Data Description:

A short (non medically exhaustive) description of the feature meaning

analysis of umbilical artery blood sample

- **pH** : Is the ph of the blood of the baby (n.v. 7.35-7.45). A slight increase causes blood alkalosis while a slight decrease causes acidosis. Both conditions are extremely life threatening. This value is inverse proportional to **pCO2**.
- **BDecf** : Base excess of extracellular fluid is a quantity that reflects only the non-respiratory (metabolic) component of acid-base disturbances. (Reference : Here)
- **pCO2** : is the relative pressure of CO2 in the blood (n.v. 4.5-6.0Kpa). In Respiratory Acidosis, **pH** and **pCO2** are inverse proportional while in Metabolic Acidosis they are directly proportional.
- **BE** : Is the excess or deficit (if negative) of bases in the blood (e.g. HCO3). The normal range is between -2 and +2 mEq/L or mmol/L. A value above the range is indicative of Metabolic Alkalosis while below the range is indicative of Metabolic Acidosis.
- **Apgar1** : It's the Apgar score at 1min from birth. It indicates the overall health status of the baby at birth. It can have values between 0 and 10 where a score above 7 is considered good. (Reference and table : Here)
- **Apgar5** : It's the Apgar score at 5min from birth. See **Apgar1**.
- **Gest. weeks** : It's the number of weeks of gestation where 39-40 weeks represent a normal term delivery.
- **Weight(g)** : Is the weigth of the baby in grams at birth. This is various but in general the normal range would be between 2500g and 4500g.
- **Sex** : This is a boolean for 1 and 2 where is not clear which is male/female but shouldn't matter.
- **Age** : The Age in years of the mom.
- **Gravidity** : Is the number of times the woman has been pregnant in her life.
- **Parity** : Is the number of times the woman has been pregnant for more than 24 weeks (in a single pregnancy).
- **Diabetes** : Boolean value for Diabetes of 0 (False) and 1 (True).
- **Hypertension** : Boolean value for Hypertension of 0 (False) and 1 (True).
- **Preeclampsia** : Boolean value for Preeclampsia of 0 (False) and 1 (True). where Preeclampsia indicate a disorder of pregnancy that could lead to complications.
- **Liq.** : It referes to Liquor which in this case is the Amniotic Fluid. I'm not sure why is a boolean in the data.
- **Pyrexia** : Is a boolean value that indicate the presence of pyrexia (high temperature) in the mom or not.
- **Meconium** : Is a boolean value that indicate the presence or not of Meconium which is the earliest stool of the baby that could happen before partum.
- **Presentation** : This indicate the presentation of the baby during delivery which can be head first, legs first etc. The problem here is that this value is a number which most probably refers to an internal classification or a scale I don't know how to interpret. **See also Deliv. type**
- **Induced** : Is a boolean value that indicate if the delivery has been medically induced.
- **I.stage** : It should indicate the time in between contractions in the stage of the delivery but this is only my observational opinon based on the data.
- **NoProgress** : Is a boolean value that indicate if there has been an abort of the pregnancy or not.
- **CK/KP** : It should refer to the level of Creatine Kinase?
- **II.stage** : see **I.stage**.
- **Deliv. type** : (1: vaginal; 2: operative vaginal; 3: CS)
- **dbID** : is just an ID of the record
- **Rec. type** : No idea
- **Pos. II.st.** : No idea

In [93]:
```
class CTG_data:
    import pandas as pd
    import numpy as np
    import os
    from tqdm import tqdm
    import seaborn as sns
    import matplotlib.pyplot as plt

    df = pd.DataFrame()

    # Initialize dataframe, converts floats to integer where possible,
    # Optimise datatype (e.g. from Float64 to Float16) where possible
    # Drop columns that contains only unique values
    # Store nan values and unique values as:
    #     self.nan_values and self.unique_values
    # Store the name of the features that contains nan values in a list:
    #     self.contains_nan
    def __init__(self,*signal):
        if signal:
            df_signal = pd.read_csv("database/signals/%s" % signal)
            df_signal = df_signal.set_index("seconds")
            df_signal.index.rename("",inplace=True)
            self.df = df_signal
            self.floats_to_integers()
            self.optimize_datatypes()
        else:
            df_ann = pd.read_csv("database/ann_db.csv")
            df_ann = df_ann.set_index('Unnamed: 0')
            df_ann.index.rename('', inplace=True)
            df_ann = df_ann.T
            self.df = df_ann
            self.floats_to_integers()
            self.optimize_datatypes()
            self.drop_unique_columns()
            self.get_nan_values()
            self.get_unique_values_numbers()

    def get_nan_values(self):
        df = self.df
        self.nan_values = {"TOTAL_RECORDS" : df.shape[0]}
        self.contains_nan = []
        for col in tqdm(df.columns):
            self.nan_values[col] = df[col].loc[df[col].isna() == True].size
            if self.nan_values[col] > 0:
                self.contains_nan.append(col)

    def get_unique_values_numbers(self):
        df = self.df
        self.unique_dict = {}
        for col in tqdm(df.columns):
            col_dict = {}
            unique_values = df[col].unique()
            nan_values = df[col].loc[df[col].isna() == True].size
            if nan_values > 0:
                col_dict["nan"] = nan_values
            for val in unique_values:
                col_dict[val] = df[col].loc[df[col] == val].shape[0]
            self.unique_dict[col] = col_dict

    def floats_to_integers(self):
        df = self.df
        for col in df.columns:
            if df[col].dtype == "float64" or df[col].dtype == "float32":
                isint = df[col].apply(lambda x : x.is_integer())
                if False not in np.array(isint):
                    df[col] = df[col].astype("int64")
        self.df = df

    def optimize_datatypes(self):
        df = self.df
        for col in df.columns:
            if df[col].dtype == "float64":
                df[col] = df[col].astype("float32")
            elif df[col].dtype == "int64":
                maxvalue = df[col].max()
                minvalue = df[col].min()
                if (minvalue >= -128 and maxvalue <= 127) or (minvalue >= 0 and maxvalue <= 255):
                    df[col] = df[col].astype("int8")
                else:
                    df[col] = df[col].astype("int16")
        self.df = df

    def drop_unique_columns(self):
        df = self.df
        unique_values = {}
        for col in tqdm(df.columns):
            unique_values[col] = df[col].unique().size
            if unique_values[col] < 2:
                df = df.drop([col],axis=1)
        self.df = df

    def convert_nan_values(self):
        df = self.df
        for col in tqdm(self.contains_nan):
            isint = df[col].apply(lambda x : x.is_integer())
            isint = isint.loc[isint == False].index
            uniques_values = df[col].loc[df[col].index.isin(isint)].unique()
            if uniques_values.size < 2 :
                if str(uniques_values[0]) == "nan":
                    df[col].fillna(value=np.around(df[col].mean()),inplace=True)
            else:
                df[col].fillna(value=df[col].mean(),inplace=True)

        self.df = df
```

In [94]:
```
# Get CTG Annotations data
ctg_data = CTG_data()
ctg_data.df.head()
```

```
100%|██████████| 35/35 [00:00<00:00, 1843.07it/s]
100%|██████████| 28/28 [00:00<00:00, 1831.72it/s]
100%|██████████| 28/28 [00:00<00:00, 60.58it/s]
```

Out[94]:

	pH	BDecf	pCO2	BE	Apgar1	Apgar5	Gest. weeks	Weight(g)	Sex	Age	...	Presentation	Induced	I.stage	NoProgress	CK/KP	II.stage	Deliv. type	dbID
1220	7.30	3.52	6.0	-4.7	9	10	42	3100.0	2	34	...	1.0	1	165	0	0	15	1	3056
1234	7.29	2.50	6.5	-4.2	8	9	41	3200.0	1	29	...	1.0	0	135	0	0	10	1	5619
1208	7.23	5.84	6.6	-7.4	9	9	40	3900.0	2	26	...	1.0	0	260	0	0	30	1	960
1038	7.33	2.72	5.7	-4.0	10	10	39	2740.0	1	24	...	2.0	0	15	0	0	10	1	19468
1004	7.30	5.19	5.5	-6.4	8	9	41	3370.0	1	36	...	1.0	1	55	0	0	10	1	237

5 rows × 28 columns

In [76]:
```
ctg_data.df.describe().T
```

Out[76]:

	count	mean	std	min	25%	50%	75%	max
pH	552.0	7.230055	0.105039	6.850000	7.17	7.25	7.30	7.470000
BDecf	541.0	4.601905	3.553392	-3.400000	2.49	4.13	6.14	26.110001
pCO2	541.0	7.069500	1.556687	0.700000	5.90	7.00	7.90	12.300000
BE	541.0	-6.384105	3.827454	-26.799999	-8.00	-5.60	-4.00	-0.200000
Apgar1	552.0	8.262681	1.624959	1.000000	8.00	9.00	9.00	10.000000
Apgar5	552.0	9.068841	1.085613	4.000000	9.00	9.00	10.00	10.000000
Gest. weeks	552.0	39.994565	1.132737	37.000000	39.00	40.00	41.00	43.000000
Weight(g)	551.0	3400.426514	454.781921	1970.000000	3100.00	3410.00	3700.00	4750.000000
Sex	552.0	1.481884	0.500125	1.000000	1.00	1.00	2.00	2.000000
Age	552.0	29.673913	4.538863	18.000000	27.00	30.00	33.00	46.000000
Gravidity	548.0	1.406934	1.031719	1.000000	1.00	1.00	1.00	11.000000
Parity	552.0	0.409420	0.724814	0.000000	0.00	0.00	1.00	7.000000
Diabetes	552.0	0.067029	0.250299	0.000000	0.00	0.00	0.00	1.000000
Hypertension	552.0	0.079710	0.271090	0.000000	0.00	0.00	0.00	1.000000
Preeclampsia	552.0	0.030797	0.172924	0.000000	0.00	0.00	0.00	1.000000
Liq.	552.0	0.266304	0.442426	0.000000	0.00	0.00	1.00	1.000000
Pyrexia	552.0	0.010870	0.103783	0.000000	0.00	0.00	0.00	1.000000
Meconium	552.0	0.115942	0.320446	0.000000	0.00	0.00	0.00	1.000000
Presentation	549.0	1.149362	0.494037	1.000000	1.00	1.00	1.00	3.000000
Induced	552.0	0.393116	0.488885	0.000000	0.00	0.00	1.00	1.000000
I.stage	552.0	222.451087	111.882609	-30.000000	135.00	216.50	290.00	648.000000
NoProgress	552.0	0.099638	0.299788	0.000000	0.00	0.00	0.00	1.000000
CK/KP	552.0	0.025362	0.157366	0.000000	0.00	0.00	0.00	1.000000
II.stage	552.0	12.456522	8.233101	-1.000000	5.00	10.00	20.00	30.000000
Deliv. type	552.0	1.083333	0.276636	1.000000	1.00	1.00	1.00	2.000000
dbID	552.0	1189.831522	18321.436802	-32668.000000	-13699.00	1863.50	16895.50	32735.000000
Rec. type	552.0	1.875000	2.668079	-1.000000	1.00	1.00	1.00	12.000000
Pos. II.st.	552.0	13241.315217	4012.185116	-1.000000	14400.00	14400.00	14400.00	19277.000000

We can notice that:

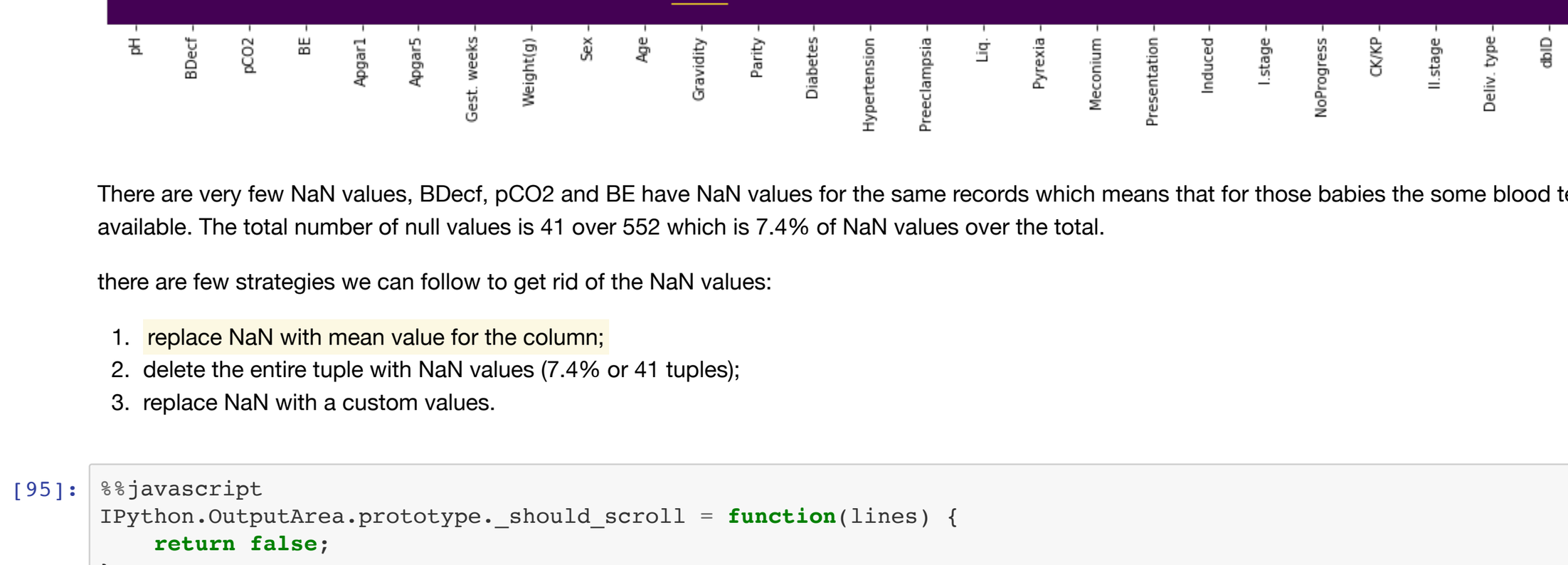
- there are few NaN values in the dataset;
- the number of decimal points for some of the features (e.g. weight) is too high which means that is not been converted appropriately from float to int. This may be due to the presence of null values. We'll tackle that later.

In [77]:
```
print(ctg_data.nan_values)
```

```
{'TOTAL_RECORDS': 552, 'pH': 0, 'BDecf': 11, 'pCO2': 11, 'BE': 11, 'Apgar1': 0, 'Apgar5': 0, 'Gest. weeks': 0, 'Weigh
t(g)': 1, 'Sex': 0, 'Age': 0, 'Gravidity': 4, 'Parity': 0, 'Diabetes': 0, 'Hypertension': 0, 'Preeclampsia': 0, 'Liq.
': 0, 'Pyrexia': 0, 'Meconium': 0, 'Presentation': 3, 'Induced': 0, 'I.stage': 0, 'NoProgress': 0, 'CK/KP': 0, 'II.st
age': 0, 'Deliv. type': 0, 'dbID': 0, 'Rec. type': 0, 'Pos. II.st.': 0}
```

In [78]:
```
plt.figure(figsize=(20, 5))
sns.heatmap(ctg_data.df.isnull(),yticklabels=False,cbar=False,cmap='viridis')
```

Out[78]: <matplotlib.axes._subplots.AxesSubplot at 0x1a1943fb90>



There are very few NaN values, BDecf, pCO2 and BE have NaN values for the same records which means that for those babies the some blood test wasn't available. The total number of null values is 41 over 552 which is 7.4% of NaN values over the total.

there are few strategies we can follow to get rid of the NaN values:

1. replace NaN with mean value for the column;
2. delete the entire tuple with NaN values (7.4% or 41 tuples);
3. replace NaN with a custom values.

In [95]:
```
%%javascript
IPython.OutputArea.prototype._should_scroll = function(lines) {
    return false;
}
```

Let's display now the unique values for each of the annotation features to see what is the distribution of the data and if the data are effectively skewed or balanced and for what features.

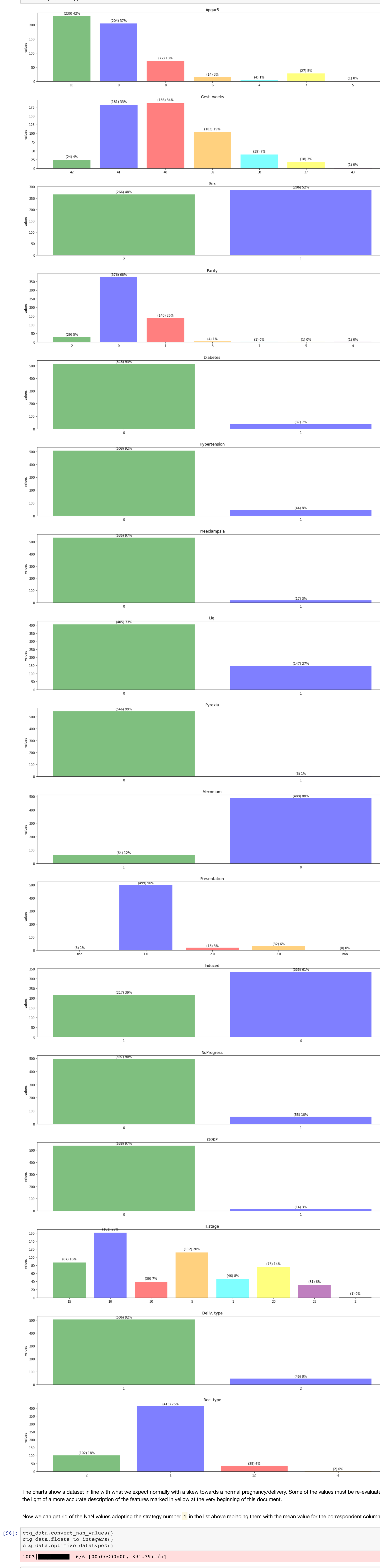
In [80]:
```
unique_values = ctg_data.unique_dict
for col in list(unique_values.keys()):
    if len(list(unique_values[col].keys())) < 10:
        y_pos = np.arange(len(list(unique_values[col].keys())))
        objects = list(unique_values[col].values())

        plt.figure(figsize=(20,4))
        plt.bar(y_pos, objects, align='center', alpha=0.5, color=['g','b','r','orange','cyan','yellow','purple','black
','brown','gray'])
        plt.xticks(y_pos,list(unique_values[col].keys()))
        plt.ylabel('values')
        plt.title(col)

        ax = plt.gca()
        rects = ax.patches
        labels = ["(%i) " % x + str(round((x*100)/sum(objects))) + "%" for x in objects]

        for rect, label in zip(rects, labels):
            height = rect.get_height()
            ax.text(rect.get_x() + rect.get_width() / 2, height + 5, label,
                    ha='center', va='bottom')

        plt.show()
```



The charts show a dataset in line with what we expect normally with a skew towards a normal pregnancy/delivery. Some of the values must be re-evaluated in the light of a more accurate description of the features marked in yellow at the very beginning of this document.

Now we can get rid of the NaN values adopting the strategy number 1 in the list above replacing them with the mean value for the correspondent column.

In [96]:
```
ctg_data.convert_nan_values()
ctg_data.floats_to_integers()
ctg_data.optimize_datatypes()
```

```
100%|██████████| 6/6 [00:00<00:00, 391.39it/s]
```

In [97]:
```
ctg_data.df.head()
```

Out[97]:

	pH	BDecf	pCO2	BE	Apgar1	Apgar5	Gest. weeks	Weight(g)	Sex	Age	...	Presentation	Induced	I.stage	NoProgress	CK/KP	II.stage	Deliv. type	dbID
1220	7.30	3.52	6.0	-4.7	9	10	42	3100	2	34	...	1	1	165	0	0	15	1	3056
1234	7.29	2.50	6.5	-4.2	8	9	41	3200	1	29	...	1	0	135	0	0	10	1	5619
1208	7.23	5.84	6.6	-7.4	9	9	40	3900	2	26	...	1	0	260	0	0	30	1	960
1038	7.33	2.72	5.7	-4.0	10	10	39	2740	1	24	...	2	0	15	0	0	10	1	19468
1004	7.30	5.19	5.5	-6.4	8	9	41	3370	1	36	...	1	1	55	0	0	10	1	237

5 rows × 28 columns

We can see we optimised the datatypes as well so to reduce the memory usage and speed up our computations.

In [83]:
```
ctg_data.df.dtypes
```

Out[83]:
```
pH               float32
BDecf            float32
pCO2             float32
BE               float32
Apgar1              int8
Apgar5              int8
Gest. weeks         int8
Weight(g)          int16
Sex                 int8
Age                 int8
Gravidity           int8
Parity              int8
Diabetes            int8
Hypertension        int8
Preeclampsia        int8
Liq.                int8
Pyrexia             int8
Meconium            int8
Presentation        int8
Induced             int8
I.stage            int16
NoProgress          int8
CK/KP               int8
II.stage            int8
Deliv. type         int8
dbID               int16
Rec. type           int8
Pos. II.st.        int16
dtype: object
```

Danger:

The following is a very computationally expensive process that will take the **FHR** and **UC** signal of each baby and match it with the appropriate annotations. This process will create a single dataframe with a lot of redundancy (1.3Gb). If there is a better way to combine the annotations with the signals, please let me know! :)

In [ ]:
```
df = pd.DataFrame()
files = []
for directory, subdir, files in os.walk("database/signals/"):
    pass

total = len(files)
with tqdm(total=total, position=0, leave=True) as pbar:
    for file in files:
        pbar.update()
        if file[file.find("."):] == ".csv":
            df_signal = CTG_data(file)
            filename = file[:file.find(".")]
            ann = ctg_data.df.loc[ctg_data.df.index == filename]
            for f in ann.columns:
                feature_list = []
                for i in range(df_signal.df.shape[0]):
                    feature_list.append(ann[f][0])
                df_signal.df[f] = feature_list
            if df.shape[0] == 0:
                df = df_signal.df
            else:
                df = pd.concat([df,df_signal.df])
        break

print(df.shape)
df.head()
```

In [48]:
```
df.to_csv("database/full.csv", index=False)
```

In [ ]: