

Paleobiogeography of crown deer

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Table S3. Biostratigraphic and zoogeographic distribution of deer from the Late Miocene to the Late Pleitocene and their body mass diversity: data processing and visualisation (Python 3).


```
In [1]: import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
import warnings
warnings.simplefilter("ignore")
```

```
In [2]: deer_geo = pd.read_excel('deer distribution2.xlsx')
```

```
In [3]: deer_geo.head()
```

Out[3]:

	species	synonym	subfamily	site	zone MN	period	realm	source	body mass	source
0	gen. et sp. indet. 1	"Muntiacinae"	Capreolinae	Creventille- 2	MN11	Late Miocene	Western Palearctic	Azanza (2000)	15.0	tl stu
1	Lucentia iberica	NaN	Capreolinae	Creventille- 2	MN11	Late Miocene	Western Palearctic	Azanza (2000)	27.5	tl stu
2	Lucentia pierensis	Eostyloceros pierensis	Capreolinae	Piera	MN11	Late Miocene	Western Palearctic	Azanza (2000)	53.0	tl stu
3	Turiacemas concudensis	NaN	Capreolinae	Concud-3	MN12	Late Miocene	Western Palearctic	Azanza (2000)	47.0	tl stu
4	Procapreolus sp. 1	Pliocervus aff. matheroni	Capreolinae	El Arquillo	MN13	Late Miocene	Western Palearctic	Azanza (2000)	35.0	tl stu



```
In [4]: deer_geo['species'].nunique()
```

Out[4]: 204

Comment: the database includes 204 accepted deer species and cervid forms that likely are undescribed true species.

Deer species of the subfamily Cervinae selected:

```
In [5]: cervinae = deer_geo.loc[deer_geo['subfamily'] == 'Cervinae']
```

```
In [6]: cervinae.head()
```

Out[6]:

	species	synonym	subfamily	site	zone MN	period	realm	source	body mass	sc
23	Eocervinus ruscinensis	Cervus ruscinensis	Cervinae	Mas Belrich, Vlleneuve- La-Raho	MN14	Early Pliocene	Western Palearctic	Deperet (1890)	50.0	
24	Metacervocerus pardinensis	Cervus pardinensis	Cervinae	Perrier- Etouaires	MN16	Late Pliocene	Western Palearctic	Heintz (1970)	85.0	
25	Praeclaphus perrieri	Cervus perrieri	Cervinae	Perrier- Etouaires	MN16	Late Pliocene	Western Palearctic	Heintz (1970)	180.0	
26	Rucervus ardei	Arvernoceros ardei	Cervinae	Perrier- Etouaires	MN16	Late Pliocene	Western Palearctic	Heintz (1970)	180.0	
27	Metacervocerus rhenanus	Cervus philisi	Cervinae	Seneze	MN17	Early Pleistocene	Western Palearctic	Heintz (1970)	70.0	

The records of Cervinae are grouped by species with a calculation of mean body size for species:

In [7]:

```
cervinae_group_species = cervinae.groupby('species').mean()
```

Comment: the calculation of predicted mean body size is needed since the predicted body masses of fossil species from different sub-epochs may be not the same according to the available craniodental variables.

The obtained result is a mean body mass for each Cervinae species in case if there are different body mass estimations in different sub-epochs:

In [8]:

```
cervinae_group_species.head()
```

Out[8]:

	body mass
species	
"Muntiacus" minor	36.300000
Axis axis	70.266667
Axis fenqii	95.000000
Axis flerovi	170.000000
Axis javanicus	40.000000

The records of representatives of the subfamily Capreolinae selected:

In [9]:

```
capreolinae = deer_geo.loc[deer_geo['subfamily'] == 'Capreolinae']
```

The records of Capreolinae grouped by species:

```
In [10]: capreolinae_group_species = capreolinae.groupby('species').mean()
```

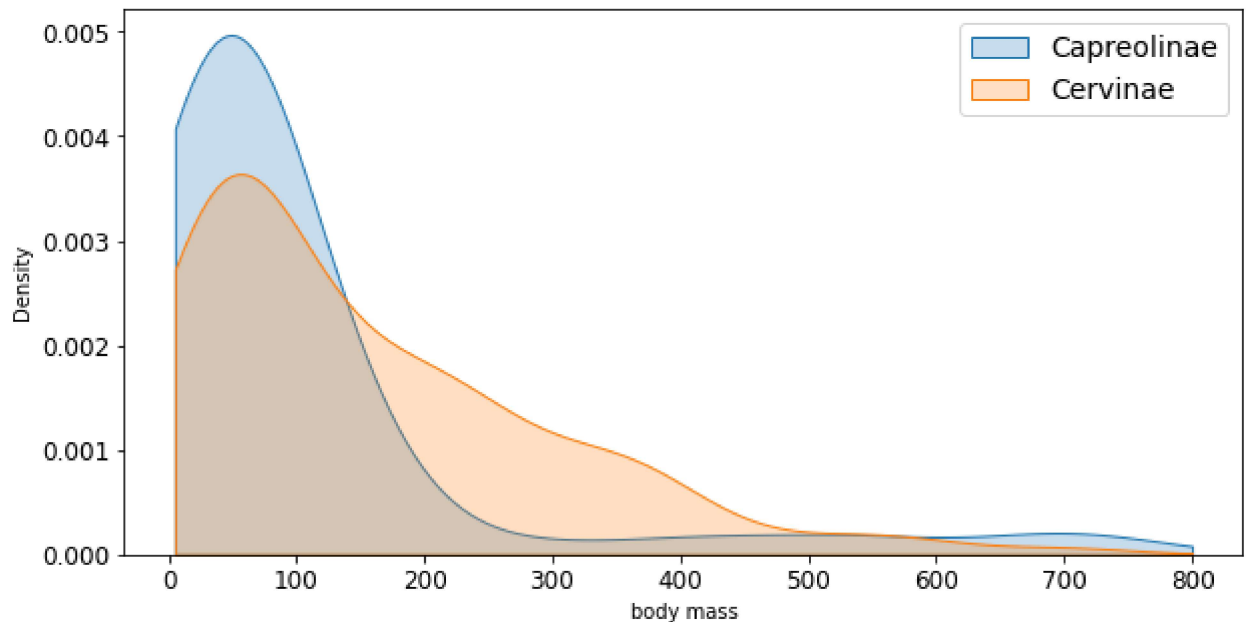
The obtained data plotted in order to visualize the species body mass distribution within the subfamilies Capreolinae and Cervinae:

```
In [11]: fig = plt.figure(figsize=(10, 5))

sns.kdeplot(x = "body mass", data = capreolinae_group_species, shade=True, clip = (5.0,
sns.kdeplot(x = "body mass", data = cervinae_group_species, shade=True, clip = (5.0, 80

plt.legend (labels = ["Capreolinae", "Cervinae"], fontsize=14)
plt.tick_params(axis='both', which='major', labelsize=12)

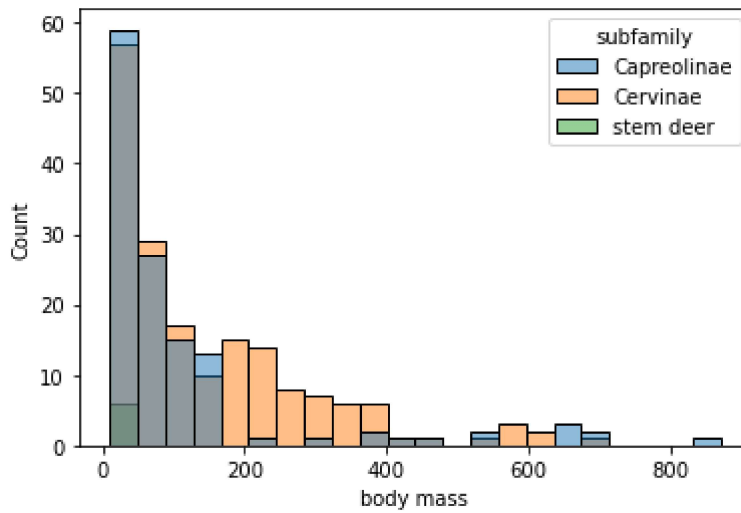
# plt.savefig("cervae_body_size_general.jpg", dpi = 600)
```



The same data represented as a histogram (including the stem genus *Eostyloceros*):

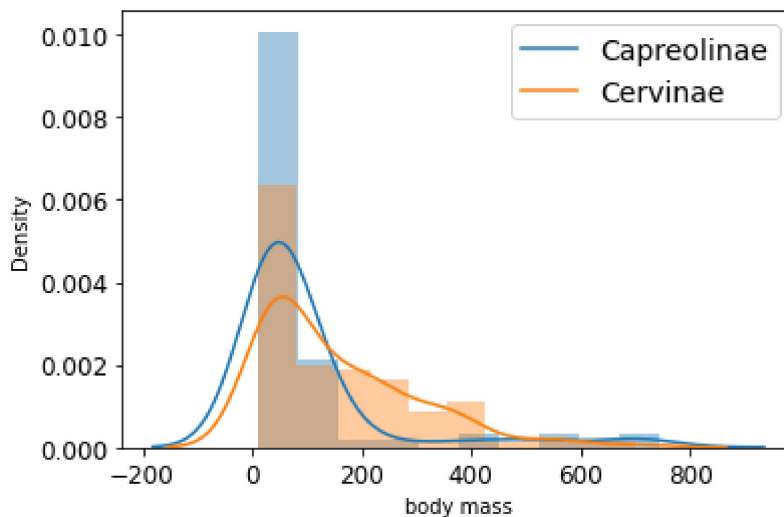
```
In [12]: sns.histplot(data=deer_geo, x="body mass", hue="subfamily")
```

```
Out[12]: <AxesSubplot:xlabel='body mass', ylabel='Count'>
```



```
In [13]: sns.distplot(capreolinae_group_species['body mass'], bins=10, kde=True)
sns.distplot(cervinae_group_species['body mass'], bins=10, kde=True)

plt.legend (labels = ["Capreolinae", "Cervinae"], fontsize=14)
plt.tick_params(axis='both', which='major', labelsize=12)
```



Data grouped by species, biogeographic region, and subfamily with calculation of mean species body mass:

```
In [14]: deer_geo_group = deer_geo.groupby(['species', 'realm', 'subfamily'], as_index = False)['
```

```
In [15]: deer_geo_group.head()
```

```
Out[15]:
```

	species	realm	subfamily	body mass
0	Cervcerus huadeensis	Sino-Malayan	Capreolinae	125.0
1	"Axis" flerowi	Eastern Palearctic	Capreolinae	40.0
2	"Bretzia" sp.	Sino-Malayan	Capreolinae	50.0
3	"Cervavitus" flerowi	Sino-Malayan	Capreolinae	40.0

	species	realm	subfamily	body mass
4	"Eostyloceros" propria	Sino-Malayan	Capreolinae	20.0

```
In [16]: df_cervinae = cervinae[cervinae.subfamily.isin(cervinae.subfamily.value_counts().head(5))
df_cervinae.head()
```

```
Out[16]:
```

	species	synonym	subfamily	site	zone MN	period	realm	source	body mass	sc
23	Eocervinus ruscinensis	Cervus ruscinensis	Cervinae	Mas Belrich, Vlleneuve-La-Raho	MN14	Early Pliocene	Western Palearctic	Deperet (1890)	50.0	
24	Metacervocerus pardinensis	Cervus pardinensis	Cervinae	Perrier-Etouaires	MN16	Late Pliocene	Western Palearctic	Heintz (1970)	85.0	
25	Praeelaphus perrieri	Cervus perrieri	Cervinae	Perrier-Etouaires	MN16	Late Pliocene	Western Palearctic	Heintz (1970)	180.0	
26	Rucervus ardei	Arvernoceros ardei	Cervinae	Perrier-Etouaires	MN16	Late Pliocene	Western Palearctic	Heintz (1970)	180.0	
27	Metacervocerus rhenanus	Cervus philisi	Cervinae	Seneze	MN17	Early Pleistocene	Western Palearctic	Heintz (1970)	70.0	

```
In [17]: df_capreolinae = capreolinae[capreolinae.subfamily.isin(capreolinae.subfamily.value_cou
df_capreolinae.head()
```

```
Out[17]:
```

	species	synonym	subfamily	site	zone MN	period	realm	source	body mass	source
0	gen. et sp. indet. 1	"Muntiacinae"	Capreolinae	Creventille-2	MN11	Late Miocene	Western Palearctic	Azanza (2000)	15.0	tl stu
1	Lucentia iberica	NaN	Capreolinae	Creventille-2	MN11	Late Miocene	Western Palearctic	Azanza (2000)	27.5	tl stu
2	Lucentia pierensis	Eostyloceros pierensis	Capreolinae	Piera	MN11	Late Miocene	Western Palearctic	Azanza (2000)	53.0	tl stu
3	Turiacemas concudensis	NaN	Capreolinae	Concud-3	MN12	Late Miocene	Western Palearctic	Azanza (2000)	47.0	tl stu
4	Procapreolus sp. 1	Pliocervus aff. matheroni	Capreolinae	El Arquillo	MN13	Late Miocene	Western Palearctic	Azanza (2000)	35.0	tl stu

The diagram showing the diversity of species of the subfamily Cervinae according to biogeographic area and sub-epochs (dark areas represent higher species diversity):

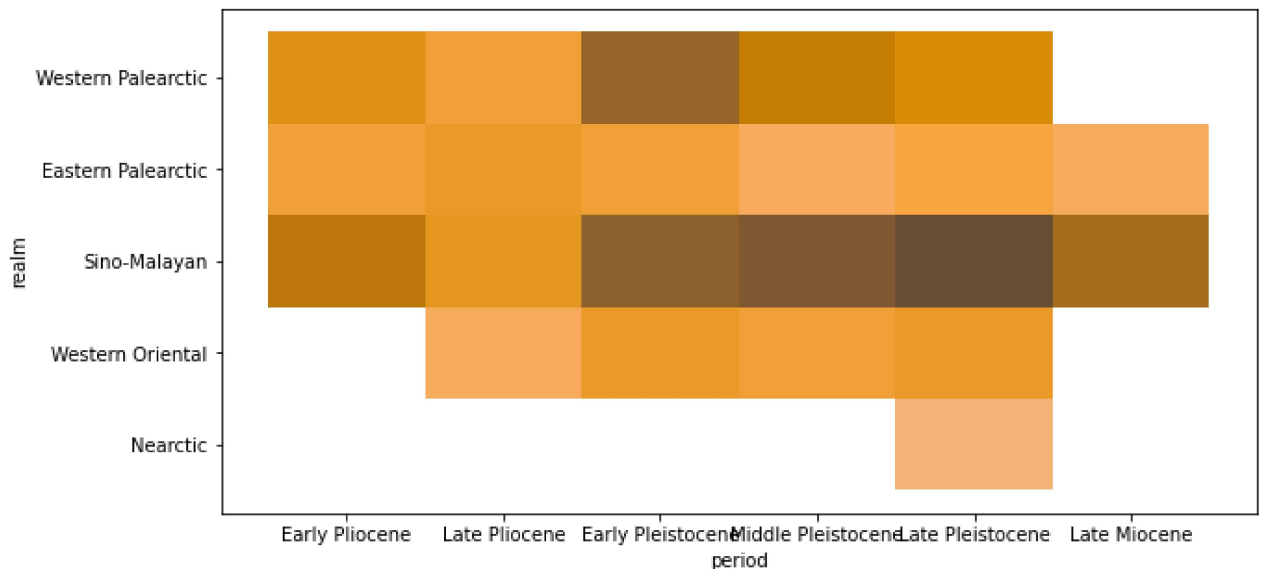
```
In [18]: fig = plt.figure(figsize=(10, 5))
```

```
sns.histplot(cervinae, x="period", y = 'realm', color='orange')
```

```
# plt.xlabel(fontsize=14)
```

```
# plt.ylabel(fontsize=14)
```

Out[18]: <AxesSubplot:xlabel='period', ylabel='realm'>

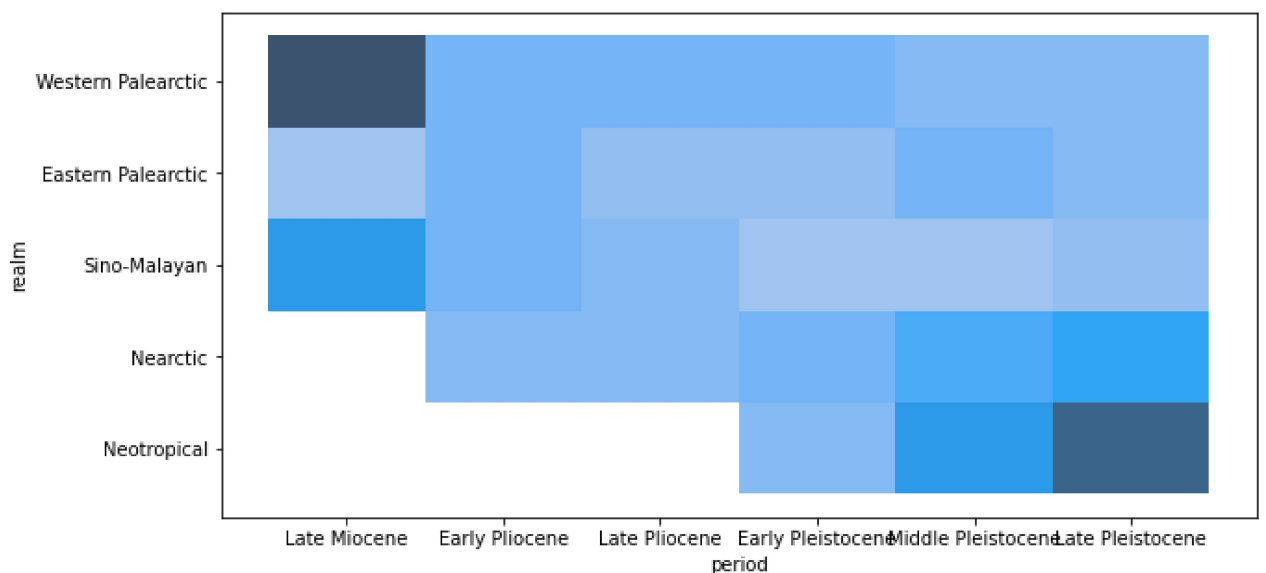


Comment: dark rectangles show the highest diversity of Cervinae

The diagram showing the diversity of species of the subfamily Capreolinae according to biogeographic area and sub-epochs:

```
In [19]: fig = plt.figure(figsize=(10, 5))
sns.histplot(capreolinae, x="period", y = 'realm')
```

Out[19]: <AxesSubplot:xlabel='period', ylabel='realm'>



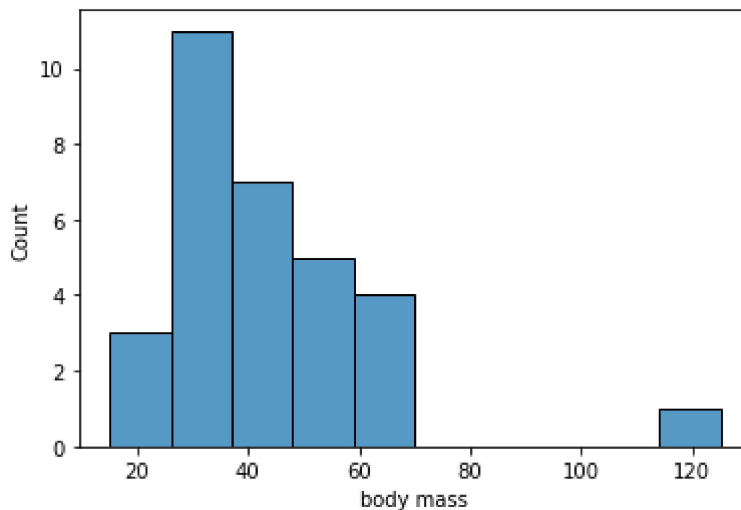
Comment: the diagram shows two biogeographic areas with highest diversity that correspond to two important evolutionary radiations of Capreolinae in the Late Miocene of Western Palearctic and the Late Pleistocene of Neotropic realm.

```
In [20]: capreolinae_radiation = capreolinae.loc[deer_geo['period'] == 'Late Miocene']
```

The species body mass distribution within the Late Miocene evolutionary radiation of the subfamily Capreolinae in western Palearctic:

```
In [21]: sns.histplot(data=capreolinae_radiation, x="body mass", bins = 10)
```

```
Out[21]: <AxesSubplot:xlabel='body mass', ylabel='Count'>
```

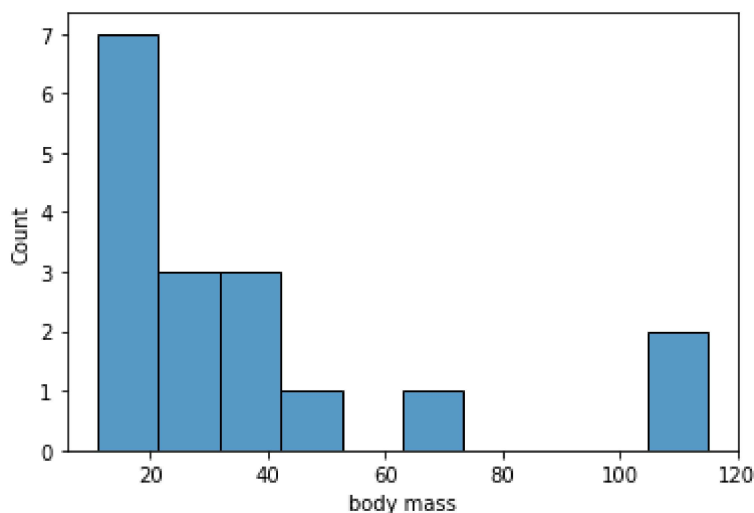


```
In [22]: cervinae_radiation = cervinae.loc[cervinae['period'] == 'Late Miocene']
```

The species body mass distribution within the Late Miocene evolutionary radiation of the subfamily Cervinae in Sino-Malayan area:

```
In [23]: sns.histplot(data=cervinae_radiation, x="body mass", bins = 10)
```

```
Out[23]: <AxesSubplot:xlabel='body mass', ylabel='Count'>
```

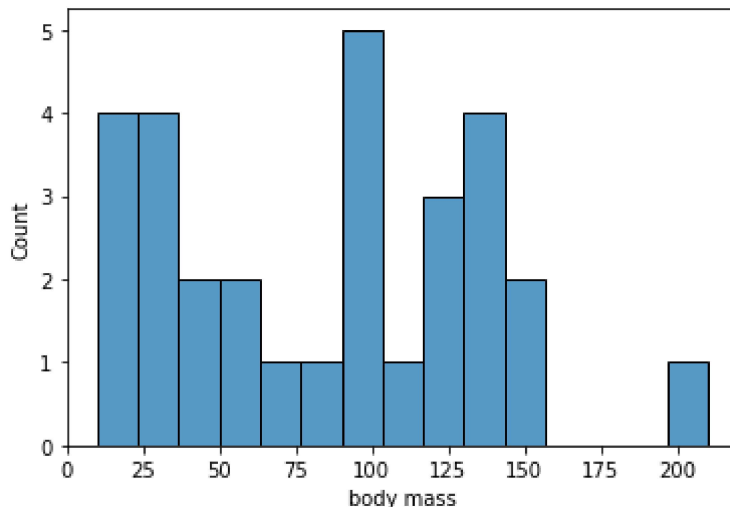


```
In [24]: capreolinae_radiation2 = capreolinae.loc[deer_geo['realm'] == 'Neotropical']
```

The species body mass distribution within the Pleistocene evolutionary radiation of the subfamily Capreolinae in South America:

```
In [25]: sns.histplot(data=capreolinae_radiation2, x="body mass", bins = 15)  
# plt.savefig("cerv_second_rad_capreolinae.jpg")
```

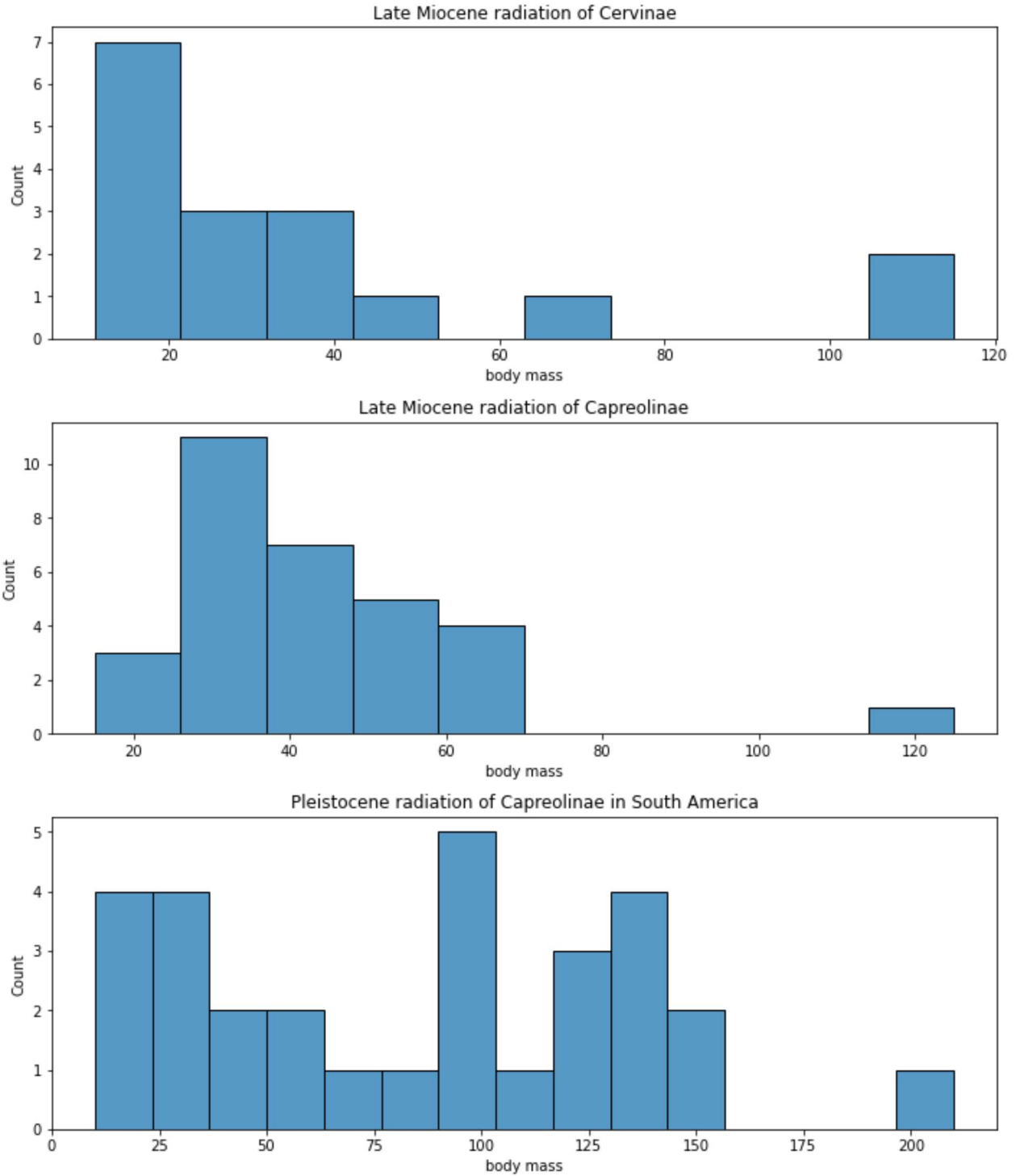
```
Out[25]: <AxesSubplot:xlabel='body mass', ylabel='Count'>
```



Combined diagrams of body mass diversity within evolutionary radiations of crown deer:

```
In [30]: fig, axes = plt.subplots(3, 1, figsize=(10,12))  
plt.suptitle('Body size distribution of evolutionary radiations of Cervidae', fontsize=  
sns.histplot(data=cervinae_radiation, x="body mass", bins = 10, ax=axes[0]).set(title='  
sns.histplot(data=capreolinae_radiation, x="body mass", bins = 10, ax=axes[1]).set(titl  
sns.histplot(data=capreolinae_radiation2, x="body mass", bins = 15, ax=axes[2]).set(tit  
  
fig.tight_layout()  
plt.savefig("cervae_radiations.jpg", dpi = 600)
```

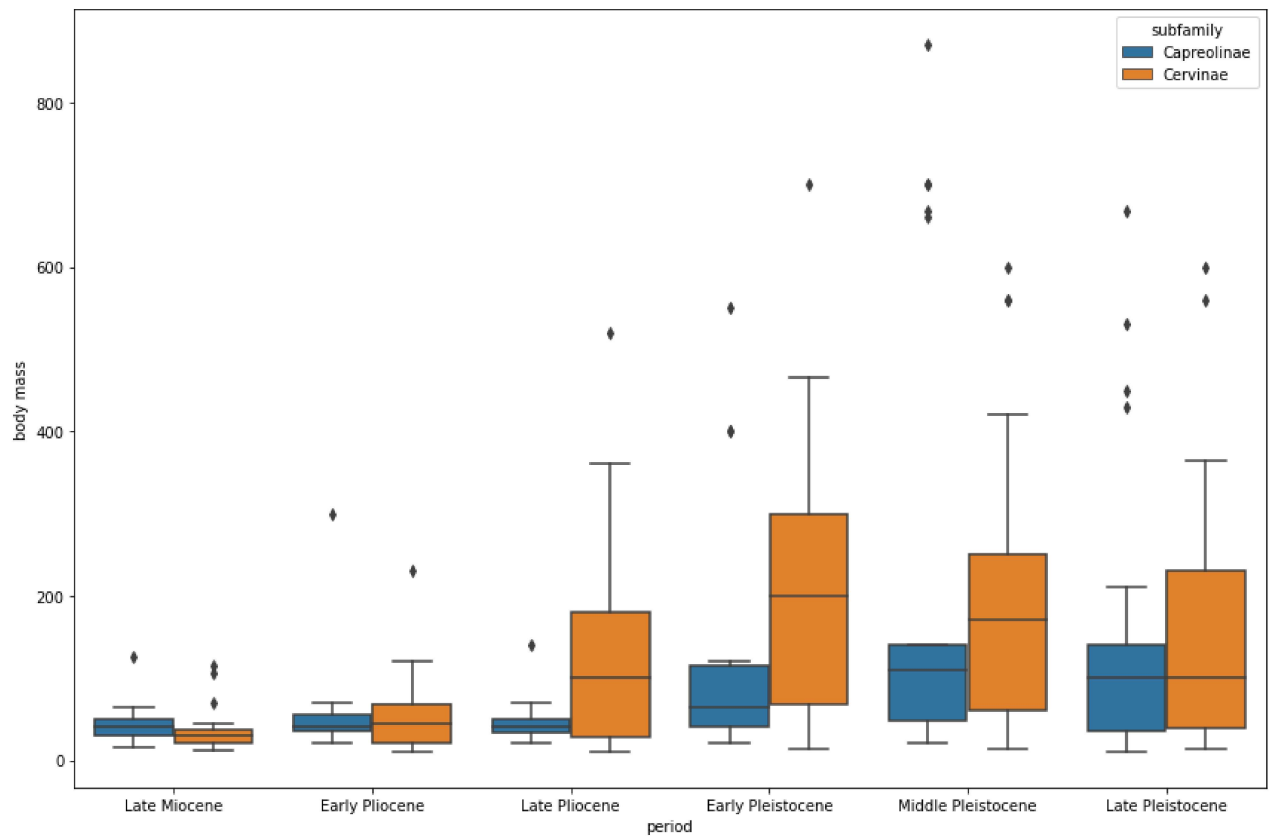

Body size distribution of evolutionary radiations of Cervidae



```
In [27]: deer_geo_drop = deer_geo.drop(deer_geo[deer_geo.subfamily == "stem deer"].index)
```

Species body mass range of crown deer in sub-epochs (with outliers, i.e. extremely large-sized species):

```
In [31]: fig = plt.figure(figsize=(12, 8))
sns.boxplot(y='body mass', x='period', data=deer_geo_drop, hue='subfamily')
fig.tight_layout()
plt.savefig("cervae_body_size_boxplot_outliers.jpg", dpi = 600)
```

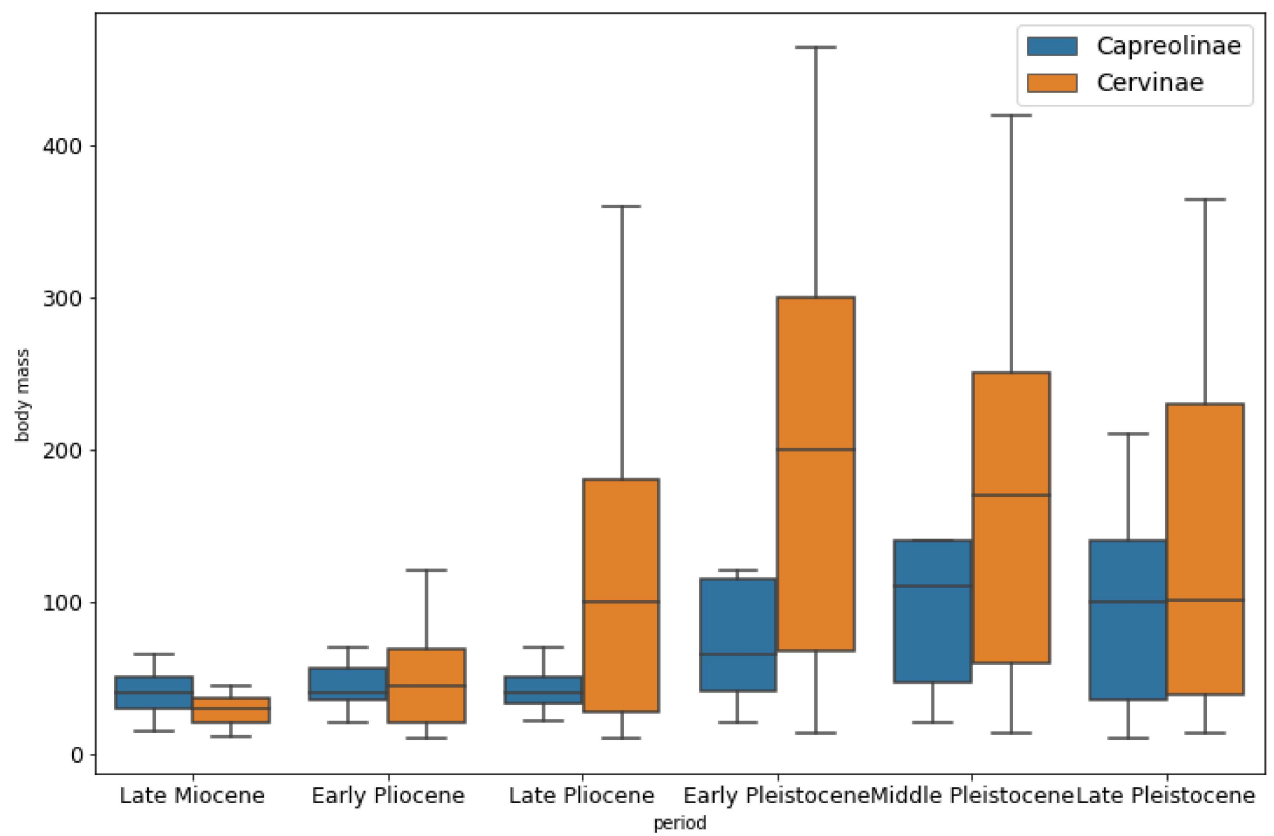


Species body mass range of crown deer in sub-epochs (outliers excluded):

```
In [29]: fig = plt.figure(figsize=(12, 8))
sns.boxplot(y='body mass', x='period', data=deer_geo_drop, hue='subfamily', showfliers=

plt.legend (fontsize=14)
plt.tick_params(axis='both', which='major', labelsz=12.5)

# plt.savefig("cervidae_body_size_boxplot.jpg", dpi = 600)
```



In []: