plot presents all the species in the canis genus, along with their occurrences over time. The dataset used to make this R plot is different from the one used in class, as the class example used the entire Canidae dataset from the PaleoBio database, whereas the dataset I used for this project grepped only the Canis species within the Canis genus, excluding all the other genres within Canidae. Most of the species as seen in this plot are extant species, which makes sense considering that Canis is one of the more recent genres of the Canidae family. Moreover, a lot of the species have wide ranges, including Canis etruschus that ranges from 0 to about 4.5 Ma which has the largest range in terms of occurrences.

4.0.8 8. Generate a graph to show the different Canis fossil occurrences over time periods, not species.

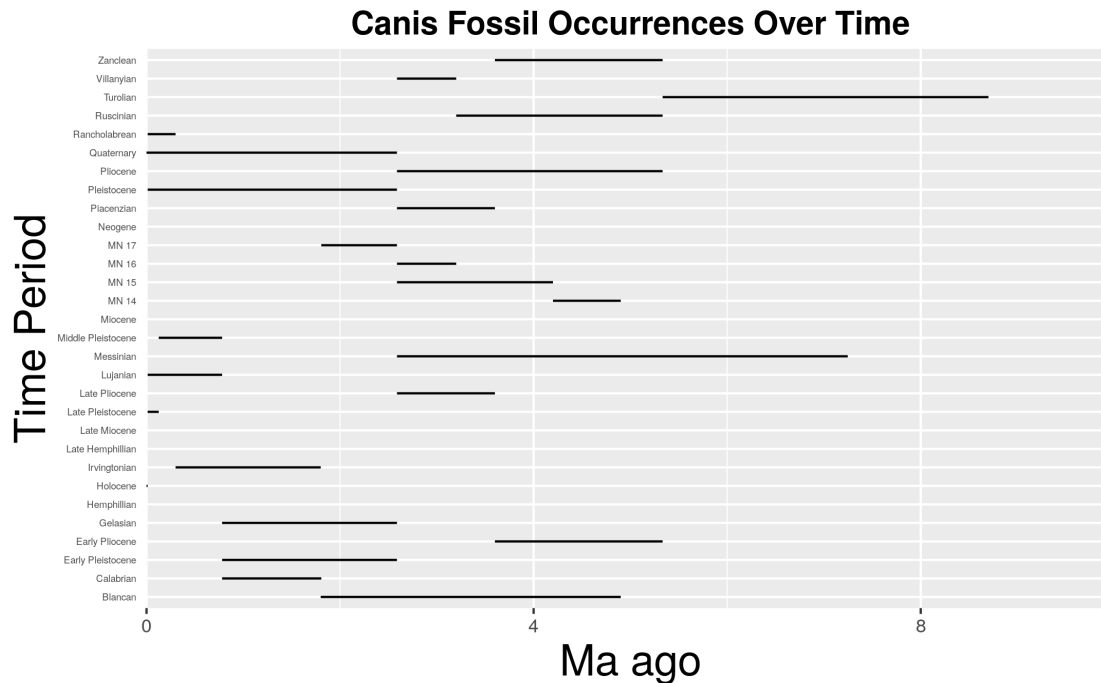
```
In [ ]: #library(ggplot2)
#setwd("/home/eeb177-student/Desktop/eeb-177/eeb177-final-project/")
#canis <- read.csv("/home/eeb177-student/Desktop/eeb-177/eeb177-final-project/canis.csv")
#names(canis) <- c("timeperiod", "minage", "maxage")
#head(canis)

#canis_occ <- ggplot(canis, aes(timeperiod, ymin =maxage, ymax=minage), col = "timeperiod")
#canis_occ <- canis_occ + geom_linerange()
#canis_occ <- canis_occ + theme(legend.position = "none")
#canis_occ <- canis_occ + coord_flip()
#canis_occ <- canis_occ + theme(axis.text.y = element_text(size=4.5))
#canis_occ <- canis_occ + theme(axis.ticks.y=element_blank())
#canis_occ <- canis_occ + scale_y_continuous(limits=c(0,10),expand=c(0,0),breaks=c(0,2,4,6,8,10))
```

```
#canis_occ <- canis_occ + labs(title="Canis Fossil Occurrences",x="Time Period")
#canis_occ
```

```
In [2]: from IPython.display import Image
Image(filename = '/home/eeb177-student/Desktop/eeb-177/eeb177-final-project')
```

Out [2]:



This R graph presents the time periods rather than species for the various occurrences, which shows that Blancan, Pleistocene, and Quaternary periods seem to be the more prominent in terms of number of occurrences. This shows that most species are from these time periods, including *Canis familiaris* and *Canis lupus* which are found mostly in the Pleistocene and Quaternary periods.

4.0.9 9. Generate a graph to show *Canis familiaris* and *Canis lupus* fossil occurrences over different time periods.

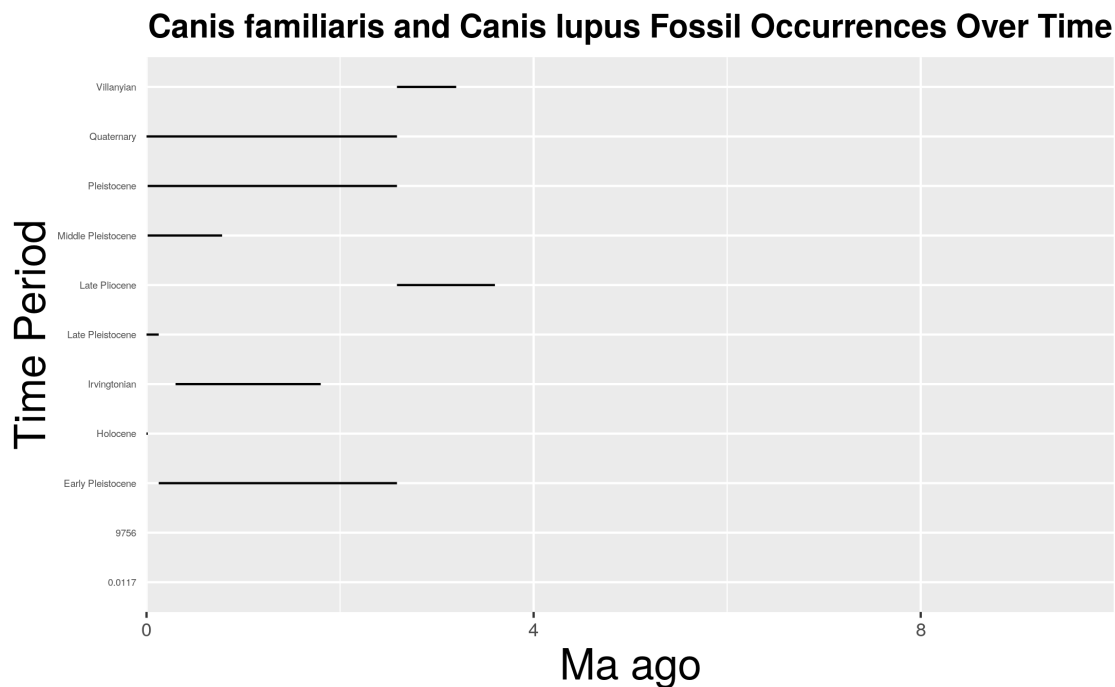
```
In [ ]: #library(ggplot2)
#setwd("/home/eeb177-student/Desktop/eeb-177/eeb177-final-project/")
#canis <- read.csv("/home/eeb177-student/Desktop/eeb-177/eeb177-final-project/canis.csv")
#names(canis) <- c("timeperiod", "minage", "maxage")
#head(canis)

#canis_occ2 <- ggplot(canis, aes(species, ymin =maxage, ymax=minage), color = species)
#canis_occ2 <- canis_occ2 + geom_linerange()
#canis_occ2 <- canis_occ2 + theme(legend.position = "none")
```

```
#canis_occ2 <- canis_occ2 + coord_flip()
#canis_occ2 <- canis_occ2 + theme(axis.text.y = element_text(size=4.5))
#canis_occ2 <- canis_occ2 + theme(axis.ticks.y=element_blank())
#canis_occ2 <- canis_occ2 + scale_y_continuous(limits=c(0,10),expand=c(0,0))
#canis_occ2 <- canis_occ2 + labs(title="Canis Fossil Occurrences",x="Time B")
#canis_occ2
```

In [1]: `from IPython.display import Image`
`Image(filename = '/home/eeb177-student/Desktop/eeb-177/eeb177-final-project')`

Out [1]:



The Holocene and Quaternary periods correspond to the *Canis familiaris* species while the rest are present for the *Canis lupus* species. This shows that *Canis lupus* is more prominent in the older time periods, especially the Pleistocene eras and *Canis familiaris* are from the more recent time periods and not as prominent, which may hint that *Canis familiaris* may have descended from *Canis lupus*, the older of the two species.

5 Conclusion

Based on the different types of evidence presented, it is clear that *Canis familiaris* and *Canis lupus* are two species that clearly have a close relationship between them. According to Manwell, C. & Baker 1983, the origin of the dog may have been most likely from the *Canis lupus*, the grey wolf, because of the geologic time scale trend, shown in the R graphs above that present the *Canis lupus* as the older of the two species and *Canis familiaris* the more recent. When *Canis lupus* became less prominent in the Holocene era, *Canis familiaris* became more apparent, which most

likely show that it may have descended from the grey wolf, merely due to this evolutionary trend. However, there is no definite conclusion, as simply looking at evolutionary trends may not be enough evidence to state for sure whether or not *Canis familiaris* has descended from the *Canis lupus* or whether they are independent lineages that are just closely related. Therefore, further research needs to be conducted, taking into consideration DNA evidence to come to a conclusion on this topic.

6 References

1. Koler-Matznick, J. 2002. "The origin of the dog revisited". *Anthrozoos* 15, 98-118.
2. Jhala, Y. & Sharma, D.K. 2004. "The ancient wolves of India". *International Wolf Summer* 2004, 15-16.
3. Dobney, K. & Larson, G. 2006. "Genetics and animal domestication: new windows on an elusive process". *Journal of Zoology* 269, 261-271.
4. Manwell, C. & Baker, C.M.A. 1983. "Origin of the dog: from wolf or wild *Canis familiaris*?" *Speculations in Science and Technology* 6, 213-224.

In []: