Survival_Analysis

July 12, 2021

0.1 Input

[1]:
```
#import necessary libraries
import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
import warnings


#import lifelines library for survival analysis & regression
from lifelines import AalenAdditiveFitter, CoxPHFitter, KaplanMeierFitter,␣
↪NelsonAalenFitter, WeibullAFTFitter, WeibullFitter, LogNormalFitter,␣
↪LogLogisticFitter, ExponentialFitter
from lifelines.utils import qth_survival_times, k_fold_cross_validation,␣
↪find_best_parametric_model
from lifelines.calibration import survival_probability_calibration
from lifelines.plotting import qq_plot


#set standard options for dataframe viewing and plotting
pd.set_option('display.max_columns', None)
pd.set_option('display.max_rows', 50)
plt.rcParams["figure.figsize"] = (15,5)
plt.style.use(["ggplot","seaborn-whitegrid"])

#ignore warnings for functions that will soon be outdated
warnings.simplefilter(action="ignore", category=FutureWarning)
```

[2]:
```
##########INPUT CLEANED DATA###########

file = 'data.sas7bdat'

########################################
```

[3]:
```
data = pd.read_sas(file, index='ID')
```

0.2 Data Transformation

[4]:
```
#Transform certain columns of dataframe into integers (mainly to remove .0)

liste = ['AGE', 'GENDER', 'HR', 'SYSBP', 'DIASBP', 'CVD', 'AFB', 'SHO', 'CHF',␣
↪'AV3', 'MIORD', 'MITYPE', 'YEAR', 'LOS', 'DSTAT', 'LENFOL', 'FSTAT']

for i in liste:
    data[i] = data[i].astype('int64')

data.index = data.index.astype('int64')
```

0.2.1 Data Viewing

[5]:
```
data.shape
```

[5]: (500, 18)

[6]:
```
data.head()
```

[6]:
```
    AGE  GENDER  HR  SYSBP  DIASBP        BMI  CVD  AFB  SHO  CHF  AV3  MIORD  \
ID
1    83       0  89    152      78  25.540510    1    1    0    0    0      1
2    49       0  84    120      60  24.023979    1    0    0    0    0      0
3    70       1  83    147      88  22.142900    0    0    0    0    0      0
4    70       0  65    123      76  26.631870    1    0    0    1    0      0
5    70       0  63    135      85  24.412550    1    0    0    0    0      0

    MITYPE  YEAR  LOS  DSTAT  LENFOL  FSTAT
ID
1        0     1    5      0    2178      0
2        1     1    5      0    2172      0
3        1     1    5      0    2190      0
4        1     1   10      0     297      1
5        1     1    6      0    2131      0
```

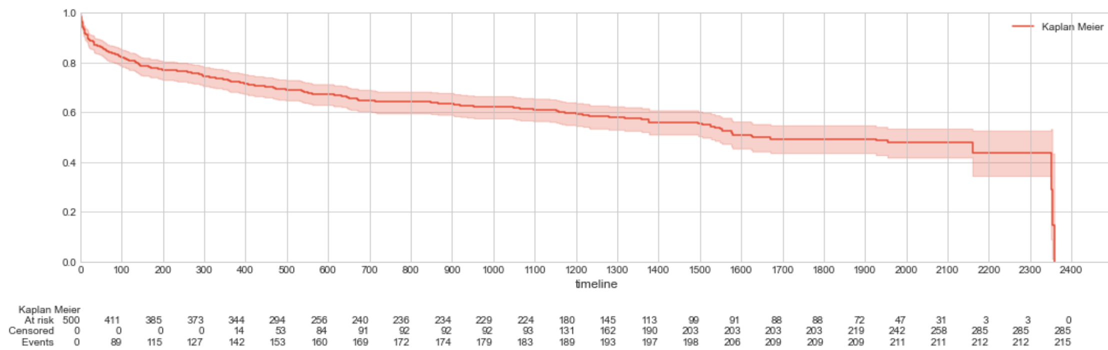
For detailed description of columns see documentary.

0.3 First Testing

Here we do a first testing on our data with the univariate survival model Kaplan Meier.

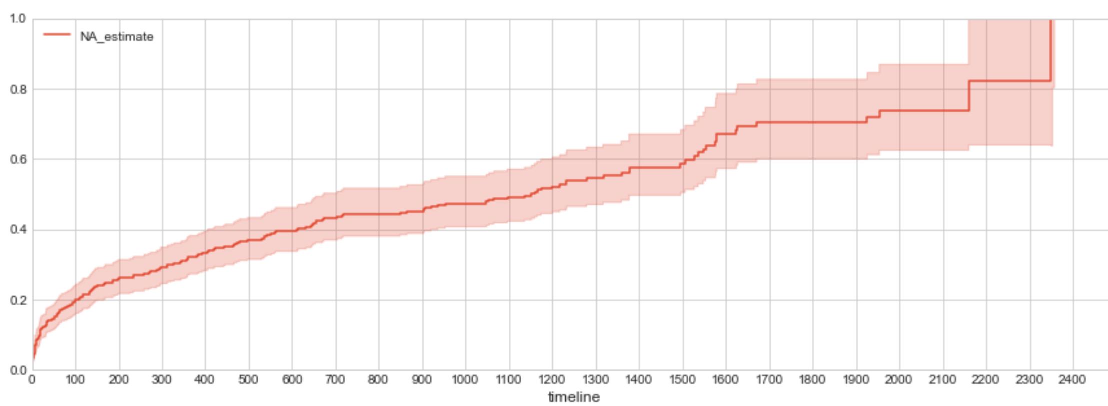
[7]:
```
kmf = KaplanMeierFitter()
kmf.fit(data['LENFOL'], event_observed=data['FSTAT'], label='Kaplan Meier')

#customizing plot (also done in future plots)
plt.axis([0,2500,0,1])
plt.xticks(np.arange(0, 2500, step=100))
kmf.plot_survival_function(at_risk_counts=True)
```

```
plt.grid(b=True, which='both')

plt.savefig('Kaplan_Meier.svg', transparent=True, bbox_inches='tight')
```



This is the Nelson Aalen Model which is the corresponding Hazard for Kaplan Meier.

[8]:
```
naf = NelsonAalenFitter()
naf.fit(data['LENFOL'],event_observed=data['FSTAT'])

naf.plot_cumulative_hazard()
plt.axis([0,2500,0,1])
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both');
```



0.4 Descriptive Analysis

General overview about the data

[9]:
```
data.describe()
```

[9]:

	AGE	GENDER	HR	SYSBP	DIASBP	BMI	\
count	500.000000	500.000000	500.000000	500.000000	500.000000	500.000000	
mean	69.846000	0.400000	87.018000	144.704000	78.266000	26.613780	
std	14.491456	0.490389	23.586231	32.294865	21.545293	5.405655	
min	30.000000	0.000000	35.000000	57.000000	6.000000	13.045460	
25%	59.000000	0.000000	69.000000	123.000000	63.000000	23.223774	
50%	72.000000	0.000000	85.000000	141.500000	79.000000	25.945925	
75%	82.000000	1.000000	100.250000	164.000000	91.250000	29.391962	
max	104.000000	1.000000	186.000000	244.000000	198.000000	44.838860	

	CVD	AFB	SHO	CHF	AV3	MIORD	\
count	500.000000	500.000000	500.000000	500.000000	500.00000	500.000000	
mean	0.750000	0.156000	0.044000	0.310000	0.02200	0.342000	
std	0.433446	0.363219	0.205301	0.462956	0.14683	0.474855	
min	0.000000	0.000000	0.000000	0.000000	0.00000	0.000000	
25%	0.750000	0.000000	0.000000	0.000000	0.00000	0.000000	
50%	1.000000	0.000000	0.000000	0.000000	0.00000	0.000000	
75%	1.000000	0.000000	0.000000	1.000000	0.00000	1.000000	
max	1.000000	1.000000	1.000000	1.000000	1.00000	1.000000	

	MITYPE	YEAR	LOS	DSTAT	LENFOL	FSTAT
count	500.000000	500.000000	500.000000	500.00000	500.000000	500.000000
mean	0.306000	1.984000	6.116000	0.07800	882.436000	0.430000
std	0.461291	0.790566	4.714127	0.26844	705.665133	0.495572
min	0.000000	1.000000	0.000000	0.00000	1.000000	0.000000
25%	0.000000	1.000000	3.000000	0.00000	296.500000	0.000000
50%	0.000000	2.000000	5.000000	0.00000	631.500000	0.000000
75%	1.000000	3.000000	7.000000	0.00000	1363.500000	1.000000
max	1.000000	3.000000	47.000000	1.00000	2358.000000	1.000000

[10]:
```
#Variance of used attributes
data.var()
```

[10]:
```
AGE          210.002289
GENDER         0.240481
HR           556.310297
SYSBP       1042.958301
DIASBP       464.199643
BMI           29.221109
CVD            0.187876
AFB            0.131928
SHO            0.042148
CHF            0.214329
AV3            0.021559
MIORD          0.225487
MITYPE         0.212790
YEAR           0.624994
```

```
LOS             22.222990
DSTAT            0.072060
LENFOL      497963.280465
FSTAT            0.245591
dtype: float64
```

[11]:
```
data.nunique()
```

[11]:
```
AGE        66
GENDER      2
HR        105
SYSBP     133
DIASBP     97
BMI       411
CVD         2
AFB         2
SHO         2
CHF         2
AV3         2
MIORD       2
MITYPE      2
YEAR        3
LOS        27
DSTAT       2
LENFOL    395
FSTAT       2
dtype: int64
```

0.4.1 Correlation Table & Matrix

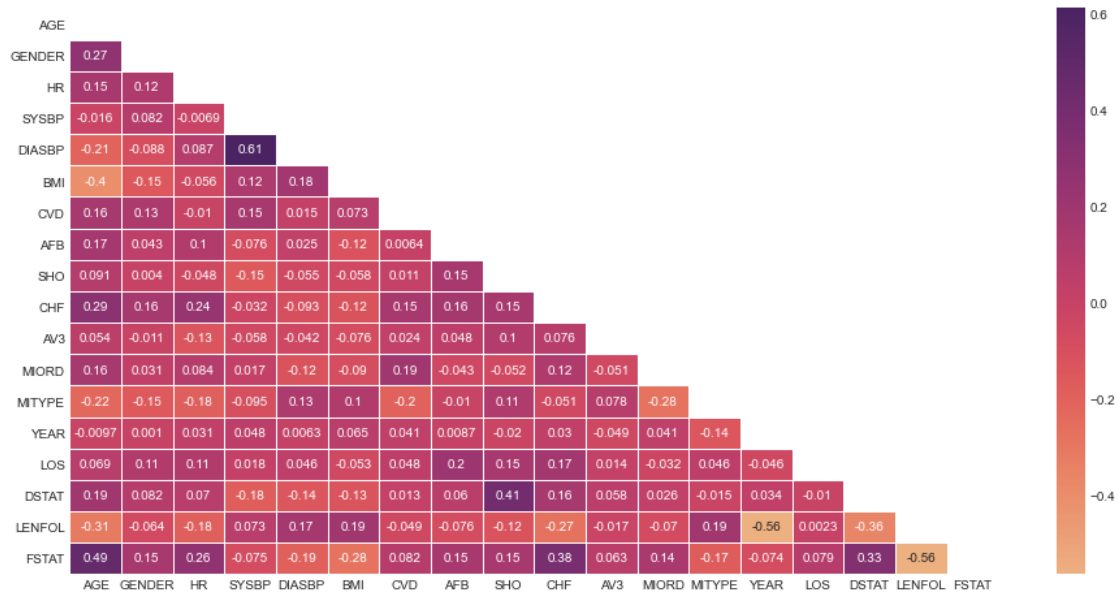
[12]:
```
data.corr()
```

[12]:
```
             AGE    GENDER        HR     SYSBP    DIASBP       BMI       CVD  \
AGE     1.000000  0.274892  0.149137 -0.015599 -0.206044 -0.402484  0.159443
GENDER  0.274892  1.000000  0.115981  0.081517 -0.088236 -0.148578  0.131993
HR      0.149137  0.115981  1.000000 -0.006947  0.086745 -0.055788 -0.010340
SYSBP  -0.015599  0.081517 -0.006947  1.000000  0.610916  0.121719  0.149319
DIASBP -0.206044 -0.088236  0.086745  0.610916  1.000000  0.177371  0.015290
BMI    -0.402484 -0.148578 -0.055788  0.121719  0.177371  1.000000  0.073024
CVD     0.159443  0.131993 -0.010340  0.149319  0.015290  0.073024  1.000000
AFB     0.169050  0.042754  0.102364 -0.075669  0.025417 -0.118545  0.006365
SHO     0.090523  0.003981 -0.048171 -0.154903 -0.054753 -0.058418  0.011260
CHF     0.293591  0.158888  0.238808 -0.031515 -0.093069 -0.120548  0.147304
AV3     0.054338 -0.011133 -0.129156 -0.057791 -0.042396 -0.076024  0.023616
MIORD   0.156484  0.030981  0.083546  0.017461 -0.122323 -0.090315  0.192296
MITYPE -0.220474 -0.152375 -0.181934 -0.095337  0.125076  0.101250 -0.197950
YEAR   -0.009661  0.001034  0.031183  0.047773  0.006251  0.065174  0.040938
```

```
LOS     0.068994  0.107319  0.107005  0.017641  0.045629 -0.053005  0.047567
DSTAT   0.187005  0.082206  0.070044 -0.176483 -0.141500 -0.125764  0.012917
LENFOL -0.312208 -0.063674 -0.179739  0.073307  0.166732  0.192634 -0.048612
FSTAT   0.486135  0.148431  0.259253 -0.074674 -0.188289 -0.277481  0.081633

             AFB       SHO       CHF       AV3     MIORD    MITYPE      YEAR  \
AGE     0.169050  0.090523  0.293591  0.054338  0.156484 -0.220474 -0.009661
GENDER  0.042754  0.003981  0.158888 -0.011133  0.030981 -0.152375  0.001034
HR      0.102364 -0.048171  0.238808 -0.129156  0.083546 -0.181934  0.031183
SYSBP  -0.075669 -0.154903 -0.031515 -0.057791  0.017461 -0.095337  0.047773
DIASBP  0.025417 -0.054753 -0.093069 -0.042396 -0.122323  0.125076  0.006251
BMI    -0.118545 -0.058418 -0.120548 -0.076024 -0.090315  0.101250  0.065174
CVD     0.006365  0.011260  0.147304  0.023616  0.192296 -0.197950  0.040938
AFB     1.000000  0.149637  0.164702  0.048248 -0.042712 -0.010382  0.008710
SHO     0.149637  1.000000  0.151389  0.100784 -0.051885  0.111476 -0.020348
CHF     0.164702  0.151389  1.000000  0.076356  0.118415 -0.050955  0.030006
AV3     0.048248  0.100784  0.076356  1.000000 -0.050644  0.077934 -0.048754
MIORD  -0.042712 -0.051885  0.118415 -0.050644  1.000000 -0.277446  0.041297
MITYPE -0.010382  0.111476 -0.050955  0.077934 -0.277446  1.000000 -0.140414
YEAR    0.008710 -0.020348  0.030006 -0.048754  0.041297 -0.140414  1.000000
LOS     0.203591  0.150015  0.172648  0.013677 -0.032082  0.046310 -0.046283
DSTAT   0.059934  0.410322  0.159803  0.058063  0.026129 -0.015116  0.034222
LENFOL -0.075755 -0.123494 -0.274633 -0.016746 -0.069898  0.185414 -0.564792
FSTAT   0.149855  0.148516  0.378654  0.062518  0.140257 -0.173486 -0.074476

             LOS     DSTAT    LENFOL     FSTAT
AGE     0.068994  0.187005 -0.312208  0.486135
GENDER  0.107319  0.082206 -0.063674  0.148431
HR      0.107005  0.070044 -0.179739  0.259253
SYSBP   0.017641 -0.176483  0.073307 -0.074674
DIASBP  0.045629 -0.141500  0.166732 -0.188289
BMI    -0.053005 -0.125764  0.192634 -0.277481
CVD     0.047567  0.012917 -0.048612  0.081633
AFB     0.203591  0.059934 -0.075755  0.149855
SHO     0.150015  0.410322 -0.123494  0.148516
CHF     0.172648  0.159803 -0.274633  0.378654
AV3     0.013677  0.058063 -0.016746  0.062518
MIORD  -0.032082  0.026129 -0.069898  0.140257
MITYPE  0.046310 -0.015116  0.185414 -0.173486
YEAR   -0.046283  0.034222 -0.564792 -0.074476
LOS     1.000000 -0.010332  0.002342  0.078970
DSTAT  -0.010332  1.000000 -0.361629  0.334877
LENFOL  0.002342 -0.361629  1.000000 -0.564037
FSTAT   0.078970  0.334877 -0.564037  1.000000
```

[13]:
```
plt.figure(figsize = (16, 8))
```

```
corr = data.corr()
mask = np.triu(np.ones_like(corr, dtype = bool))
sns.heatmap(corr, mask = mask, annot = True, fmt = '.2g', linewidths = 1,␣
 ↪cmap="flare")
plt.show()
plt.savefig('correlation.png')
```




```
<Figure size 1080x360 with 0 Axes>
```

We will filter out columns with high correlation (i.e. SYSBP/DIASBP, YEAR/LENFOL, SHO/DSTAT, AGE/BMI). Note that correlations with columns LENFOL or FSTAT will not be taken into account, as these are the target variables

0.4.2 Transform certain columns into categories

[14]:
```
categories = ['GENDER', 'CVD', 'AFB', 'SHO', 'CHF', 'AV3', 'MIORD', 'MITYPE']

for i in categories:
    data[i] = data[i].astype("category")
```

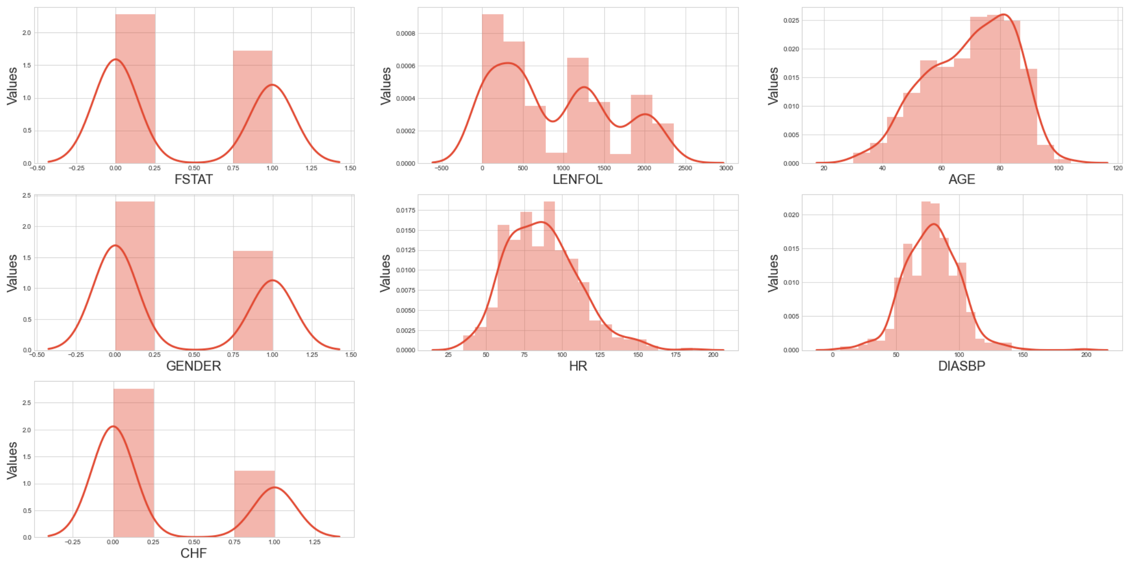
0.5 Filter Data

[15]:
```
data = data[['FSTAT', 'LENFOL', 'AGE', 'GENDER', 'HR', 'DIASBP', 'CHF']]
```

We filtererd out columns with high correlation (1 of each pair) & chose the 5 most interesting and significant attributes (+ the necessary columns for time and event)

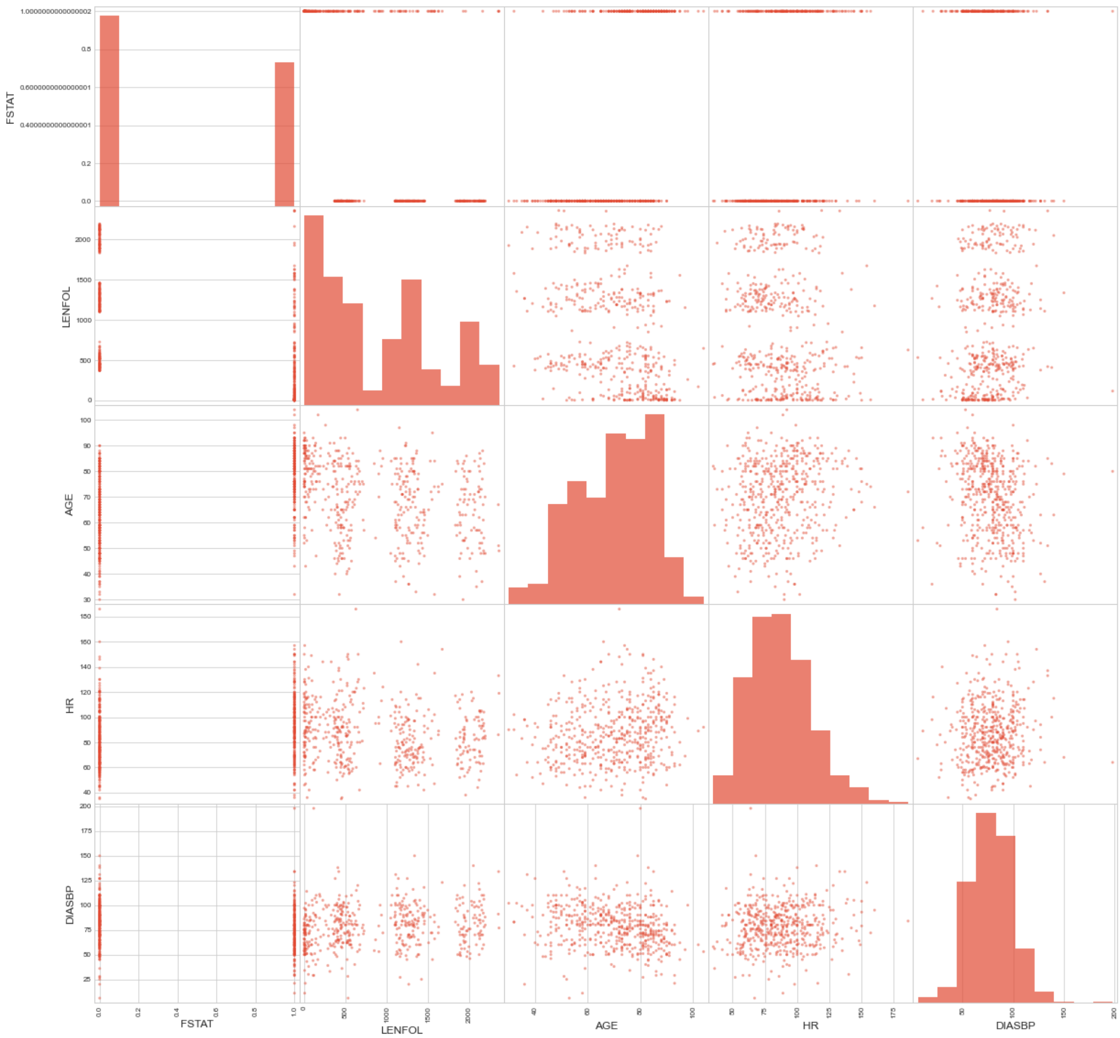
0.5.1 List number of unique values and plot distributions of every attribute

[16]:
```
plt.figure(figsize=(30,15))
plotnumber=1

for column in data:
    if plotnumber<8:
        ax=plt.subplot(3,3,plotnumber)
        sns.distplot(data[column], kde_kws={"linewidth":3})
        plt.xlabel(column,fontsize=20)
        plt.ylabel('Values',fontsize=20)
    plotnumber+=1
plt.show()
```



Plot Scatter Matrix to identify further relations between attributes (e.g. examine clusters)

[17]:
```
pd.plotting.scatter_matrix(data, figsize=(20,20), hist_kwds={"alpha":0.7});
```



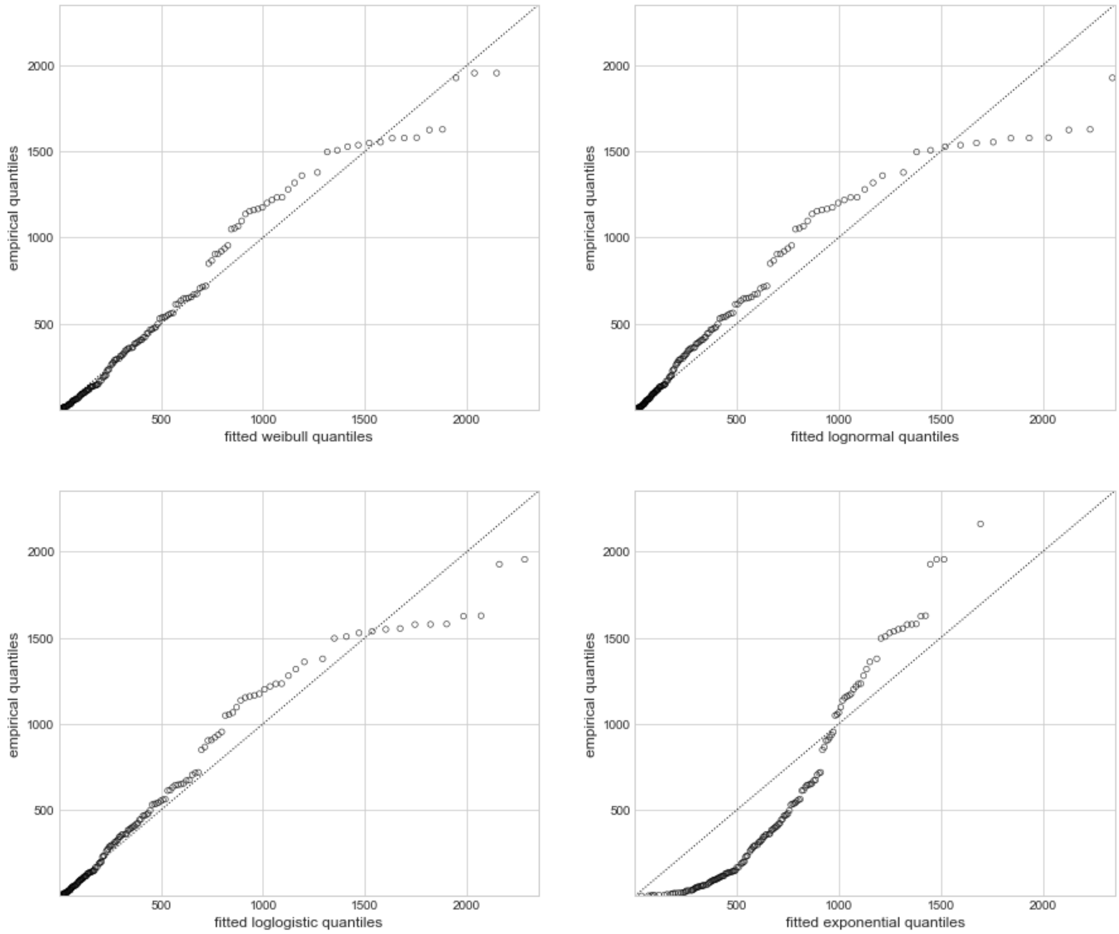
You can see clusters on columns/rows related to the time attribute LENFOL, which means the data was collected in a regimented fashion. Overall the Variance remains the same over time.

0.6 Model Selection

Our first approach is to use univariate parametric models which need a certain distribution of data (we already used the only non parametric univariate model: Kaplan Meier). Lifelines has the most important distributions implemented. Lifelines also provides qqplots to help to graphically choose the right distribution

[18]:
```
fig, axes = plt.subplots(2, 2, figsize=(15, 13))
axes = axes.reshape(4,)

for i, model in enumerate([WeibullFitter(), LogNormalFitter(),
↪LogLogisticFitter(), ExponentialFitter()]):
    model.fit(data['LENFOL'], data['FSTAT'])
```

```
    qq_plot(model, ax=axes[i])
```

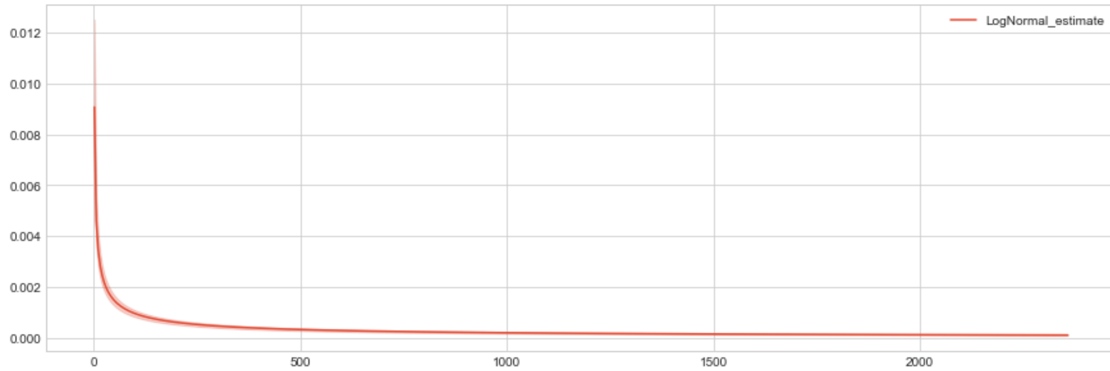


The more the datapoints are on the line, the better the distribution is. Note that datapoints more to the right are allowed to spread more. Nevertheless, none of the plots below are as appropriate as we want them to. But for general testing we continued with the best model:

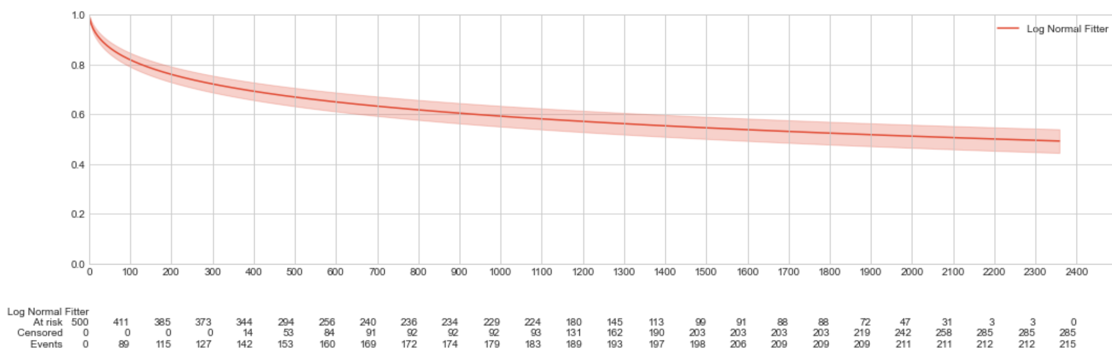
[19]:
```
#let lifelines choose the best model out of the parametric models
best_model, best_aic_ = find_best_parametric_model(data['LENFOL'],␣
 ↪data['FSTAT'], scoring_method="AIC")
print(best_model)
print(best_aic_)
#plot the hazard of the best model (Log Normal Fitter)
best_model.plot_hazard()
```

```
<lifelines.LogNormalFitter:"LogNormal_estimate", fitted with 500 total
observations, 285 right-censored observations>
3506.4392661978636
```

[19]:
```
<AxesSubplot:>
```



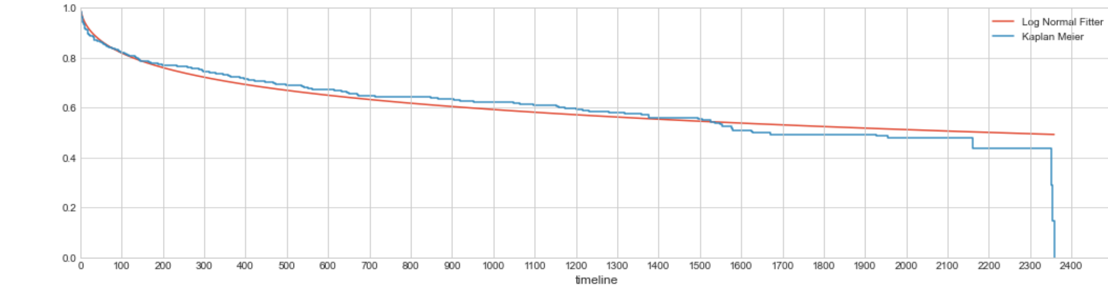

```
[20]: #fit and plot the basline survival curve of the fitted data with the Log Normal␣
      ↪Model
      lnf = LogNormalFitter()
      lnf.fit(data['LENFOL'], event_observed=data['FSTAT'], label='Log Normal Fitter')

      plt.axis([0,2500,0,1])
      plt.xticks(np.arange(0, 2500, step=100))
      lnf.plot_survival_function(at_risk_counts=True)
      plt.grid(b=True, which='both')
```



Note that these two univariate models (Log Normal: parametric, Kaplan Meier: non-parametric) seem alike. The qq plot of the Log Normal Model was not as good as wanted though, which means the univariate models are not the best solution for this analysis either.

```
[21]: ax=lnf.plot_survival_function(at_risk_counts=False, ci_show=False)
      plt.axis([0,2500,0,1])
      plt.xticks(np.arange(0, 2500, step=100))
      kmf.plot_survival_function(at_risk_counts=True, ax=ax, ci_show=False)
      plt.grid(b=True, which='both')
```

```
#plt.savefig('Cox_lognormal.svg', transparent=True, bbox_inches='tight')
```



Kaplan Meier																									
At risk	500	411	385	373	344	294	256	240	236	234	229	224	180	145	113	99	91	88	88	72	47	31	3	3	0
Censored	0	0	0	0	14	53	84	91	92	92	92	93	131	162	190	203	203	203	203	219	242	258	285	285	285
Events	0	89	115	127	142	153	160	169	172	174	179	183	189	193	197	198	206	209	209	209	211	211	212	212	215

0.7 Cox Probability Hazard Model

The Cox PH Fitter is a semi-parametric survival regression model, which firstly means it's a hybrid of both parametric and non-parametric models, and secondly it is multivariate and can deal with more attributes than just the event. This is the model we want to use and optimise.

In our first attempt we split up our data into train and test samples, which led to normal results. However lifelines provides an integrated cross_validation function to validate the model which we eventually used

[22]:
```
#use data_train for train and data_test as a score method

#data2 = data.sample(frac=1, random_state=25367)

#data_train = data2.iloc[:450]
#data_test = data2.iloc[450:]
```

The Cox PH Fitter provides different options for the estimation method, penalization and stratification. Fortunately we don't need any penalty as the model has it's best scores without penalties. The Cox Model fits the data with specified time and event columns and furthermore includes every other column.

[23]:
```
Cox = CoxPHFitter(penalizer=0.0, l1_ratio=0.0)
Cox.fit(data, duration_col='LENFOL', event_col='FSTAT')
Cox.print_summary()
```

covariate	coef	exp(coef)	se(coef)	coef lower 95%	coef upper 95%	exp(coef) lower 95%	exp(coef) up
AGE	0.06	1.06	0.01	0.04	0.07	1.04	
GENDER	-0.25	0.78	0.14	-0.53	0.03	0.59	
HR	0.01	1.01	0.00	0.01	0.02	1.01	
DIASBP	-0.01	0.99	0.00	-0.02	-0.00	0.98	
CHF	0.77	2.16	0.15	0.48	1.06	1.62	

The tables above show several evaluations of the model. (See documentary for a more detailed description) The column exp(coef) gives the ratio of the influence of each attribute. This can be well intepreted for categorical attributes. For example, the value 0.78 for GENDER means, that the ratio of people having a 1/true (=female) in column GENDER with people having a 0/false (=male) is 0.78:1. This means that whenever "0.78" female persons die, then this is equivalent to 1 male person dying.

0.7.1 Checking and validation of the model

The following built-in function of lifelines checks in several ways if the data fitted to the model + the model itself have no statistical semantic errors. If any error occurs, lifelines shows you waht error happend, why it happend and gives links on how to solve these errors. Note that this is not a direct validation of the model.

[24]:
```
Cox.check_assumptions(data, show_plots=True)
```

```
Proportional hazard assumption looks okay.
```

[24]:
```
[]
```

The following is a built-in cross validation of the model which uses the concordance index as the scoring method. The result of .8 means that the model is almost overfitted, but it's just in the acceptable region. (use the penalizer and optionally the l1_ratio parameter in the fit above to handle overfitting)

[25]:
```
scores = np.mean(k_fold_cross_validation(Cox, data, 'LENFOL',␣
↪event_col='FSTAT', k=100, scoring_method="concordance_index"))
print(scores)
```

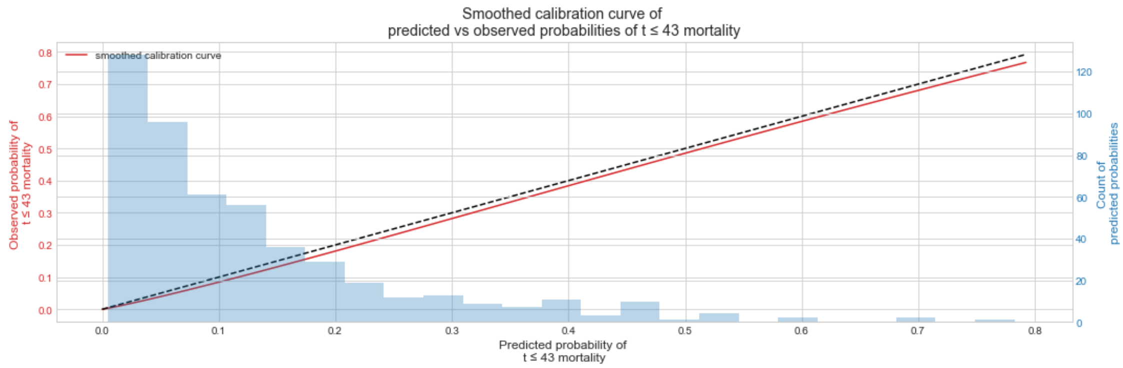
```
0.7954801587301588
```

The following is a built-in graphical method to see how good the model predicts the survival rate of data with a specified event-rate. The more the red curve looks like the black one, the better the model. In this case the result is really good.

[26]:
```
survival_probability_calibration(Cox, data, t0=43)
#plt.savefig('Test.svg', transparent=True, bbox_inches='tight')
```

```
ICI =  0.013070767082751697
E50 =  0.014457868747542069
```

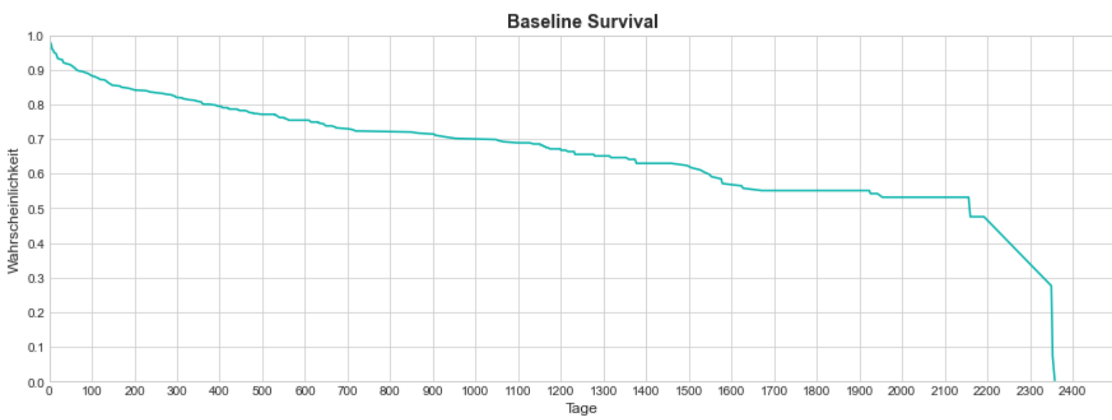
[26]:
```
(<AxesSubplot:title={'center':'Smoothed calibration curve of \npredicted vs
observed probabilities of t   43 mortality'}, xlabel='Predicted probability of
\nt   43 mortality', ylabel='Observed probability of \nt   43 mortality'>,
 0.013070767082751697,
 0.014457868747542069)
```



0.7.2 Survival graphs of Cox PH Model

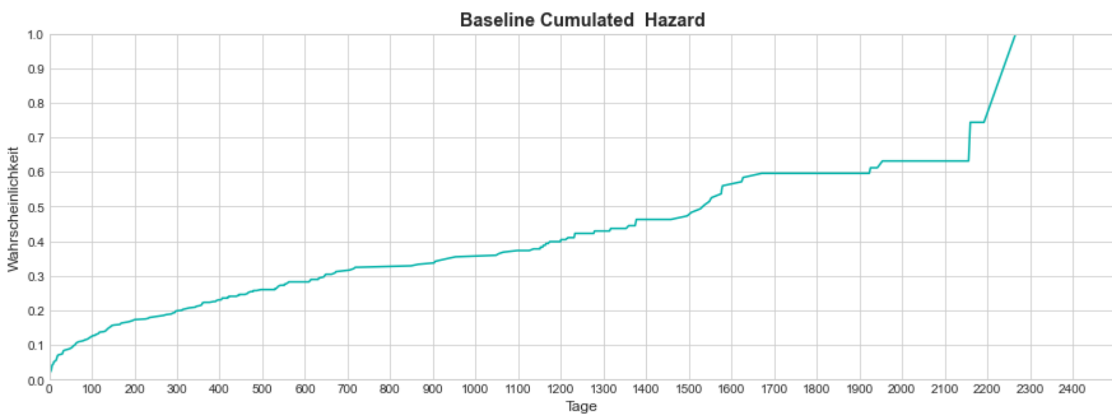
The following shows the survival curve predicted by the Cox model.

[27]:
```
Cox.baseline_survival_.plot(color='#00b2a9',ls='-').legend('')

#this section of code is for configuration of the graphical output and is used␣
↪in every other of the following code snippets
plt.axis([0,2500,0,1])
plt.title('Baseline Survival', fontweight='bold')
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.yticks(np.arange(0, 1.1, step=0.1))
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
#plt.savefig('Baseline_Survival.svg', transparent=True, bbox_inches='tight')
```

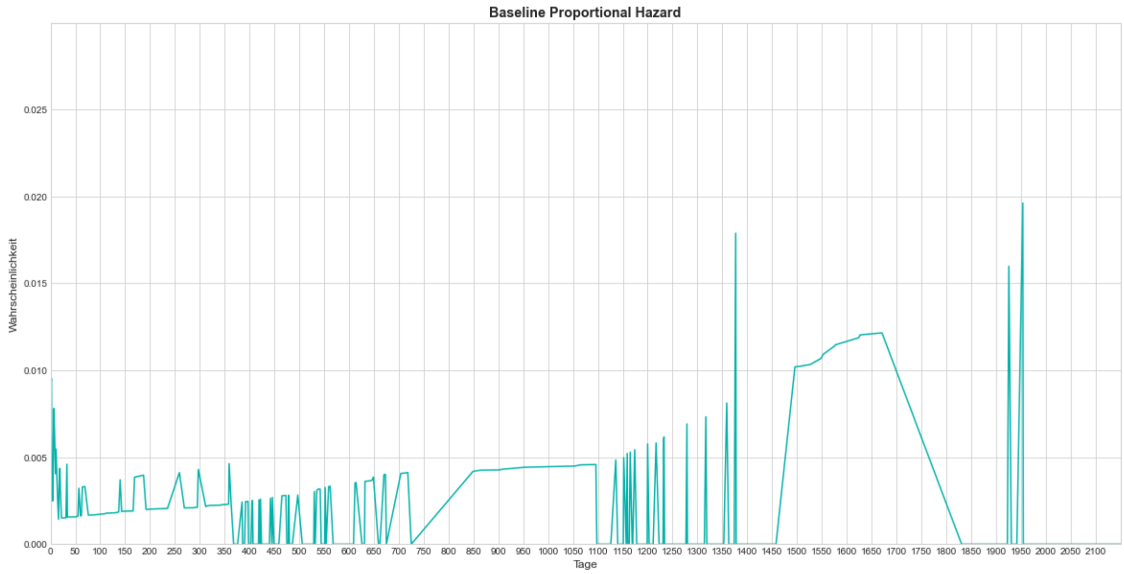


The next graph shows the cumulated hazard and the hazard corresponding to the survival curve. (See documentary for more a more detailed description)

[28]:
```
Cox.baseline_cumulative_hazard_.plot(color='#00b2a9',ls='-').legend('')

plt.axis([0,2500,0,1])
plt.title('Baseline Cumulated  Hazard', fontweight='bold')
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.yticks(np.arange(0, 1.1, step=0.1))
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
#plt.savefig('Baseline_Cumulated.svg', transparent=True, bbox_inches='tight')
```

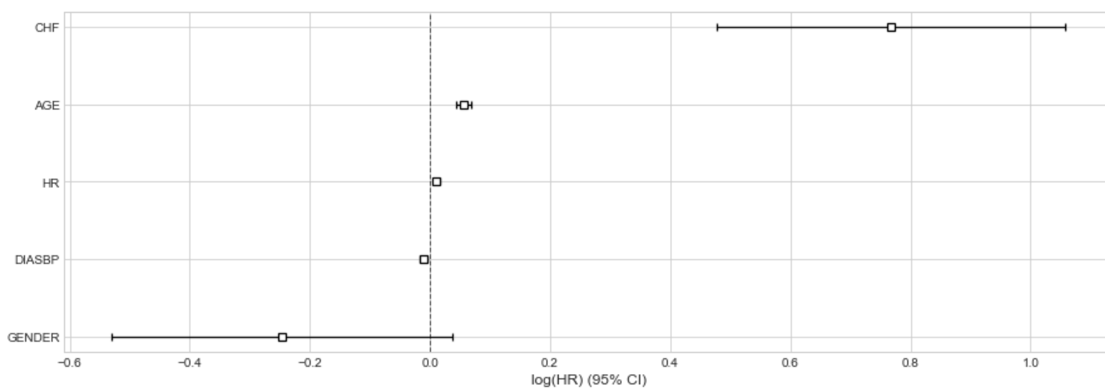


[29]:
```
Cox.baseline_hazard_.plot(color='#00b2a9',ls='-', figsize=(20,10)).legend('')

plt.axis([0,2150,0,0.03])
plt.title('Baseline Proportional Hazard', fontweight='bold')
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.yticks(np.arange(0, 0.03, step=0.005))
plt.xticks(np.arange(0, 2150, step=50))
plt.grid(b=True, which='both')
#plt.savefig('Baseline_Hazard.svg', transparent=True, bbox_inches='tight')
```



0.7.3 Impact of the attributes on the survival probability

[30]:
```
Cox.plot()
plt.grid(b=True, which='both', axis='x')
#plt.savefig('Variables.svg', transparent=True, bbox_inches='tight')
```



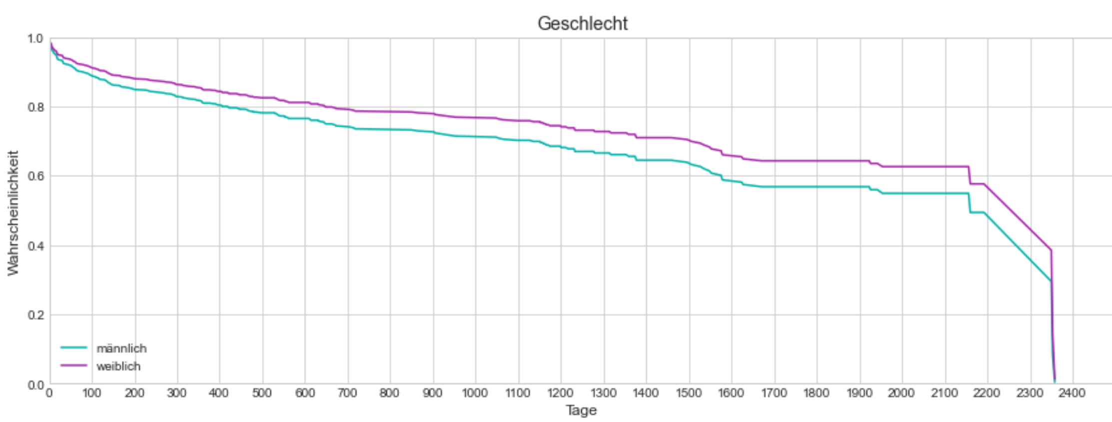
The graphic above shows the influence of each attribute on the probability. An attribute which is to the right of the dotted line means that this attribute has a negative impact on the survival probability. In this case having a 1/True in the CHF attribute (which means that this person has the CHF illness) has a negative influence on the probability curve. A 1/True in GENDER (which means that the person is female) has a positive influence on the probability curve respectfully.

0.8 Data Visualization

The following graphs show the influence of each of the used attributes. In most cases no further explanation is needed. See the documentary on the critical interpretation for these graphs.

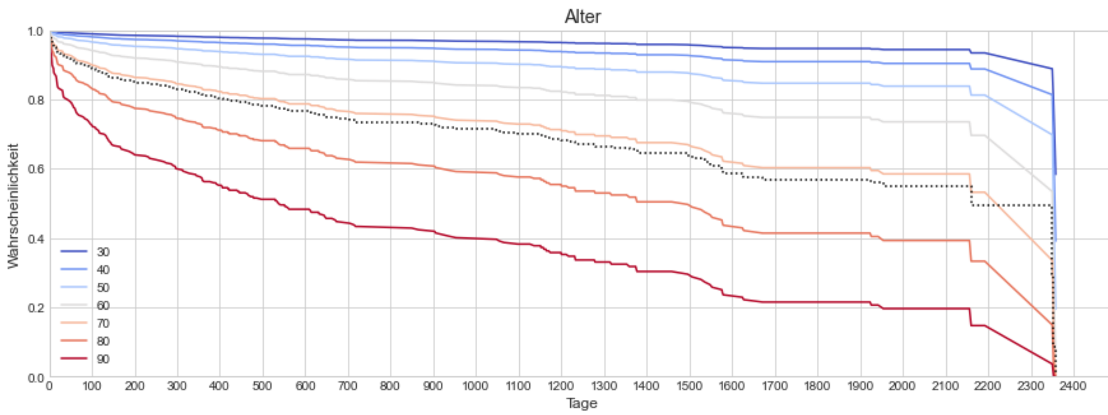
[31]:
```
Cox.plot_partial_effects_on_outcome(covariates='GENDER', values=[0, 1],␣
↪color=['#00b2a9','#a626aa'], plot_baseline=False, drawstyle='default').
↪legend(['männlich','weiblich'], loc='lower left', bbox_to_anchor=(0,0))

plt.axis([0,2500,0,1])
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
plt.title('Geschlecht')
#plt.savefig('Gender.svg', transparent=True, bbox_inches='tight')
```

[31]: Text(0.5, 1.0, 'Geschlecht')



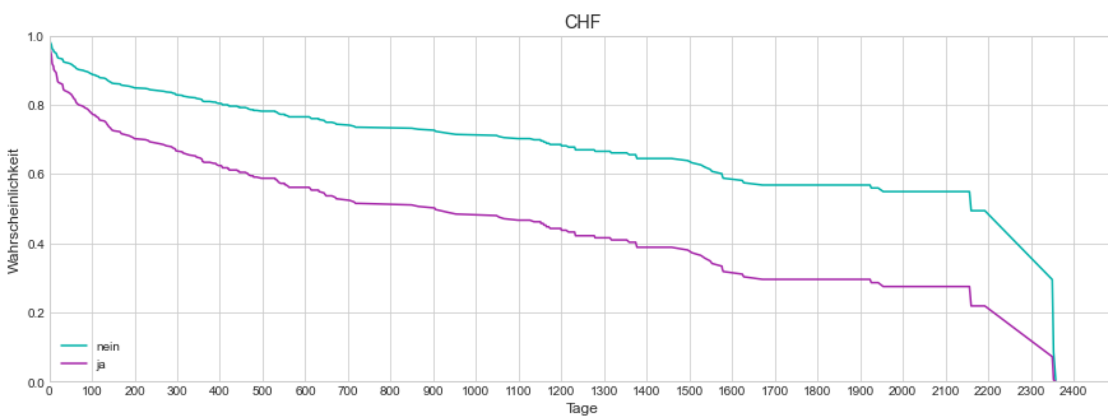
[32]:
```
Cox.plot_partial_effects_on_outcome(covariates='AGE', values=[30, 40, 50, 60,␣
↪70, 80, 90], cmap='coolwarm', drawstyle='default').legend(['30', '40', '50',␣
↪'60', '70', '80', '90'], loc='lower left',  bbox_to_anchor=(0,0))

plt.axis([0,2500,0,1])
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
plt.title('Alter')
#plt.savefig('Age.svg', transparent=True, bbox_inches='tight')
```

[32]: Text(0.5, 1.0, 'Alter')



[33]:
```
Cox.plot_partial_effects_on_outcome(covariates='CHF', values=[0, 1], color=['#00b2a9','#a626aa'], plot_baseline=False, drawstyle='default').legend(['nein','ja'], loc='lower left', bbox_to_anchor=(0,0))

plt.axis([0,2500,0,1])
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
plt.title('CHF')
#plt.savefig('CHF.svg', transparent=True, bbox_inches='tight')
```

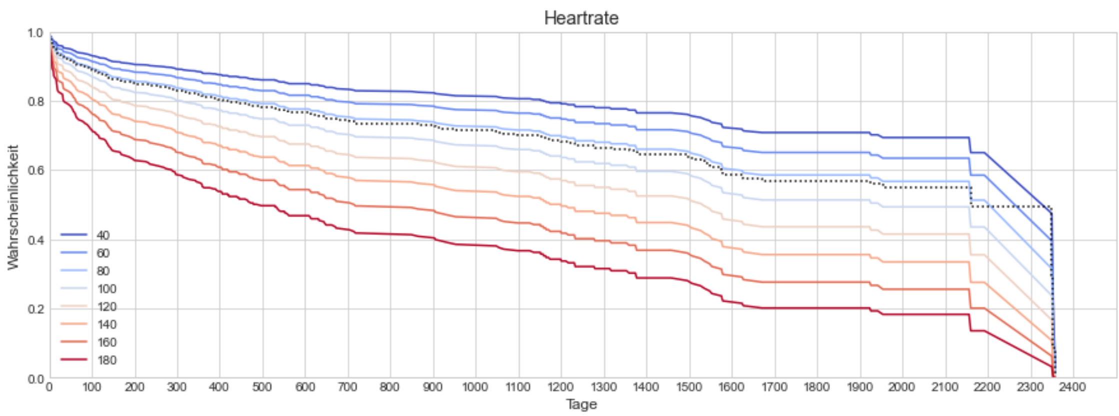
[33]: Text(0.5, 1.0, 'CHF')



[34]:

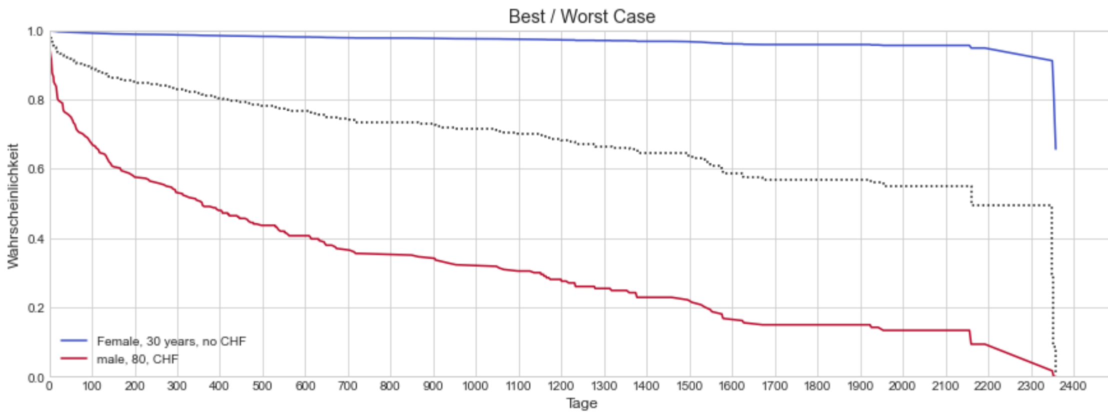
```
Cox.plot_partial_effects_on_outcome(covariates='HR', values=[40, 60, 80, 100,␣
↪120, 140, 160, 180], cmap='coolwarm', drawstyle='default').legend(['40',␣
↪'60', '80', '100', '120', '140', '160', '180'], loc='lower left', ␣
↪bbox_to_anchor=(0,0))

plt.axis([0,2500,0,1])
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
plt.title('Heartrate')
#plt.savefig('HR.svg', transparent=True, bbox_inches='tight')
```

[34]: Text(0.5, 1.0, 'Heartrate')



You can compare different combinations of attributes to see the outcome of the survival curve:

[35]:
```
Cox.plot_partial_effects_on_outcome(covariates=['GENDER', 'AGE', 'CHF'],␣
↪values=[[1,30,0],[0,80,1]], cmap='coolwarm', drawstyle='default').
↪legend(['Female, 30 years, no CHF', 'male, 80, CHF'], loc='lower left', ␣
↪bbox_to_anchor=(0,0))

plt.axis([0,2500,0,1])
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
plt.title('Best / Worst Case')
#plt.savefig('best.svg', transparent=True, bbox_inches='tight')
```



0.8.1 Prediction

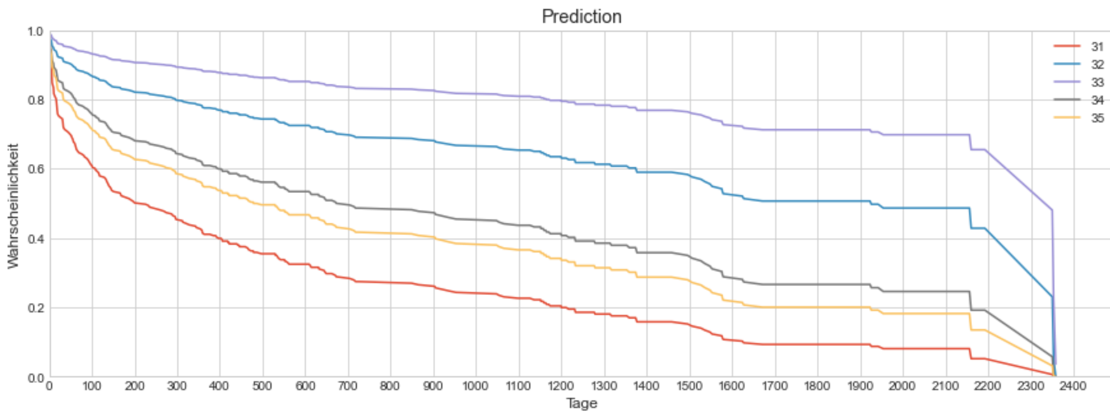
This is what the model predicts on some random data:

[37]:
```
t_data = data.iloc[30:35,]
t_data
```

[37]:

ID	FSTAT	LENFOL	AGE	GENDER	HR	DIASBP	CHF
31	1	849	83	0	135	54	0
32	1	714	61	1	111	80	1
33	0	2057	58	1	86	103	1
34	1	2	90	1	97	82	0
35	1	7	84	1	69	76	1

[39]:
```
Cox.predict_survival_function(t_data).plot()

plt.axis([0,2500,0,1])
plt.xlabel('Tage')
plt.ylabel('Wahrscheinlichkeit')
plt.xticks(np.arange(0, 2500, step=100))
plt.grid(b=True, which='both')
plt.title('Prediction')
#plt.savefig('prediction.svg', transparent=True, bbox_inches='tight')
```


Prediction
Wahrscheinlichkeit
Tage
31
32
33
34
35
1.0
0.8
0.6
0.4
0.2
0.0
0
100
200
300
400
500
600
700
800
900
1000
1100
1200
1300
1400
1500
1600
1700
1800
1900
2000
2100
2200
2300
2400

```
[ ]:
```