

```
In [1]: # inputting Libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
%matplotlib inline
sns.set(color_codes=True)
```

```
In [2]: mri = pd.read_csv("E:/R-programming/mri.csv")
anavex2 = pd.read_csv("E:/R-programming/anavex2.csv")
```

```
In [4]: anavex2
```

```
Out[4]:
```

	Subject ID	Subject birth year	Subject sex	Scan date	Timepoint	Date of form completion	ICV (ml)	Whole brain (combined WM and GM) (ml)	Whole brain (combined WM and GM) (% ICV)
0	101001	1942	M	8/8/2019	Week48	8/27/2021	1744.44	1233.303	70.699038
1	101002	1951	F	9/13/2018	Baseline	1/31/2019	1391.85	1029.378	73.957539
2	101003	1945	M	9/13/2018	Baseline	1/15/2019	1623.29	1007.688	62.076893
3	101003	1945	M	8/22/2019	Week48	11/22/2019	1624.22	995.623	61.298644
4	101004	1934	F	9/27/2018	Baseline	1/31/2019	1398.50	972.417	69.532707
...
886	460015	1942	M	5/20/2021	Baseline	5/20/2021	1830.85	1044.045	57.025246
887	460015	1942	M	4/26/2022	Week48	4/29/2022	1824.77	1050.492	57.568555
888	460018	1938	M	6/3/2021	Baseline	6/3/2021	1502.69	1084.067	72.141759
889	460020	1944	F	6/16/2021	Baseline	6/16/2021	1431.21	1032.476	72.140077
890	460020	1944	F	5/25/2022	Week48	5/27/2022	1429.91	995.734	69.636228

891 rows × 225 columns

```
In [5]: mri
```

Out[5]:

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BTD	RS.HOMN	RS.GENE.neg	MMSE	BTD.group
0	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0	Y	Y	17	BTD 10-20 mg
1	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0	Y	Y	17	BTD 10-20 mg
2	101004	84	F	Placebo	-8.0	Baseline	0.0	Y	N	22	Placebo
3	101005	77	M	Placebo	-13.0	Baseline	0.0	Y	Y	22	Placebo
4	101005	77	M	Placebo	338.0	Week 48	0.0	Y	Y	22	Placebo
...
429	113098	83	F	Anavex2- 73 50 mg	339.0	Week 48	20.0	Y	Y	21	BTD 10-20 mg
430	115001	72	M	Anavex2- 73 50 mg	-10.0	Baseline	40.0	Y	Y	17	BTD 40-50 mg
431	115003	74	F	Anavex2- 73 50 mg	-2.0	Baseline	50.0	Y	Y	21	BTD 40-50 mg
432	115003	74	F	Anavex2- 73 50 mg	334.0	Week 48	50.0	Y	Y	21	BTD 40-50 mg
433	115005	56	M	Anavex2- 73 30 mg	-10.0	Baseline	30.0	Y	Y	19	BTD 30 mg

434 rows × 11 columns

In [6]: `mri.dtypes`

```
Out[6]: SUBJID      int64
AGE        int64
SEX        object
TRT01A     object
Day        float64
AVISIT     object
BTD        float64
RS.HOMN    object
RS.GENE.neg object
MMSE       int64
BTD.group  object
dtype: object
```

In [7]: `mri.columns`

```
Out[7]: Index(['SUBJID', 'AGE', 'SEX', 'TRT01A', 'Day', 'AVISIT', 'BTD', 'RS.HOMN',
              'RS.GENE.neg', 'MMSE', 'BTD.group'],
              dtype='object')
```

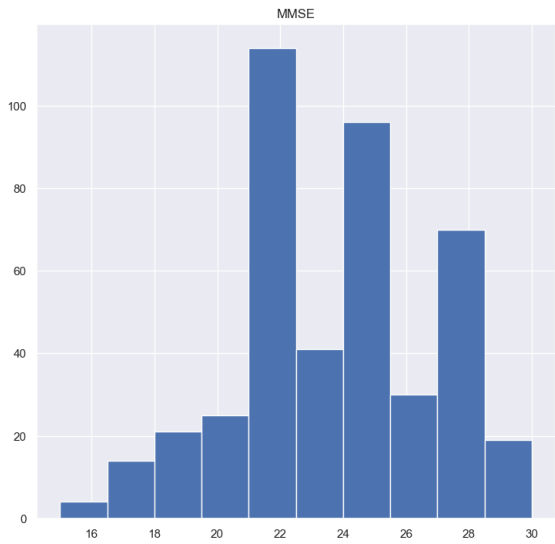
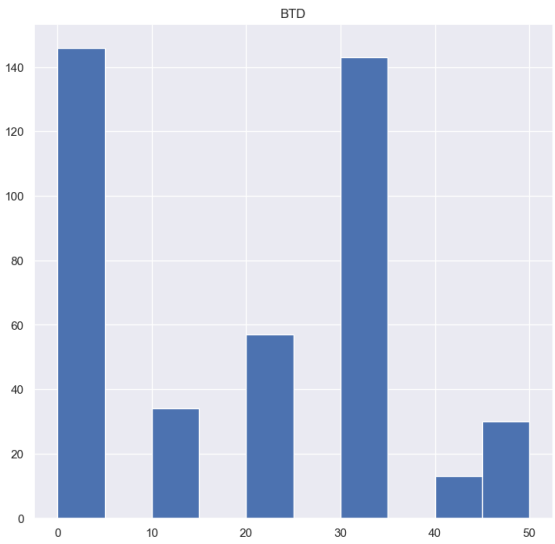
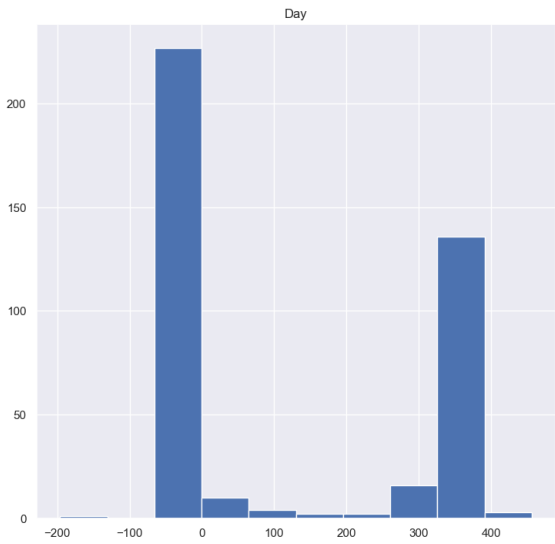
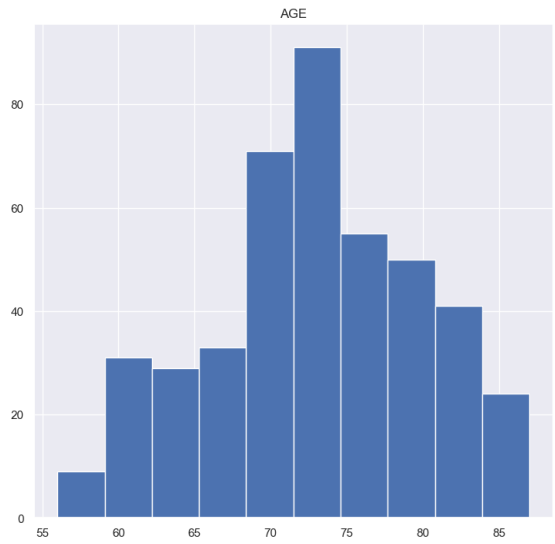
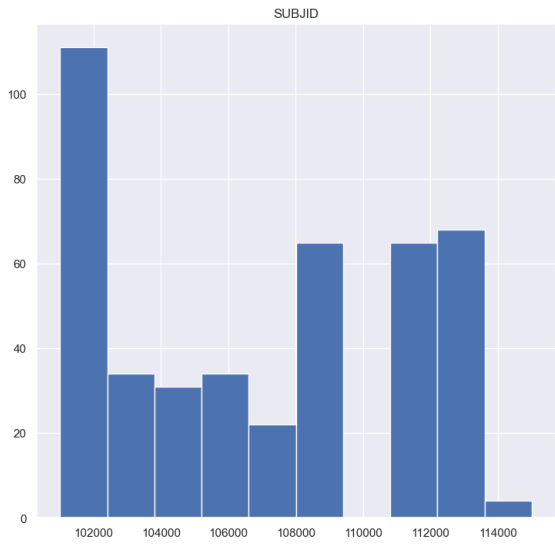
```
In [8]: #analytical summary of dataset
mri.describe(include='all')
```

Out[8]:

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BTD	RS.HOMN	RS.G
count	434.000000	434.000000	434	434	401.000000	434	423.000000	434	
unique	NaN	NaN	2	3	NaN	4	NaN	2	
top	NaN	NaN	F	Anavex2- 73 30 mg	NaN	Baseline	NaN	Y	
freq	NaN	NaN	220	157	NaN	232	NaN	419	
mean	107008.110599	72.900922	NaN	NaN	129.047382	NaN	18.416076	NaN	
std	4524.428438	6.761995	NaN	NaN	170.739964	NaN	15.941151	NaN	
min	101003.000000	56.000000	NaN	NaN	-196.000000	NaN	0.000000	NaN	
25%	102014.250000	69.000000	NaN	NaN	-9.000000	NaN	0.000000	NaN	
50%	107008.000000	73.000000	NaN	NaN	-3.000000	NaN	20.000000	NaN	
75%	112003.000000	78.000000	NaN	NaN	334.000000	NaN	30.000000	NaN	
max	115005.000000	87.000000	NaN	NaN	456.000000	NaN	50.000000	NaN	

```
In [9]: mri.hist(figsize=(20,30))
```

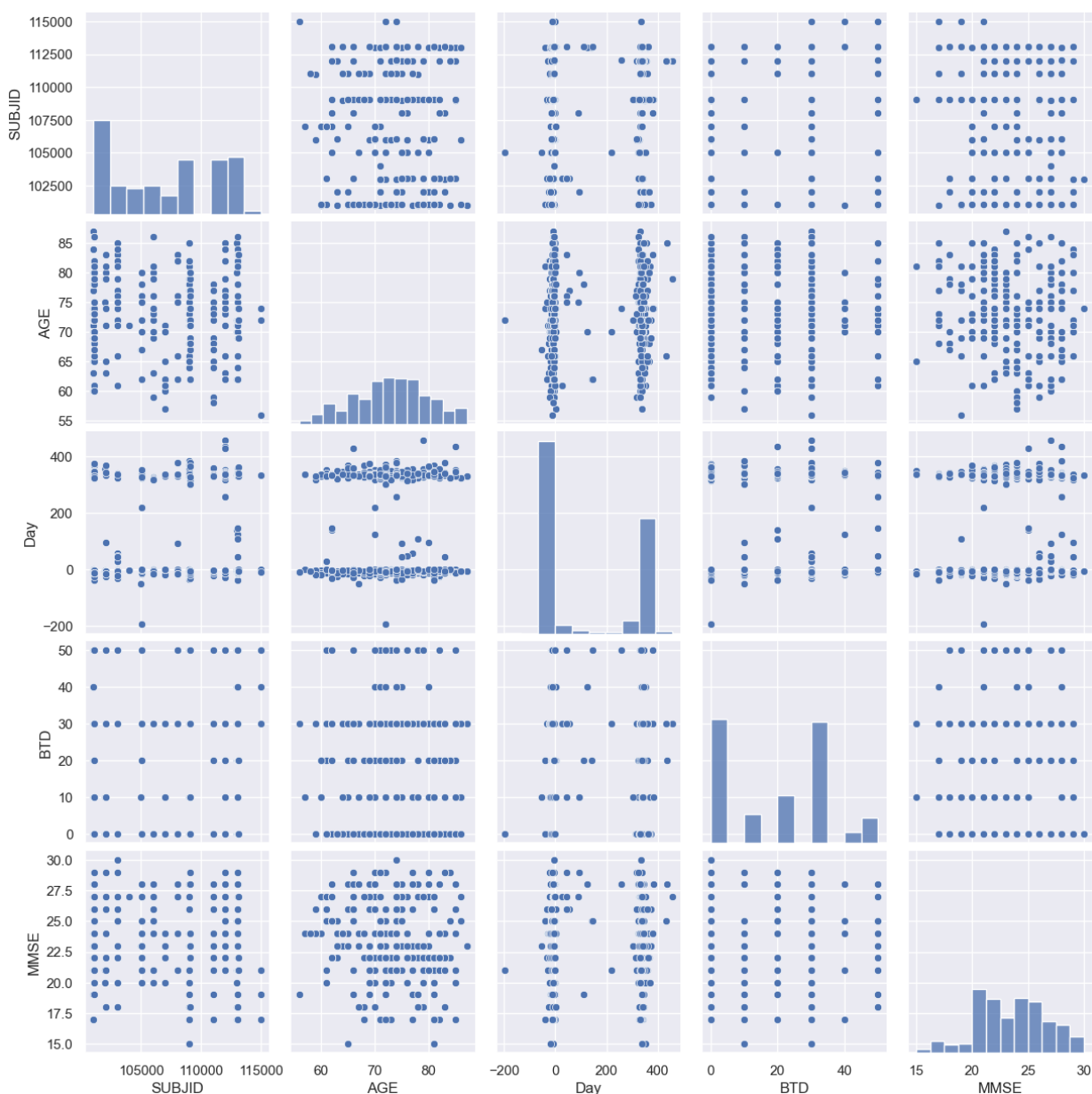
```
Out[9]: array([[<Axes: title={'center': 'SUBJID'}>,
      <Axes: title={'center': 'AGE'}>],
      [<Axes: title={'center': 'Day'}>, <Axes: title={'center': 'BTD'}>],
      [<Axes: title={'center': 'MMSE'}>, <Axes: >]], dtype=object)
```



```
In [10]: sns.pairplot(mri)
```

C:\Users\MBOGO ANGEL ALFRED\ANACONDA\Lib\site-packages\seaborn\axisgrid.py:118: UserWarning: The figure layout has changed to tight
 self._figure.tight_layout(*args, **kwargs)

Out[10]: <seaborn.axisgrid.PairGrid at 0x21b274b2a10>



In [11]: *# total number of rows and columns*
 mri.shape

Out[11]: (434, 11)

In [12]: *# rows containing duplicate data*
 duplicate_rows_mri = mri[mri.duplicated()]

In [13]: *#count number of rows before removing data*
 mri.count

```
Out[13]: <bound method DataFrame.count of
SIT   BT.D RS.HOMN \
0     101003  73   M  Anavex2-73 30 mg  -4.0  Baseline  20.0    Y
1     101003  73   M  Anavex2-73 30 mg  340.0  Week 48  20.0    Y
2     101004  84   F           Placebo  -8.0  Baseline   0.0    Y
3     101005  77   M           Placebo -13.0  Baseline   0.0    Y
4     101005  77   M           Placebo 338.0  Week 48   0.0    Y
..     ...    ...   ..           ...    ...    ...    ...
429   113098  83   F  Anavex2-73 50 mg  339.0  Week 48  20.0    Y
430   115001  72   M  Anavex2-73 50 mg  -10.0  Baseline  40.0    Y
431   115003  74   F  Anavex2-73 50 mg   -2.0  Baseline  50.0    Y
432   115003  74   F  Anavex2-73 50 mg  334.0  Week 48  50.0    Y
433   115005  56   M  Anavex2-73 30 mg  -10.0  Baseline  30.0    Y

      RS.GENE.neg  MMSE      BT.D.group
0                Y    17  BT.D 10-20 mg
1                Y    17  BT.D 10-20 mg
2                N    22           Placebo
3                Y    22           Placebo
4                Y    22           Placebo
..             ...    ...             ...
429             Y    21  BT.D 10-20 mg
430             Y    17  BT.D 40-50 mg
431             Y    21  BT.D 40-50 mg
432             Y    21  BT.D 40-50 mg
433             Y    19  BT.D 30 mg

[434 rows x 11 columns]>
```

```
In [14]: #drop the duplicates
mri = mri.drop_duplicates()
mri.head()
```

```
Out[14]:
```

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BT.D	RS.HOMN	RS.GENE.neg	MMSE	BT.D.group
0	101003	73	M	Anavex2-73 30 mg	-4.0	Baseline	20.0	Y	Y	17	BT.D 10-20 mg
1	101003	73	M	Anavex2-73 30 mg	340.0	Week 48	20.0	Y	Y	17	BT.D 10-20 mg
2	101004	84	F	Placebo	-8.0	Baseline	0.0	Y	N	22	Placebo
3	101005	77	M	Placebo	-13.0	Baseline	0.0	Y	Y	22	Placebo
4	101005	77	M	Placebo	338.0	Week 48	0.0	Y	Y	22	Placebo

```
In [15]: # find the null values
print(mri.isnull().sum())
```

```

SUBJID      0
AGE         0
SEX         0
TRT01A      0
Day        33
AVISIT      0
BTD         11
RS.HOMN     0
RS.GENE.neg 0
MMSE        0
BTD.group   11
dtype: int64

```

```

In [16]: #drop the null(missing values)
mri = mri.dropna()
mri.count()

```

```

Out[16]: SUBJID      391
AGE         391
SEX         391
TRT01A      391
Day         391
AVISIT      391
BTD         391
RS.HOMN     391
RS.GENE.neg 391
MMSE        391
BTD.group   391
dtype: int64

```

```

In [17]: # find the null values
print(mri.isnull().sum())

```

```

SUBJID      0
AGE         0
SEX         0
TRT01A      0
Day         0
AVISIT      0
BTD         0
RS.HOMN     0
RS.GENE.neg 0
MMSE        0
BTD.group   0
dtype: int64

```

```

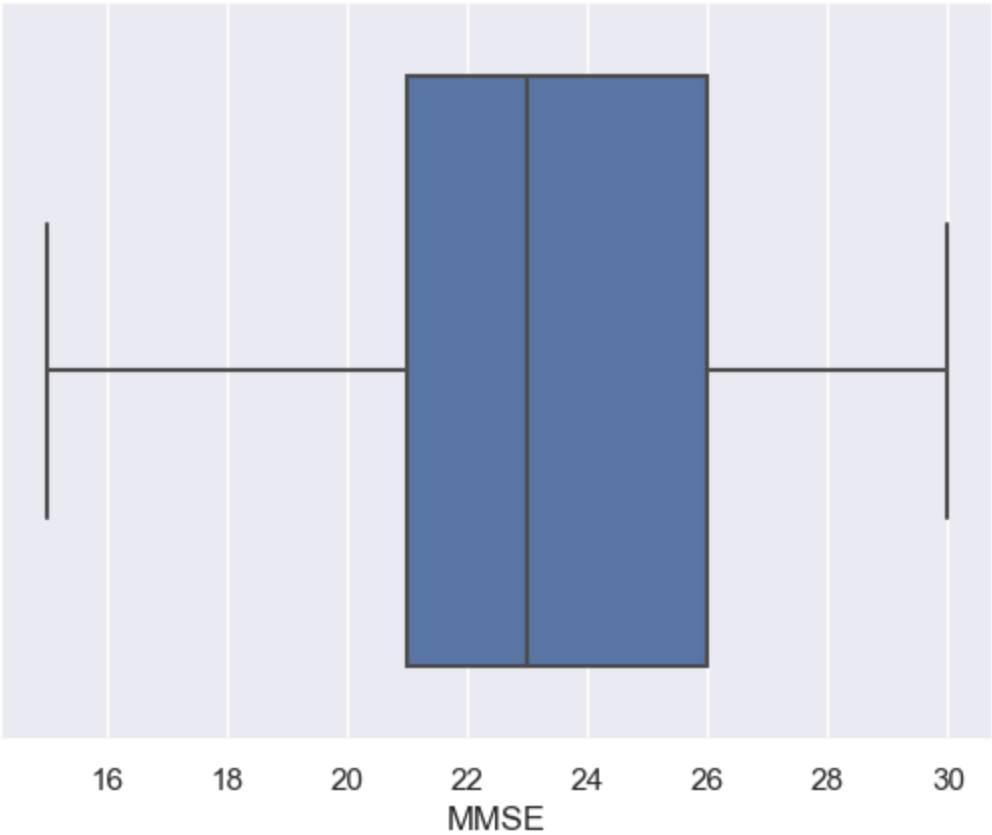
In [20]: # finding the outliers
sns.boxplot(x=mri["MMSE"])

```

```

Out[20]: <Axes: xlabel='MMSE'>

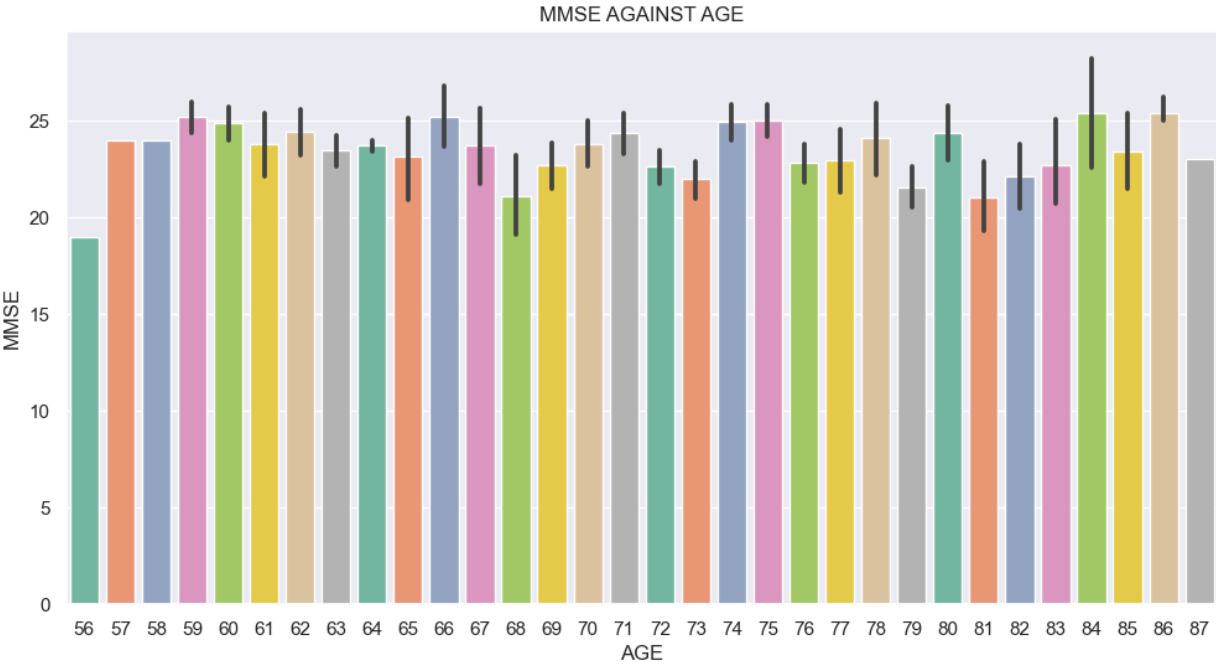
```



```
In [ ]:
```

```
In [ ]:
```

```
In [6]: #AGE AND MMSE
plt.figure(figsize=(12,6))
plt.title("MMSE AGAINST AGE")
sns.barplot(x= mri['AGE'], y= mri['MMSE'], palette = 'Set2');
```



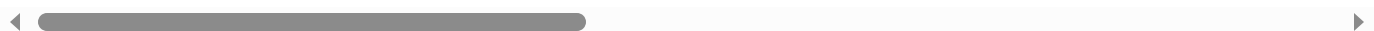
In []:

In [5]: anavex2

Out[5]:

	Subject ID	Subject birth year	Subject sex	Scan date	Timepoint	Date of form completion	ICV (ml)	Whole brain (combined WM and GM) (ml)	Whole brain (combined WM and GM) (% ICV)
0	101001	1942	M	8/8/2019	Week48	8/27/2021	1744.44	1233.303	70.699038
1	101002	1951	F	9/13/2018	Baseline	1/31/2019	1391.85	1029.378	73.957539
2	101003	1945	M	9/13/2018	Baseline	1/15/2019	1623.29	1007.688	62.076893
3	101003	1945	M	8/22/2019	Week48	11/22/2019	1624.22	995.623	61.298644
4	101004	1934	F	9/27/2018	Baseline	1/31/2019	1398.50	972.417	69.532707
...
886	460015	1942	M	5/20/2021	Baseline	5/20/2021	1830.85	1044.045	57.025246
887	460015	1942	M	4/26/2022	Week48	4/29/2022	1824.77	1050.492	57.568555
888	460018	1938	M	6/3/2021	Baseline	6/3/2021	1502.69	1084.067	72.141759
889	460020	1944	F	6/16/2021	Baseline	6/16/2021	1431.21	1032.476	72.140077
890	460020	1944	F	5/25/2022	Week48	5/27/2022	1429.91	995.734	69.636228

891 rows × 225 columns



```
In [7]: # rows containing duplicate data
duplicate_rows_anavex2 = anavex2[anavex2.duplicated()]
anavex2
```

Out[7]:

	Subject ID	Subject birth year	Subject sex	Scan date	Timepoint	Date of form completion	ICV (ml)	Whole brain (combined WM and GM) (ml)	Whole brain (combined WM and GM) (% ICV)
0	101001	1942	M	8/8/2019	Week48	8/27/2021	1744.44	1233.303	70.699038
1	101002	1951	F	9/13/2018	Baseline	1/31/2019	1391.85	1029.378	73.957539
2	101003	1945	M	9/13/2018	Baseline	1/15/2019	1623.29	1007.688	62.076893
3	101003	1945	M	8/22/2019	Week48	11/22/2019	1624.22	995.623	61.298644
4	101004	1934	F	9/27/2018	Baseline	1/31/2019	1398.50	972.417	69.532707
...
886	460015	1942	M	5/20/2021	Baseline	5/20/2021	1830.85	1044.045	57.025246
887	460015	1942	M	4/26/2022	Week48	4/29/2022	1824.77	1050.492	57.568555
888	460018	1938	M	6/3/2021	Baseline	6/3/2021	1502.69	1084.067	72.141759
889	460020	1944	F	6/16/2021	Baseline	6/16/2021	1431.21	1032.476	72.140077
890	460020	1944	F	5/25/2022	Week48	5/27/2022	1429.91	995.734	69.636228

891 rows × 225 columns

In [8]: `anavex2.dtypes`

Out[8]:

```

Subject ID
int64
Subject birth year
int64
Subject sex
object
Scan date
object
Timepoint
object

...
ASL CBF- Posterior cingulate cortex Change in perfusion in mL/min/cm3 from baseline
float64
ASL CBF- Posterior cingulate cortex (left) Perfusion in mL/min/cm3
float64
ASL CBF- Posterior cingulate cortex (left) Change in perfusion in mL/min/cm3 from baseline
float64
ASL CBF- Posterior cingulate cortex (right) Perfusion in mL/min/cm3
float64
ASL CBF- Posterior cingulate cortex (right) Change in perfusion in mL/min/cm3 from baseline
float64
Length: 225, dtype: object

```

```
In [45]: anavex2.rename(columns ={'Subject ID': 'SUBJID', 'BRAIN VOLUME': 'Whole brain (combined  
anavex2.head
```

```
Out[45]: <bound method NDFrame.head of
Timepoint \
0      101001      1942      M      8/8/2019      Week48
1      101002      1951      F      9/13/2018      Baseline
2      101003      1945      M      9/13/2018      Baseline
3      101003      1945      M      8/22/2019      Week48
4      101004      1934      F      9/27/2018      Baseline
..      ...      ...      ...      ...      ...
886    460015      1942      M      5/20/2021      Baseline
887    460015      1942      M      4/26/2022      Week48
888    460018      1938      M      6/3/2021      Baseline
889    460020      1944      F      6/16/2021      Baseline
890    460020      1944      F      5/25/2022      Week48
```

```

Date of form completion  ICV (ml)  Whole brain (combined WM and GM) (ml) \
0      8/27/2021      1744.44      1233.303
1      1/31/2019      1391.85      1029.378
2      1/15/2019      1623.29      1007.688
3      11/22/2019      1624.22      995.623
4      1/31/2019      1398.50      972.417
..      ...      ...      ...
886    5/20/2021      1830.85      1044.045
887    4/29/2022      1824.77      1050.492
888    6/3/2021      1502.69      1084.067
889    6/16/2021      1431.21      1032.476
890    5/27/2022      1429.91      995.734
```

```

Whole brain (combined WM and GM) (% ICV) \
0      70.699038
1      73.957539
2      62.076893
3      61.298644
4      69.532707
..      ...
886    57.025246
887    57.568555
888    72.141759
889    72.140077
890    69.636228
```

```

Whole brain (combined WM and GM) (mL change from baseline) ... \
0      NaN      ...
1      NaN      ...
2      NaN      ...
3      -12.065      ...
4      NaN      ...
..      ...      ...
886    NaN      ...
887    6.447      ...
888    NaN      ...
889    NaN      ...
890    -36.742      ...
```

```

ASL CBF- Precuneus (left) Perfusion in mL/min/cm3 \
0      NaN
1      NaN
2      NaN
3      NaN
4      NaN
..      ...
```

886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Precuneus (left) Change in perfusion in mL/min/cm3 from baseline \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Precuneus (right) Perfusion in mL/min/cm3 \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Precuneus (right) Change in perfusion in mL/min/cm3 from baseline \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Posterior cingulate cortex Perfusion in mL/min/cm3 \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Posterior cingulate cortex Change in perfusion in mL/min/cm3 from baseline \
--	---

0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Posterior cingulate cortex (left) Perfusion in mL/min/cm3 \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Posterior cingulate cortex (left) Change in perfusion in mL/min/cm3 from baseline \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Posterior cingulate cortex (right) Perfusion in mL/min/cm3 \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
886	NaN
887	NaN
888	NaN
889	NaN
890	NaN

	ASL CBF- Posterior cingulate cortex (right) Change in perfusion in mL/min/cm3 from baseline
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...

886

887

888

889

890

NaN

NaN

NaN

NaN

NaN

[891 rows x 225 columns]>

```
In [46]: brain = mri.merge(anavex2,how = 'left', on = 'SUBJID')
brain.head()
```

Out[46]:

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BTD	RS.HOMN	RS.GENE.neg	MMSE	...	ASL CI Precune (le Perfusior mL/min/c
0	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0	Y	Y	17	...	N
1	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0	Y	Y	17	...	N
2	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0	Y	Y	17	...	N
3	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0	Y	Y	17	...	N
4	101004	84	F	Placebo	-8.0	Baseline	0.0	Y	N	22	...	N

5 rows x 235 columns



```
In [13]: brain
```

Out[13]:

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BTD	RS.HOMN	RS.GENE.neg	MMSE	...	ASL Preci	Perfusi mL/min
0	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0	Y	Y	17	...		
1	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0	Y	Y	17	...		
2	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0	Y	Y	17	...		
3	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0	Y	Y	17	...		
4	101004	84	F	Placebo	-8.0	Baseline	0.0	Y	N	22	...		
...		
806	115003	74	F	Anavex2- 73 50 mg	-2.0	Baseline	50.0	Y	Y	21	...		
807	115003	74	F	Anavex2- 73 50 mg	334.0	Week 48	50.0	Y	Y	21	...		
808	115003	74	F	Anavex2- 73 50 mg	334.0	Week 48	50.0	Y	Y	21	...		
809	115005	56	M	Anavex2- 73 30 mg	-10.0	Baseline	30.0	Y	Y	19	...		
810	115005	56	M	Anavex2- 73 30 mg	-10.0	Baseline	30.0	Y	Y	19	...		

811 rows × 235 columns



```
In [14]: brain.hist(figsize=(20,30))
```



```
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dtype=object)
Error in callback <function flush_figures at 0x000002F05FB339C0> (for post_execute):

```

```

-----
KeyboardInterrupt                                Traceback (most recent call last)
File ~\ANACONDA\Lib\site-packages\matplotlib_inline\backend_inline.py:126, in flush_figures()
    123 if InlineBackend.instance().close_figures:
    124     # ignore the tracking, just draw and close all figures
    125     try:
--> 126         return show(True)
    127 except Exception as e:
    128     # safely show traceback if in IPython, else raise
    129     ip = get_ipython()

File ~\ANACONDA\Lib\site-packages\matplotlib_inline\backend_inline.py:90, in show(close, block)
    88 try:
    89     for figure_manager in Gcf.get_all_fig_managers():
---> 90         display(
    91             figure_manager.canvas.figure,
    92             metadata=_fetch_figure_metadata(figure_manager.canvas.figure)
    93         )
    94 finally:
    95     show._to_draw = []

File ~\ANACONDA\Lib\site-packages\IPython\core\display_functions.py:298, in display(include, exclude, metadata, transient, display_id, raw, clear, *objs, **kwargs)
    296     publish_display_data(data=obj, metadata=metadata, **kwargs)
    297 else:
--> 298     format_dict, md_dict = format(obj, include=include, exclude=exclude)
    299     if not format_dict:
    300         # nothing to display (e.g. _ipython_display_ took over)
    301         continue

File ~\ANACONDA\Lib\site-packages\IPython\core\formatters.py:179, in DisplayFormatter.format(self, obj, include, exclude)
    177 md = None
    178 try:
--> 179     data = formatter(obj)
    180 except:
    181     # FIXME: log the exception
    182     raise

File ~\ANACONDA\Lib\site-packages\decorator.py:232, in decorate.<locals>.fun(*args, **kw)
    230 if not kwsyntax:
    231     args, kw = fix(args, kw, sig)
--> 232 return caller(func, *(extras + args), **kw)

File ~\ANACONDA\Lib\site-packages\IPython\core\formatters.py:223, in catch_format_error(method, self, *args, **kwargs)
    221 """show traceback on failed format call"""
    222 try:
--> 223     r = method(self, *args, **kwargs)
    224 except NotImplementedError:
    225     # don't warn on NotImplementedError
    226     return self._check_return(None, args[0])

File ~\ANACONDA\Lib\site-packages\IPython\core\formatters.py:340, in BaseFormatter.__call__(self, obj)
    338     pass
    339 else:

```

```

--> 340     return printer(obj)
      341 # Finally look for special method names
      342 method = get_real_method(obj, self.print_method)

File ~\ANACONDA\Lib\site-packages\IPython\core\pylabtools.py:152, in print_figure(fig,
fmt, bbox_inches, base64, **kwargs)
      149     from matplotlib.backend_bases import FigureCanvasBase
      150     FigureCanvasBase(fig)
--> 152 fig.canvas.print_figure(bytes_io, **kw)
      153 data = bytes_io.getvalue()
      154 if fmt == 'svg':

File ~\ANACONDA\Lib\site-packages\matplotlib\backend_bases.py:2346, in FigureCanvasBase.print_figure(self, filename, dpi, facecolor, edgecolor, orientation, format,
bbox_inches, pad_inches, bbox_extra_artists, backend, **kwargs)
      2344 if bbox_inches:
      2345     if bbox_inches == "tight":
-> 2346         bbox_inches = self.figure.get_tightbbox(
      2347             renderer, bbox_extra_artists=bbox_extra_artists)
      2348     if pad_inches is None:
      2349         pad_inches = rcParams['savefig.pad_inches']

File ~\ANACONDA\Lib\site-packages\matplotlib\figure.py:1776, in FigureBase.get_tightbbox(self, renderer, bbox_extra_artists)
      1773     artists = bbox_extra_artists
      1775 for a in artists:
-> 1776     bbox = a.get_tightbbox(renderer)
      1777     if bbox is not None:
      1778         bb.append(bbox)

File ~\ANACONDA\Lib\site-packages\matplotlib\axes\_base.py:4388, in _AxesBase.get_tightbbox(self, renderer, call_axes_locator, bbox_extra_artists, for_layout_only)
      4386         if ba:
      4387             bb.append(ba)
-> 4388 self._update_title_position(renderer)
      4389 axbbox = self.get_window_extent(renderer)
      4390 bb.append(axbbox)

File ~\ANACONDA\Lib\site-packages\matplotlib\axes\_base.py:2963, in _AxesBase._update_title_position(self, renderer)
      2960 bb = None
      2961 if (ax.xaxis.get_ticks_position() in ['top', 'unknown']
      2962     or ax.xaxis.get_label_position() == 'top'):
-> 2963     bb = ax.xaxis.get_tightbbox(renderer)
      2964 if bb is None:
      2965     if 'outline' in ax.spines:
      2966         # Special case for colorbars:

File ~\ANACONDA\Lib\site-packages\matplotlib\axis.py:1325, in Axis.get_tightbbox(self, renderer, for_layout_only)
      1322     renderer = self.figure._get_renderer()
      1323 ticks_to_draw = self._update_ticks()
-> 1325 self._update_label_position(renderer)
      1327 # go back to just this axis's tick labels
      1328 tlb1, tlb2 = self._get_ticklabel_bboxes(ticks_to_draw, renderer)

File ~\ANACONDA\Lib\site-packages\matplotlib\axis.py:2310, in XAxis._update_label_position(self, renderer)
      2308 try:
      2309     spine = self.axes.spines['bottom']

```

```

-> 2310 spinebbox = spine.get_window_extent()
2311 except KeyError:
2312     # use Axes if spine doesn't exist
2313     spinebbox = self.axes.bbox

File ~\ANACONDA\Lib\site-packages\matplotlib\spines.py:158, in Spine.get_window_exten
t(self, renderer)
    156     return bb
    157 bboxes = [bb]
--> 158 drawn_ticks = self.axis._update_ticks()
    160 major_tick = next(iter(*drawn_ticks} & {*self.axis.majorTicks}), None)
    161 minor_tick = next(iter(*drawn_ticks} & {*self.axis.minorTicks}), None)

File ~\ANACONDA\Lib\site-packages\matplotlib\axis.py:1262, in Axis._update_ticks(sel
f)
    1257 def _update_ticks(self):
    1258     """
    1259     Update ticks (position and labels) using the current data interval of
    1260     the axes. Return the list of ticks that will be drawn.
    1261     """
-> 1262     major_locs = self.get_majorticklocs()
    1263     major_labels = self.major.formatter.format_ticks(major_locs)
    1264     major_ticks = self.get_major_ticks(len(major_locs))

File ~\ANACONDA\Lib\site-packages\matplotlib\axis.py:1484, in Axis.get_majorticklocs
(self)
    1482 def get_majorticklocs(self):
    1483     """Return this Axis' major tick locations in data coordinates."""
-> 1484     return self.major.locator()

File ~\ANACONDA\Lib\site-packages\matplotlib\ticker.py:2136, in MaxNLocator.__call__
(self)
    2134 def __call__(self):
    2135     vmin, vmax = self.axis.get_view_interval()
-> 2136     return self.tick_values(vmin, vmax)

File ~\ANACONDA\Lib\site-packages\matplotlib\ticker.py:2144, in MaxNLocator.tick_valu
es(self, vmin, vmax)
    2141     vmin = -vmax
    2142     vmin, vmax = mtransforms.nonsingular(
    2143         vmin, vmax, expander=1e-13, tiny=1e-14)
-> 2144     locs = self._raw_ticks(vmin, vmax)
    2146     prune = self._prune
    2147     if prune == 'lower':

File ~\ANACONDA\Lib\site-packages\matplotlib\ticker.py:2083, in MaxNLocator._raw_tick
s(self, vmin, vmax)
    2081     if self._nbins == 'auto':
    2082         if self.axis is not None:
-> 2083             nbins = np.clip(self.axis.get_tick_space(),
    2084                             max(1, self._min_n_ticks - 1), 9)
    2085         else:
    2086             nbins = 9

File ~\ANACONDA\Lib\site-packages\matplotlib\axis.py:2475, in XAxis.get_tick_space(se
lf)
    2474 def get_tick_space(self):
-> 2475     ends = mtransforms.Bbox.unit().transformed(
    2476         self.axes.transAxes - self.figure.dpi_scale_trans)
    2477     length = ends.width * 72

```



```
2478     # There is a heuristic here that the aspect ratio of tick text
2479     # is no more than 3:1
```

File ~\ANACONDA\Lib\site-packages\matplotlib\transforms.py:793, in Bbox.unit()

```
790 @staticmethod
791 def unit():
792     """Create a new unit `Bbox` from (0, 0) to (1, 1)."""
--> 793     return Bbox([[0, 0], [1, 1]])
```

File ~\ANACONDA\Lib\site-packages\matplotlib\transforms.py:772, in Bbox.__init__(self, points, **kwargs)

```
768 self._ignore = True
769 # it is helpful in some contexts to know if the bbox is a
770 # default or has been mutated; we store the orig points to
771 # support the mutated methods
--> 772 self._points_orig = self._points.copy()
```

KeyboardInterrupt:

```
In [15]: #counting rows and colums before cleaning
         brain.count
```

```

Out[15]: <bound method DataFrame.count of
SIT   BTID  RS.HOMN  \
0      101003    73    M  Anavex2-73  30 mg   -4.0  Baseline  20.0      Y
1      101003    73    M  Anavex2-73  30 mg   -4.0  Baseline  20.0      Y
2      101003    73    M  Anavex2-73  30 mg  340.0  Week 48  20.0      Y
3      101003    73    M  Anavex2-73  30 mg  340.0  Week 48  20.0      Y
4      101004    84    F              Placebo  -8.0  Baseline   0.0      Y
..      ...      ...    ..      ...      ...      ...      ...      ...
806    115003    74    F  Anavex2-73  50 mg   -2.0  Baseline  50.0      Y
807    115003    74    F  Anavex2-73  50 mg  334.0  Week 48  50.0      Y
808    115003    74    F  Anavex2-73  50 mg  334.0  Week 48  50.0      Y
809    115005    56    M  Anavex2-73  30 mg  -10.0  Baseline  30.0      Y
810    115005    56    M  Anavex2-73  30 mg  -10.0  Baseline  30.0      Y

      RS.GENE.neg  MMSE  ...  ASL CBF- Precuneus (left) Perfusion in mL/min/cm3  \
0                Y    17  ...                                                NaN
1                Y    17  ...                                                NaN
2                Y    17  ...                                                NaN
3                Y    17  ...                                                NaN
4                N    22  ...                                                NaN
..      ...      ...      ...      ...
806            Y    21  ...                                                NaN
807            Y    21  ...                                                NaN
808            Y    21  ...                                                NaN
809            Y    19  ...                                                NaN
810            Y    19  ...                                                NaN

      ASL CBF- Precuneus (left) Change in perfusion in mL/min/cm3 from baseline  \
0                NaN
1                NaN
2                NaN
3                NaN
4                NaN
..      ...
806            NaN
807            NaN
808            NaN
809            NaN
810            NaN

      ASL CBF- Precuneus (right) Perfusion in mL/min/cm3  \
0                NaN
1                NaN
2                NaN
3                NaN
4                NaN
..      ...
806            NaN
807            NaN
808            NaN
809            NaN
810            NaN

      ASL CBF- Precuneus (right) Change in perfusion in mL/min/cm3 from baseline  \
0                NaN
1                NaN
2                NaN
3                NaN
4                NaN
..      ...

```

806	NaN
807	NaN
808	NaN
809	NaN
810	NaN

	ASL CBF- Posterior cingulate cortex Perfusion in mL/min/cm3 \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
806	NaN
807	NaN
808	NaN
809	NaN
810	NaN

	ASL CBF- Posterior cingulate cortex Change in perfusion in mL/min/cm3 from baseline \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
806	NaN
807	NaN
808	NaN
809	NaN
810	NaN

	ASL CBF- Posterior cingulate cortex (left) Perfusion in mL/min/cm3 \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
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807	NaN
808	NaN
809	NaN
810	NaN

	ASL CBF- Posterior cingulate cortex (left) Change in perfusion in mL/min/cm3 from baseline \
0	NaN
1	NaN
2	NaN
3	NaN
4	NaN
..	...
806	NaN
807	NaN
808	NaN
809	NaN
810	NaN

```

ASL CBF- Posterior cingulate cortex (right) Perfusion in mL/min/cm3 \
0 NaN
1 NaN
2 NaN
3 NaN
4 NaN
.. ...
806 NaN
807 NaN
808 NaN
809 NaN
810 NaN

ASL CBF- Posterior cingulate cortex (right) Change in perfusion in mL/min/cm3 fr
om baseline
0 NaN
1 NaN
2 NaN
3 NaN
4 NaN
.. ...
806 NaN
807 NaN
808 NaN
809 NaN
810 NaN

[811 rows x 235 columns]>

```

```

In [16]: #drop the duplicates
brain = brain.drop_duplicates()
brain.head()

```

Out[16]:

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BTD	RS.HOMN	RS.GENE.neg	MMSE	...	ASL CI Precune (le Perfusior mL/min/c
0	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0		Y	Y	17 ...	N
1	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0		Y	Y	17 ...	N
2	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0		Y	Y	17 ...	N
3	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0		Y	Y	17 ...	N
4	101004	84	F	Placebo	-8.0	Baseline	0.0		Y	N	22 ...	N

5 rows × 235 columns



```
In [17]: brain
```

Out[17]:

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BTD	RS.HOMN	RS.GENE.neg	MMSE	...	ASL Preci	Perfusi mL/min
0	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0		Y	Y	17	...	
1	101003	73	M	Anavex2- 73 30 mg	-4.0	Baseline	20.0		Y	Y	17	...	
2	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0		Y	Y	17	...	
3	101003	73	M	Anavex2- 73 30 mg	340.0	Week 48	20.0		Y	Y	17	...	
4	101004	84	F	Placebo	-8.0	Baseline	0.0		Y	N	22	...	
...	
806	115003	74	F	Anavex2- 73 50 mg	-2.0	Baseline	50.0		Y	Y	21	...	
807	115003	74	F	Anavex2- 73 50 mg	334.0	Week 48	50.0		Y	Y	21	...	
808	115003	74	F	Anavex2- 73 50 mg	334.0	Week 48	50.0		Y	Y	21	...	
809	115005	56	M	Anavex2- 73 30 mg	-10.0	Baseline	30.0		Y	Y	19	...	
810	115005	56	M	Anavex2- 73 30 mg	-10.0	Baseline	30.0		Y	Y	19	...	

811 rows × 235 columns

```
In [18]: # find the null values
print(brain.isnull().sum())
```

SUBJID

0

AGE

0

SEX

0

TRT01A

0

Day

58

...

ASL CBF- Posterior cingulate cortex Change in perfusion in mL/min/cm3 from baseline
686

ASL CBF- Posterior cingulate cortex (left) Perfusion in mL/min/cm3

484

ASL CBF- Posterior cingulate cortex (left) Change in perfusion in mL/min/cm3 from baseline
682

ASL CBF- Posterior cingulate cortex (right) Perfusion in mL/min/cm3

478

ASL CBF- Posterior cingulate cortex (right) Change in perfusion in mL/min/cm3 from baseline
676

Length: 235, dtype: int64

```
In [19]: #drop the null(missing values)
         brain = brain.dropna()
         brain.count()
```

```
Out[19]: SUBJID
          94
          AGE
          94
          SEX
          94
          TRT01A
          94
          Day
          94
```

..

ASL CBF- Posterior cingulate cortex Change in perfusion in mL/min/cm3 from baseline
94

ASL CBF- Posterior cingulate cortex (left) Perfusion in mL/min/cm3

94

ASL CBF- Posterior cingulate cortex (left) Change in perfusion in mL/min/cm3 from baseline
94

ASL CBF- Posterior cingulate cortex (right) Perfusion in mL/min/cm3

94

ASL CBF- Posterior cingulate cortex (right) Change in perfusion in mL/min/cm3 from baseline
94

Length: 235, dtype: int64

```
In [20]: brain
```

Out[20]:

	SUBJID	AGE	SEX	TRT01A	Day	AVISIT	BTD	RS.HOMN	RS.GENE.neg	MMSE	...	ASL Preci	Perfusi mL/min
63	101025	60	F	Anavex2- 73 50 mg	-4.0	Baseline	20.0	Y	Y	24	...	13.1	
65	101026	72	F	Anavex2- 73 30 mg	-17.0	Baseline	30.0	Y	Y	19	...	15.1	
67	101026	72	F	Anavex2- 73 30 mg	338.0	Week 48	30.0	Y	Y	19	...	15.1	
69	101027	74	M	Anavex2- 73 50 mg	-14.0	Baseline	50.0	Y	Y	22	...	28.5	
71	101027	74	M	Anavex2- 73 50 mg	330.0	Week 48	50.0	Y	Y	22	...	28.5	
...	
587	111015	72	M	Placebo	338.0	Week 48	0.0	Y	Y	22	...	8.6	
590	111017	69	F	Anavex2- 73 30 mg	-22.0	Baseline	30.0	Y	Y	27	...	34.8	
592	111017	69	F	Anavex2- 73 30 mg	332.0	Week 48	30.0	Y	Y	27	...	34.8	
597	111027	67	F	Anavex2- 73 50 mg	-5.0	Baseline	30.0	Y	Y	28	...	21.1	
599	111027	67	F	Anavex2- 73 50 mg	329.0	Week 48	30.0	Y	Y	28	...	21.1	

94 rows × 235 columns

◀

▶

```
In [21]: #plots
         brain.hist(figsize=(20,30))
```



```
Out[21]: array([[<Axes: title={'center': 'SUBJID'}>,<Axes: title={'center': 'AGE'}>,<Axes: title={'center': 'Day'}>,<Axes: title={'center': 'BTD'}>,<Axes: title={'center': 'MMSE'}>,<Axes: title={'center': 'Subject birth year'}>,<Axes: title={'center': 'ICV (ml)'}>,<Axes: title={'center': 'Whole brain (combined WM and GM) (ml)'}>,<Axes: title={'center': 'Whole brain (combined WM and GM) (% ICV)'}>,<Axes: title={'center': 'Whole brain (combined WM and GM) (mL change from baseline)'}>,<Axes: title={'center': 'Whole brain (combined WM and GM) (annual % change from baseline)'}>,<Axes: title={'center': 'Whole brain (combined WM and GM) (BSI - mL change from baseline)'}>,<Axes: title={'center': 'Whole brain (combined WM and GM) (BSI - annual % change from baseline)'}>,<Axes: title={'center': 'Whole brain white matter (WM) (ml)'}>,<Axes: title={'center': 'Whole brain white matter (WM) (% ICV)'}>,<Axes: title={'center': 'Whole brain white matter (WM) (mL change from baseline)'}>,<Axes: title={'center': 'Whole brain white matter (WM) (annual % change from baseline)'}>,<Axes: title={'center': 'Whole brain grey matter (GM) (ml)'}>,<Axes: title={'center': 'Whole brain grey matter (GM) (% ICV)'}>,<Axes: title={'center': 'Whole brain grey matter (GM) (mL change from baseline)'}>,<Axes: title={'center': 'Whole brain grey matter (GM) (annual % change from baseline)'}>,<Axes: title={'center': 'Lateral Ventricles (ml)'}>,<Axes: title={'center': 'Lateral Ventricles (% ICV)'}>,<Axes: title={'center': 'Lateral Ventricles (mL change from baseline)'}>,<Axes: title={'center': 'Lateral Ventricles (annual % change from baseline)'}>,<Axes: title={'center': 'Hippocampus (ml)'}>,<Axes: title={'center': 'Hippocampus (% ICV)'}>,<Axes: title={'center': 'Hippocampus (mL change from baseline)'}>,<Axes: title={'center': 'Hippocampus (annual % change from baseline)'}>,<Axes: title={'center': 'Hippocampus (BSI - mL change from baseline)'}>,<Axes: title={'center': 'Hippocampus (BSI - annual % change from baseline)'}>,<Axes: title={'center': 'Hippocampus (left) (ml)'}>,<Axes: title={'center': 'Hippocampus (left) (% ICV)'}>,<Axes: title={'center': 'Hippocampus (left) (mL change from baseline)'}>,<Axes: title={'center': 'Hippocampus (left) (annual % change from baseline)'}>,<Axes: title={'center': 'Hippocampus (left) (BSI - mL change from baseline)'}>,<Axes: title={'center': 'Hippocampus (left) (BSI - annual % change from baseline)'}>,<Axes: title={'center': 'Hippocampus (right) (ml)'}>,<Axes: title={'center': 'Hippocampus (right) (% ICV)'}>,<Axes: title={'center': 'Hippocampus (right) (mL change from baseline)'}>,<Axes: title={'center': 'Hippocampus (right) (annual % change from baseline)'}>,<Axes: title={'center': 'Hippocampus (right) (BSI - mL change from baseline)'}>,<Axes: title={'center': 'Hippocampus (right) (BSI - annual % change from baseline)'}>,<Axes: title={'center': 'Temporal lobe (ml)'}>,<Axes: title={'center': 'Temporal lobe (% ICV)'}>],
```

```

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```

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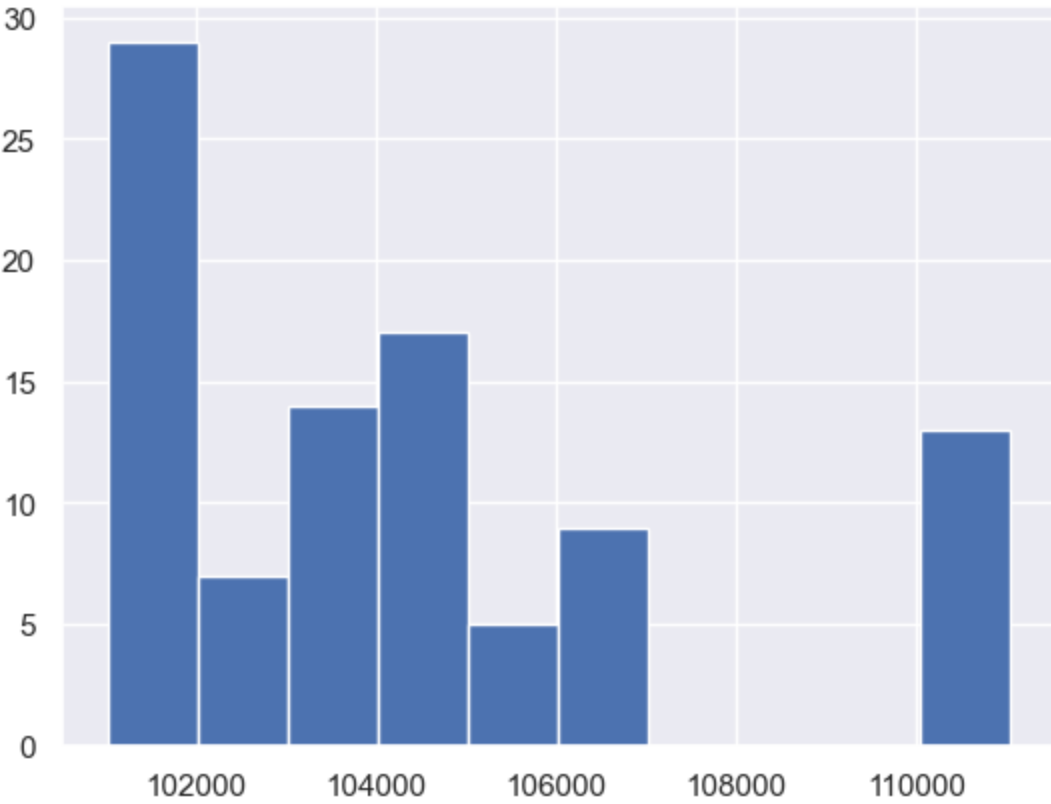
```

```

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```

```
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```



```
In [47]: anavex2
```

Out[47]:

	SUBJID	Subject birth year	Subject sex	Scan date	Timepoint	Date of form completion	ICV (ml)	Whole brain (combined WM and GM) (ml)	Whole brain (combined WM and GM) (% ICV)	(c
0	101001	1942	M	8/8/2019	Week48	8/27/2021	1744.44	1233.303	70.699038	
1	101002	1951	F	9/13/2018	Baseline	1/31/2019	1391.85	1029.378	73.957539	
2	101003	1945	M	9/13/2018	Baseline	1/15/2019	1623.29	1007.688	62.076893	
3	101003	1945	M	8/22/2019	Week48	11/22/2019	1624.22	995.623	61.298644	
4	101004	1934	F	9/27/2018	Baseline	1/31/2019	1398.50	972.417	69.532707	
...	
886	460015	1942	M	5/20/2021	Baseline	5/20/2021	1830.85	1044.045	57.025246	
887	460015	1942	M	4/26/2022	Week48	4/29/2022	1824.77	1050.492	57.568555	
888	460018	1938	M	6/3/2021	Baseline	6/3/2021	1502.69	1084.067	72.141759	
889	460020	1944	F	6/16/2021	Baseline	6/16/2021	1431.21	1032.476	72.140077	
890	460020	1944	F	5/25/2022	Week48	5/27/2022	1429.91	995.734	69.636228	

891 rows × 225 columns



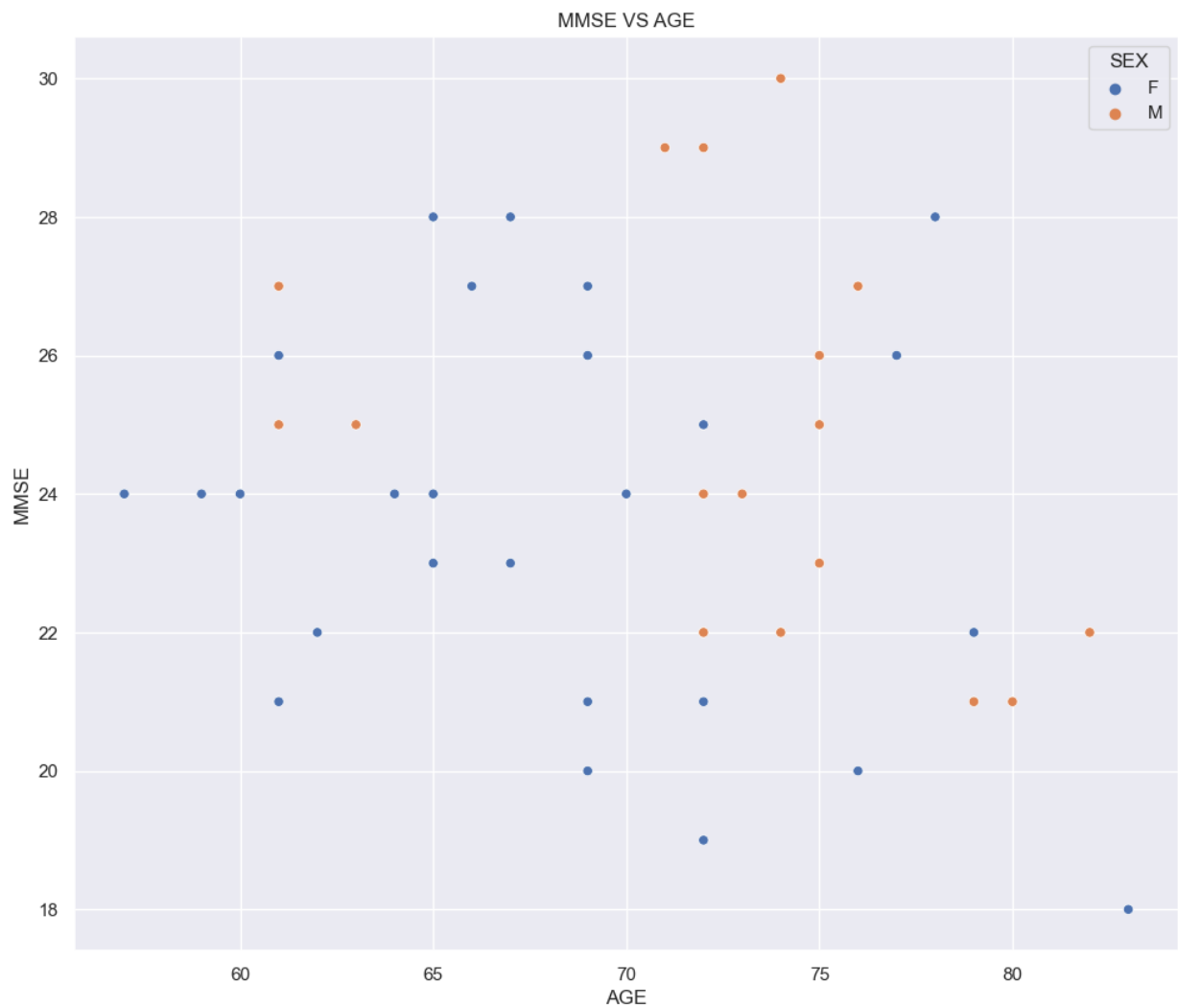
In []:

In [39]:

```
#MMSE AGAINST AGE
plt.figure(figsize=(12,10))
axis = sns.scatterplot(x="AGE", y='MMSE',data=brain, hue="SEX")
plt.title('MMSE VS AGE')
```

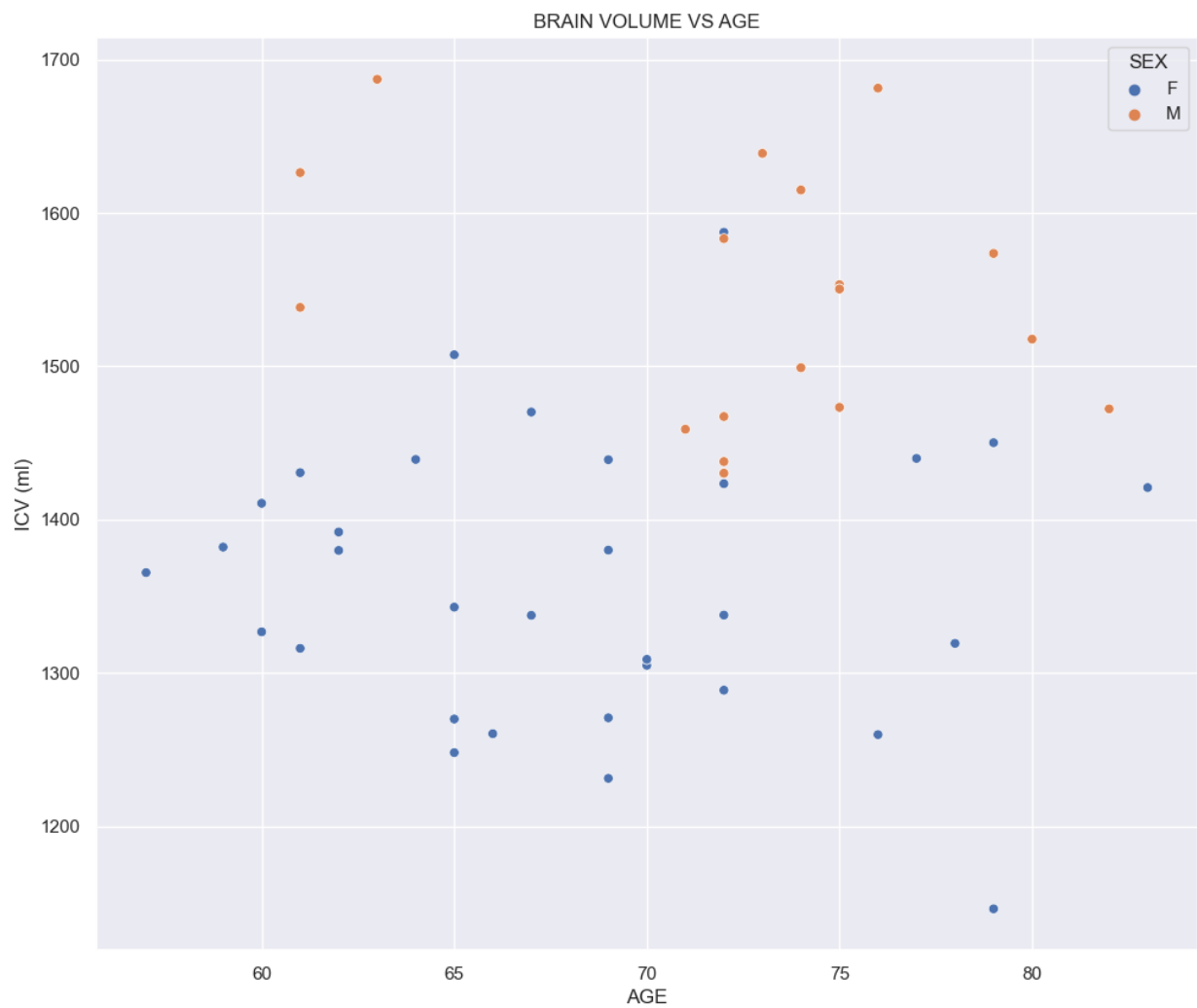
Out[39]:

Text(0.5, 1.0, 'MMSE VS AGE')



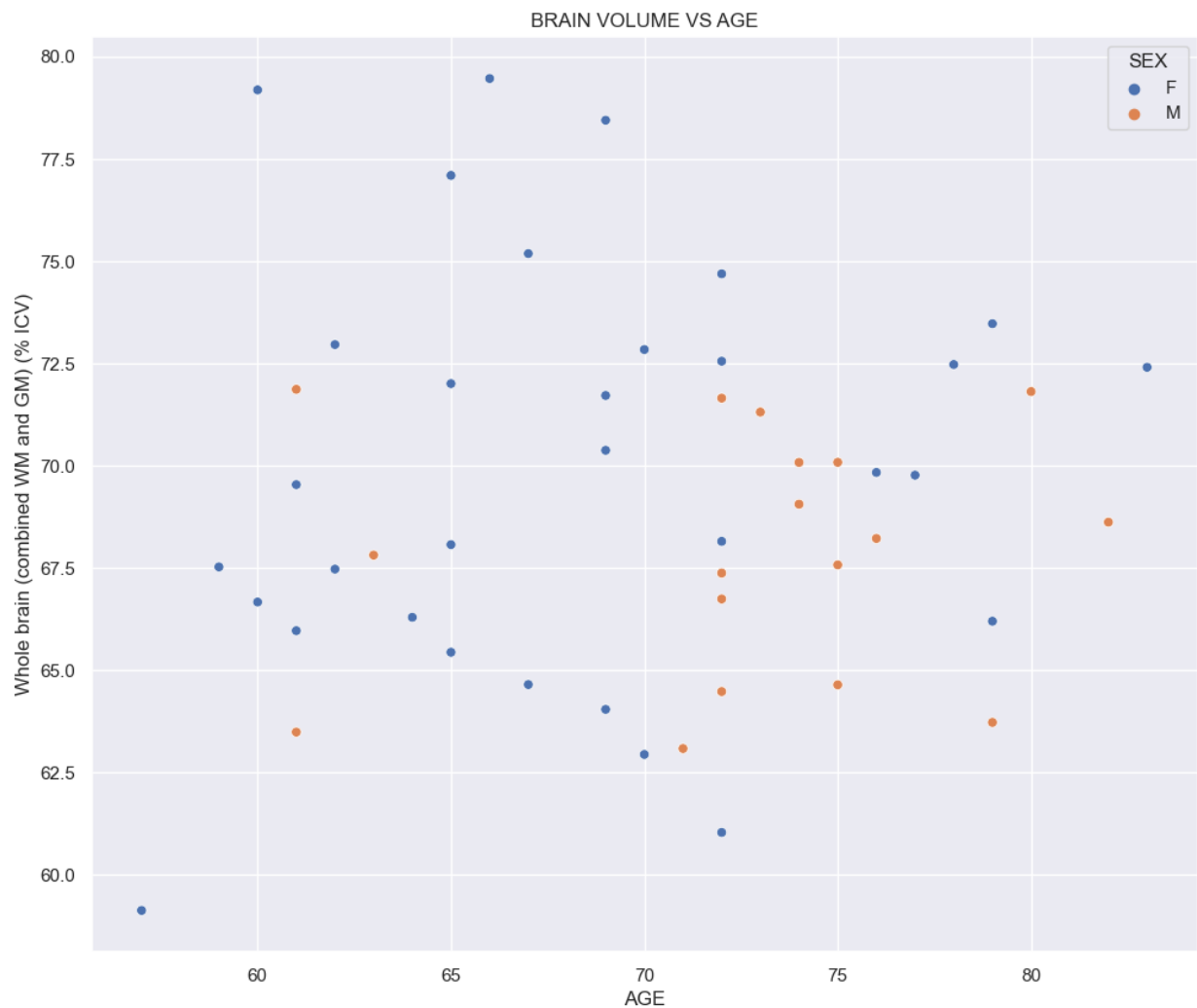
```
In [43]: #BRAIN VOLUME WITH AGE
plt.figure(figsize=(12,10))
axis = sns.scatterplot(x="AGE", y='ICV (ml)',data=brain, hue="SEX")
plt.title('BRAIN VOLUME VS AGE')
```

```
Out[43]: Text(0.5, 1.0, 'BRAIN VOLUME VS AGE')
```



```
In [44]: #BRAIN VOLUME WITH AGE
plt.figure(figsize=(12,10))
axis = sns.scatterplot(x="AGE", y='Whole brain (combined WM and GM) (% ICV)', data=brai
plt.title('BRAIN VOLUME VS AGE')
```

```
Out[44]: Text(0.5, 1.0, 'BRAIN VOLUME VS AGE')
```

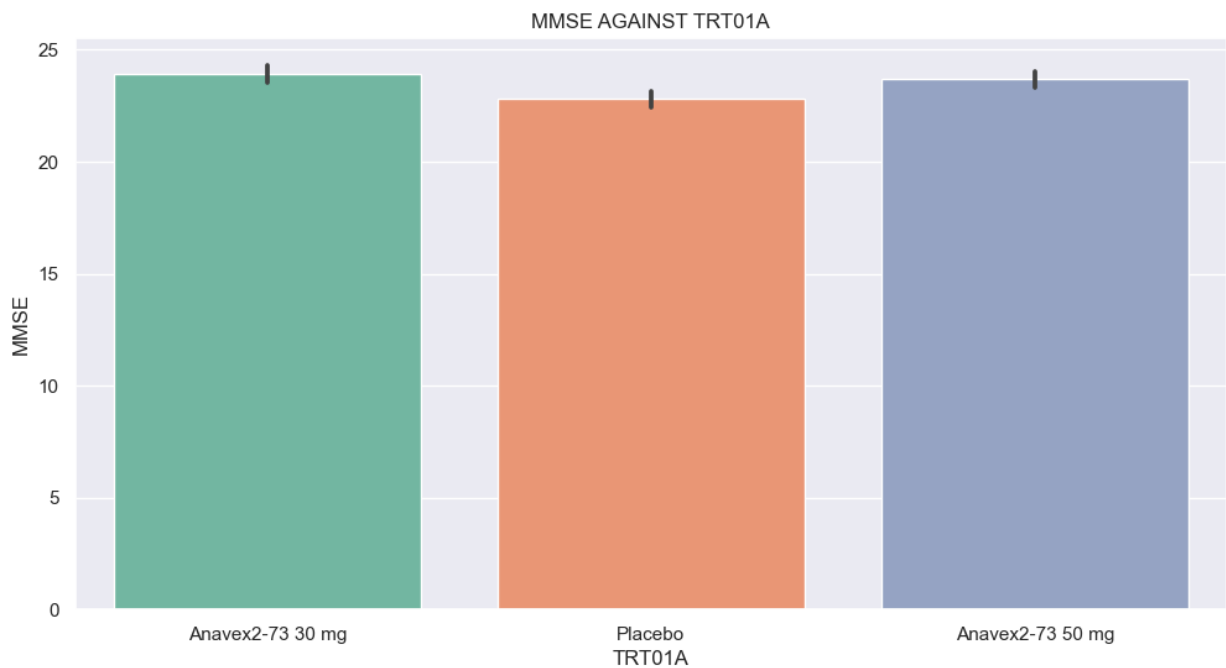


```
In [48]: #BRAIN VOLUME WITH AGE
plt.figure(figsize=(12,10))
axis = sns.scatterplot(x="AGE", y='Whole brain (combined WM and GM) (ml)',data=brain,
plt.title('BRAIN VOLUME VS AGE')
```

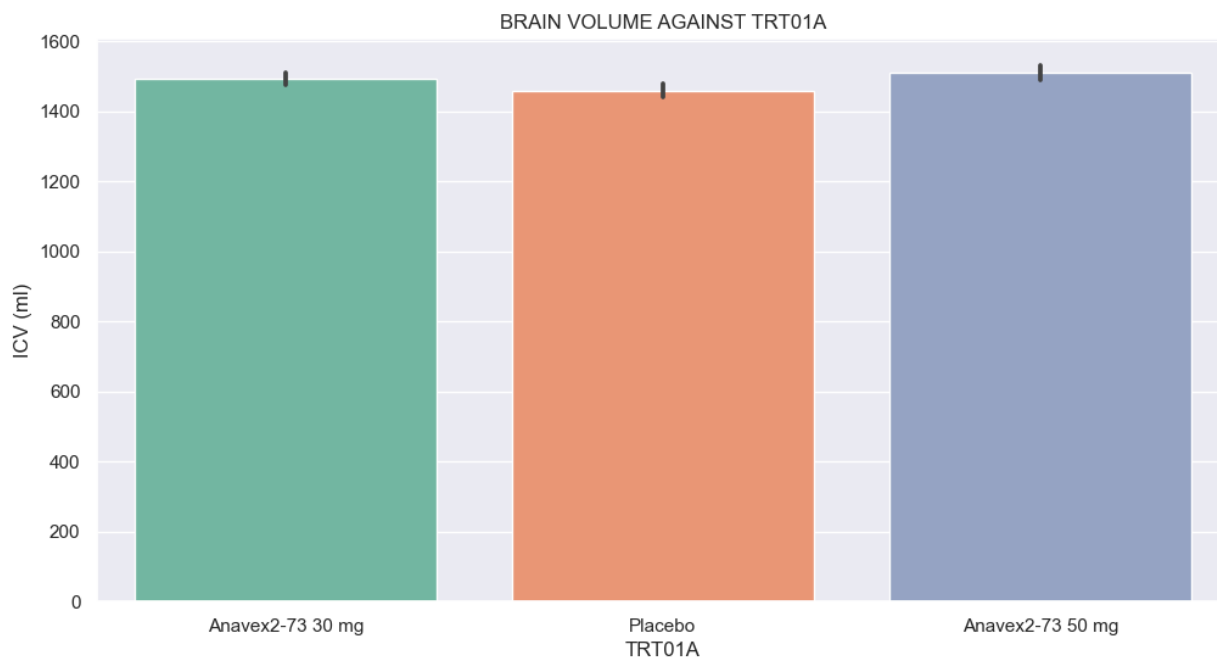
```
Out[48]: Text(0.5, 1.0, 'BRAIN VOLUME VS AGE')
```



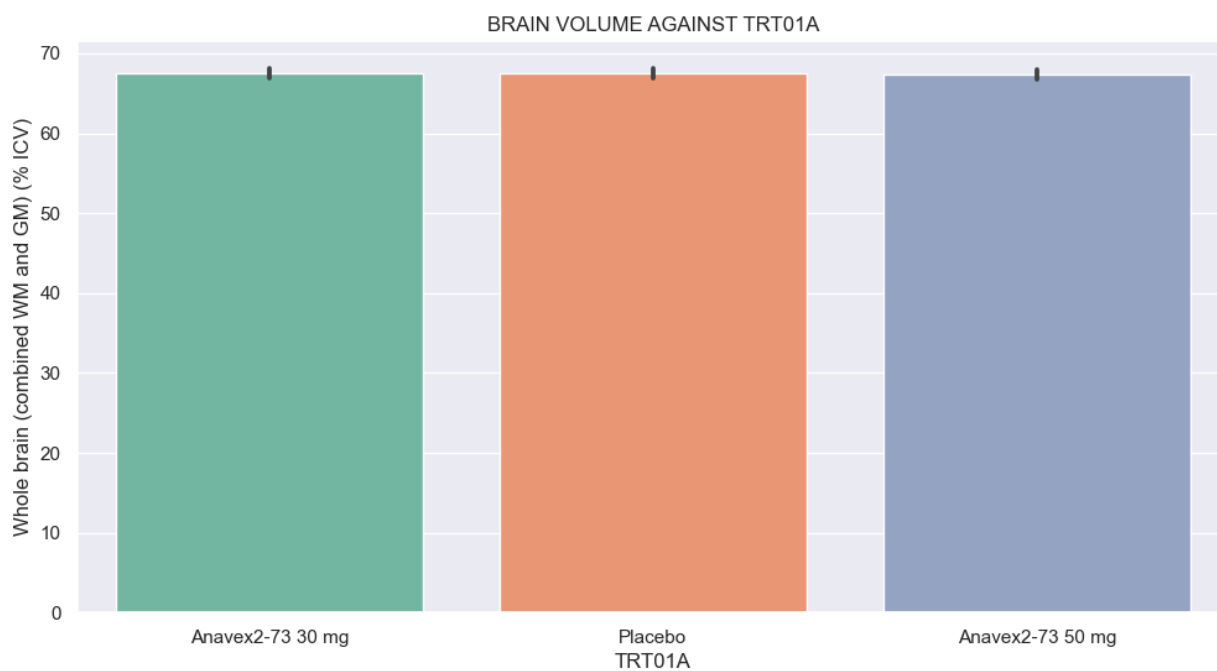
```
In [49]: #MMSE AND TREATMENT
plt.figure(figsize=(12,6))
plt.title("MMSE AGAINST TRT01A")
sns.barplot(x= brain['TRT01A'], y= brain['MMSE'], palette = 'Set2');
```



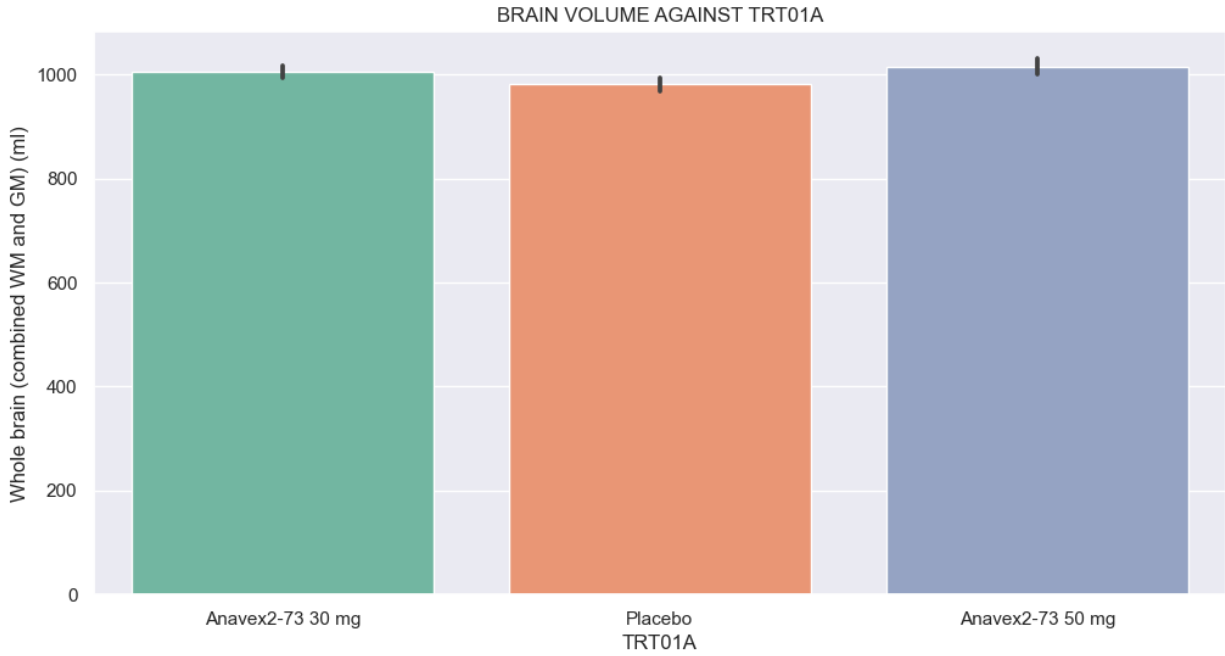
```
In [50]: #BRAIN VOLUME AND TREATMENT
plt.figure(figsize=(12,6))
plt.title("BRAIN VOLUME AGAINST TRT01A")
sns.barplot(x= brain['TRT01A'], y= brain['ICV (ml)'], palette = 'Set2');
```



```
In [51]: #BRAIN VOLUME AND TREATMENT
plt.figure(figsize=(12,6))
plt.title("BRAIN VOLUME AGAINST TRT01A")
sns.barplot(x= brain['TRT01A'], y= brain['Whole brain (combined WM and GM) (% ICV)'],
```



```
In [52]: #BRAIN VOLUME AND TREATMENT
plt.figure(figsize=(12,6))
plt.title("BRAIN VOLUME AGAINST TRT01A")
sns.barplot(x= brain['TRT01A'], y= brain['Whole brain (combined WM and GM) (ml)'], pal
```



```
In [ ]:
```