Exercise 8

The situation

It is well known that many hormones have diurnal fluctuations. Your boss wants a descriptive function to describe this fluctuation over the course of a single day. She has data on relative melatonin level vs. relative time of day that you can use.

The Basics

In [4]:
```
import numpy as np
import pandas as pd
import seaborn as sns
import matplotlib.pyplot as plt
```

In [6]:
```
md = pd.read_csv("datasets/008ExerciseFile.csv")
```

In [7]:
```
display(md)
```

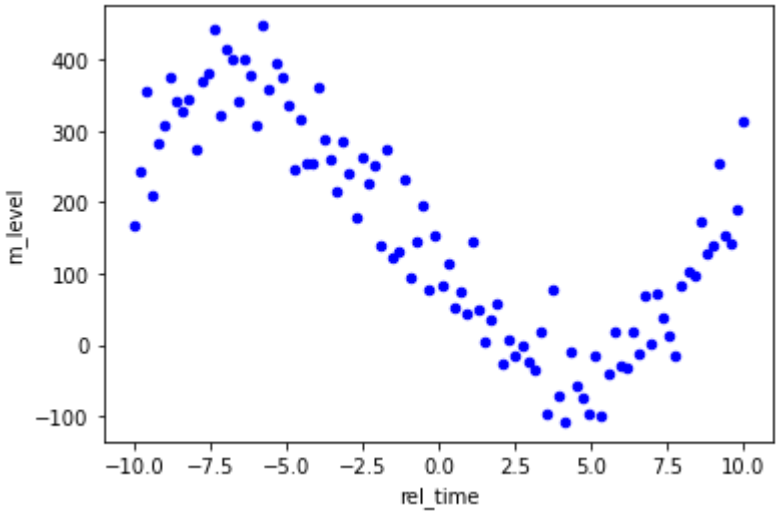
	rel_time	m_level
0	-10.000000	166.846602
1	-9.797980	243.656949
2	-9.595960	354.591642
3	-9.393939	209.023218
4	-9.191919	283.431508
...	...	...
95	9.191919	255.174991
96	9.393939	152.987761
97	9.595960	142.685158
98	9.797980	189.684193
99	10.000000	314.140057

100 rows × 2 columns

Plain Scatter Plot

In [9]:
```
md.plot(x='rel_time', y='m_level', kind='scatter', color='b')
```

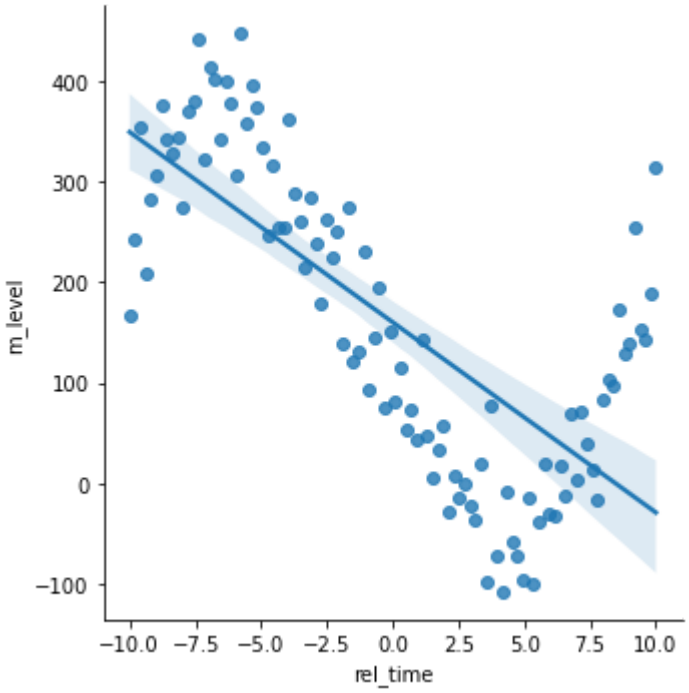
Out[9]:
```
<AxesSubplot:xlabel='rel_time', ylabel='m_level'>
```



Straight Line

In [10]:
```
sns.lmplot(data=md, x='rel_time', y='m_level')
```

Out[10]:
```
<seaborn.axisgrid.FacetGrid at 0x2066fa88400>
```

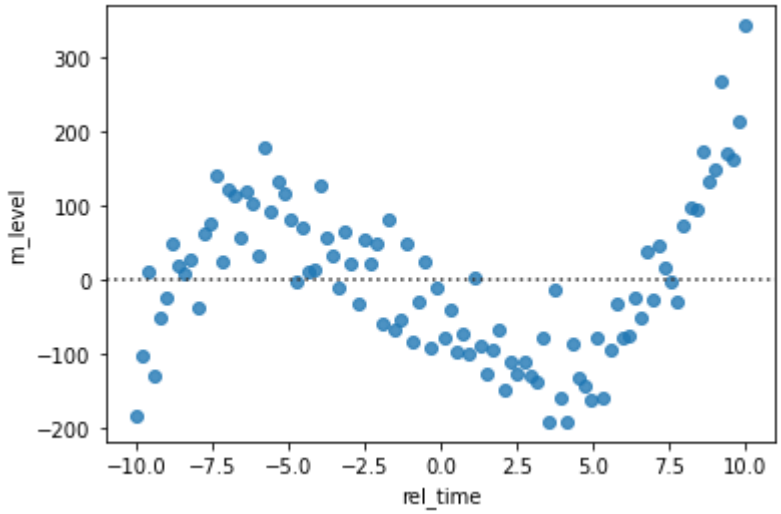


In [11]:
```
myfit = np.polyfit(x=md['rel_time'], y=md['m_level'], deg=1)
print(myfit)
```

```
[-18.91517148 160.25727447]
```

In [13]:
```
sns.residplot(data=md, x='rel_time', y='m_level')
```

Out[13]:
```
<AxesSubplot:xlabel='rel_time', ylabel='m_level'>
```

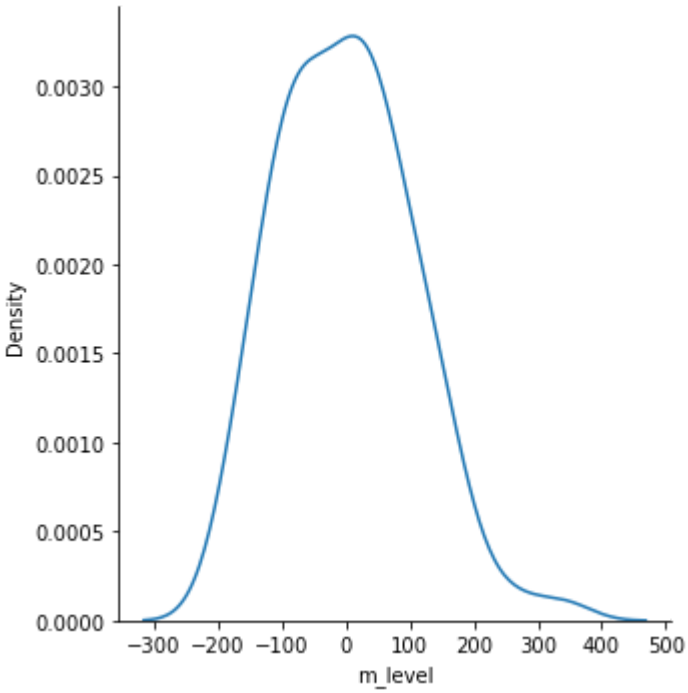


In [14]:
```
fitvals = np.polyval(myfit, md['rel_time'])
```

In [15]:
```
myres = md['m_level'] - fitvals
```

In [16]:
```
sns.displot(myres, kind='kde')
```

Out[16]:
```
<seaborn.axisgrid.FacetGrid at 0x2066fc23dc0>
```



In [22]:
```
np.std(myres)
```

Out[22]:
```
104.76481228544043
```

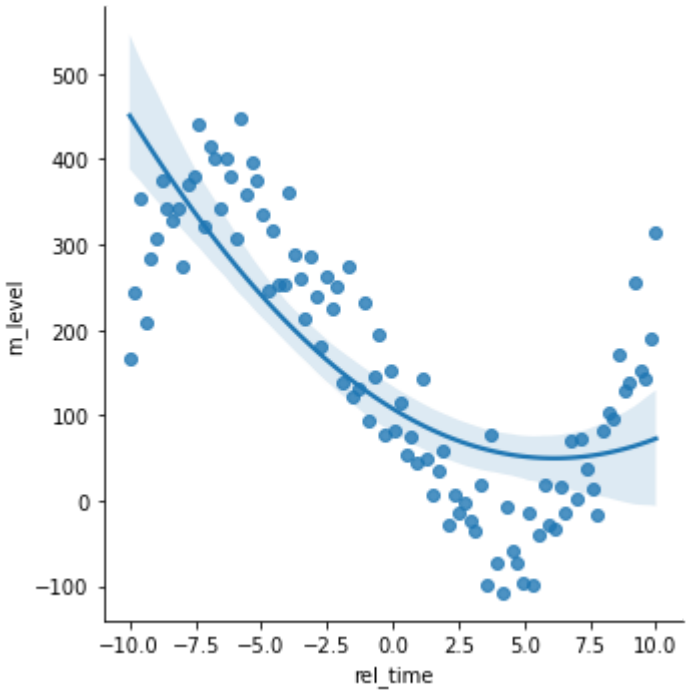
Why the first order polynomial isn't a good fit

The straight line fit doesn't properly model the data because it systematically overestimates, underestimates, overestimates, and the understimates again. Also the error bounds of the line of best fit are rather large. Looking at the residual plot, the residuals should be randomly and symmetrically distributed around 0, but this is not the case.

Another Fit: Second Order Polynomial

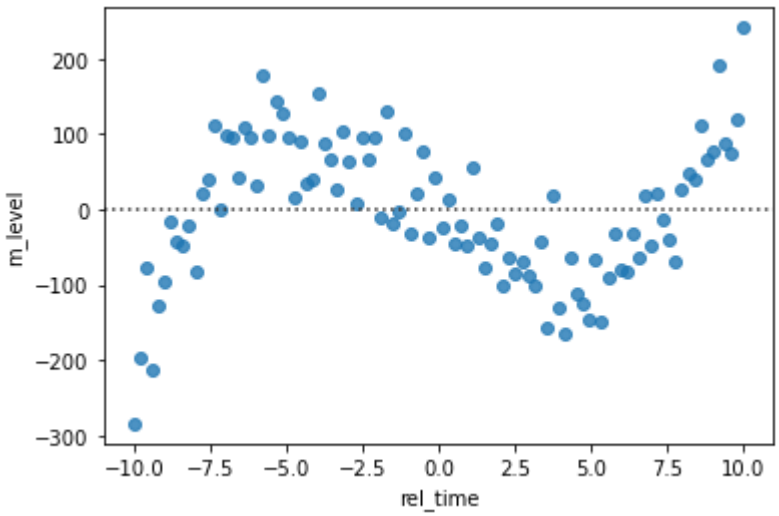
In [17]:
```
sns.lmplot(data=md, x='rel_time', y='m_level', order = 2)
```

Out[17]:
```
<seaborn.axisgrid.FacetGrid at 0x2066fc85040>
```



In [20]:
```
sns.residplot(data=md, x='rel_time', y='m_level', order=2)
```

Out[20]:
```
<AxesSubplot:xlabel='rel_time', ylabel='m_level'>
```



In [24]:
```
myfit = np.polyfit(x=md['rel_time'], y=md['m_level'], deg=2)
```

```
print(myfit)
```

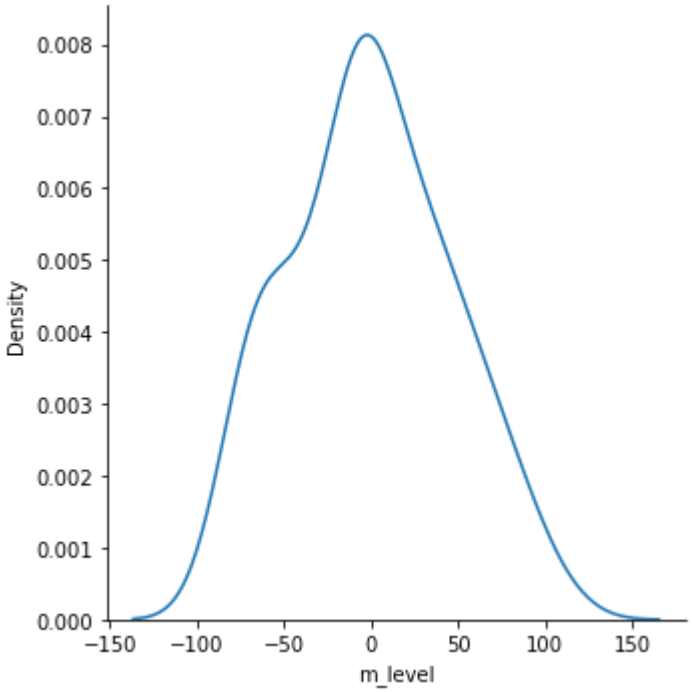
```
[  1.5417871  -18.91517148 107.82613075]
```

In [25]:
```
fitvals = np.polyval(myfit, md['rel_time'])
```

In [26]:
```
myres = md['m_level'] - fitvals
```

In [47]:
```
sns.displot(myres, kind='kde')
```

Out[47]:
```
<seaborn.axisgrid.FacetGrid at 0x20671405580>
```



In [28]:
```
np.std(myres)
```

Out[28]:
```
93.68620954635846
```

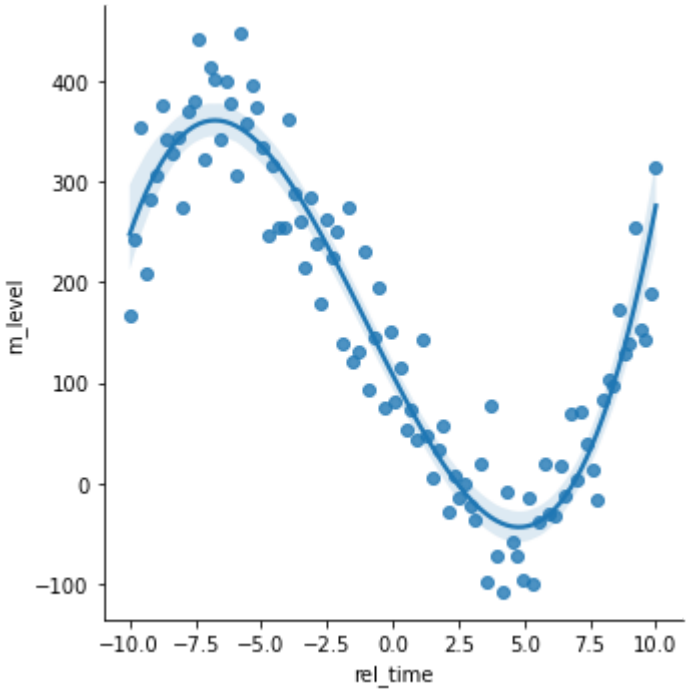
Why the second order polynomial isn't the best fit

The second order polynomial isn't the best fit for the same reason as the first order polynomial. The line of best fit systematically overestimates, underestimates, overestimates, and underestimates the data. The scatterplot of the residuals reveals that the residuals are not normally distributed around 0.

Best Fit: Third Order Polynomial

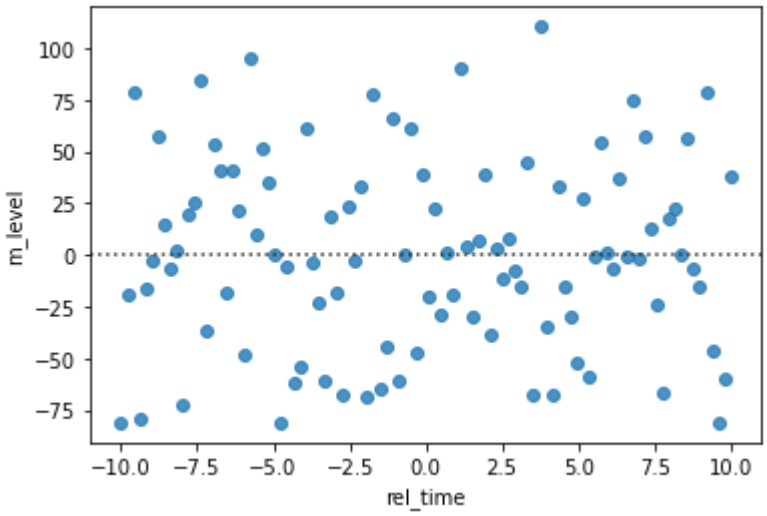
In [19]:
```
sns.lmplot(data=md, x='rel_time', y='m_level', order=3)
```

Out[19]:
```
<seaborn.axisgrid.FacetGrid at 0x2066fc8ac10>
```



In [21]:
```
sns.residplot(data=md, x='rel_time', y='m_level', order=3)
```

Out[21]:
```
<AxesSubplot:xlabel='rel_time', ylabel='m_level'>
```



In [29]:
```
myfit = np.polyfit(x=md['rel_time'], y=md['m_level'], deg=3)
print(myfit)
```

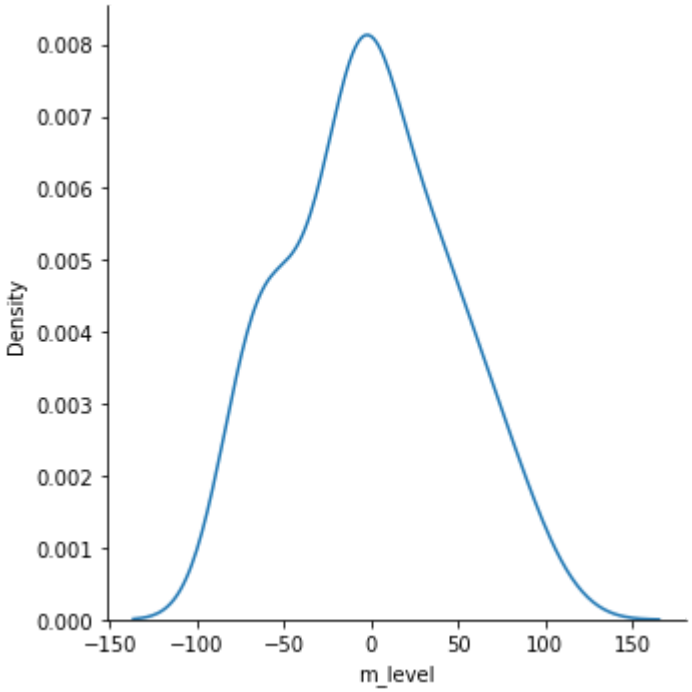
```
[  0.52406776   1.5417871  -50.9901931  107.82613075]
```

In [31]:
```
fitvals = np.polyval(myfit, md['rel_time'])
```

In [32]:
```
myres = md['m_level'] - fitvals
```

In [46]:
```
sns.displot(myres, kind='kde')
```

Out[46]: <seaborn.axisgrid.FacetGrid at 0x206711f5cd0>



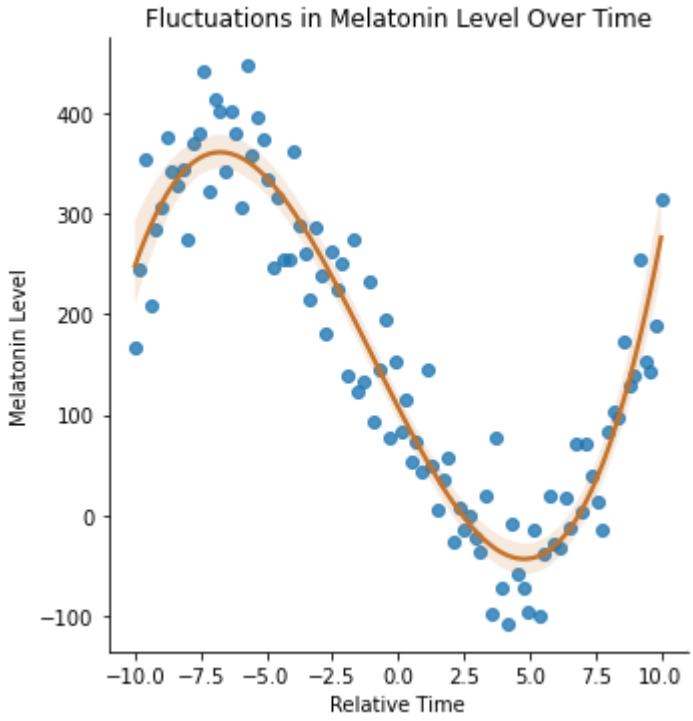
Why this is the best plot

The third order polynomial is the best fit line because it minimizes the distance between the the data points and the line throughout the whole range. Additionally, the scatter plot of the residuals is roughly normally distributed around 0, Which is further demonstrated with the kde plot above.

Pretty Plot and Fit

In [45]:
```
sns.lmplot(data=md, x='rel_time', y='m_level', order=3, line_kws={'color': '#c47229'})
plt.xlabel("Relative Time")
plt.ylabel("Melatonin Level")
plt.title("Fluctuations in Melatonin Level Over Time")
```

Out[45]: Text(0.5, 1.0, 'Fluctuations in Melatonin Level Over Time')


Fluctuations in Melatonin Level Over Time
Melatonin Level
400
300
200
100
0
−100
−10.0
−7.5
−5.0
−2.5
0.0
2.5
5.0
7.5
10.0
Relative Time