数据挖掘作业——马的疝病分析

一、 数据摘要及可视化

1. 数据摘要

该部分内容均在 python 下通过 pandas 库完成。

1.1 标称属性频次统计

在该数据集中包含以下标称属性：surgery、Age、Hospital Number、temperature of extremities、peripheral pulse、mucous membranes、capillary refill time、pain、peristalsis、abdominal distension、nasogastric tube、nasogastric reflux、rectal examination – feces、abdomen、abdominocentesis appearance、outcome、surgical lesion、cp_data。

其分别的词频统计为：

（1）Surgery：

```
1.0    214
2.0    152
Name: surgery, dtype: int64
```

（2）Age：

```
1    340
9     28
Name: Age, dtype: int64
```

（3）temperature of extremities：

```
3.0    135
1.0     95
2.0     39
4.0     34
Name: temperature of extremities, dtype: int64
```

（4）peripheral pulse：

```
1.0    151
3.0    116
4.0     12
2.0      6
Name: peripheral pulse, dtype: int64
```

（5）mucous membranes：

```
1.0    98
3.0    81
4.0    50
2.0    38
5.0    28
6.0    25
Name: mucous membranes, dtype: int64
```

(6) capillary refill time：

```
1.0    232
2.0     96
3.0      2
Name: capillary refill time, dtype: int64
```

(7) pain：

```
3.0    82
2.0    77
5.0    50
1.0    49
4.0    47
Name: pain, dtype: int64
```

(8) Peristalsis：

```
3.0    154
4.0     91
1.0     49
2.0     22
Name: peristalsis, dtype: int64
```

(9) abdominal distension：

```
1.0    101
3.0     85
2.0     75
4.0     42
Name: abdominal distension, dtype: int64
```

(10) nasogastric tube：

```
2.0    121
1.0     89
3.0     27
Name: nasogastric tube, dtype: int64
```

(11) nasogastric reflux：

```
1.0    141
3.0     49
2.0     45
Name: nasogastric reflux, dtype: int64
```

(12) rectal examination – feces：

```
4.0    97
1.0    68
3.0    61
2.0    14
Name: rectal examination - feces, dtype: int64
```

（13）abdomen：

```
5.0    96
4.0    55
1.0    31
2.0    24
3.0    19
Name: abdomen, dtype: int64
```

（14）abdominocentesis appearance：

```
2.0    62
3.0    60
1.0    52
Name: abdominocentesis appearance, dtype: int64
```

（15）outcome：

```
1.0    225
2.0     89
3.0     52
Name: outcome, dtype: int64
```

（16）surgical lesion：

```
1    232
2    136
Name: surgical lesion, dtype: int64
```

（17）cp_data：

```
2    244
1    124
Name: cp_ data, dtype: int64
```

1.2 数值型数据统计

在该数据集中包含以下数值属性：rectal temperature、pulse、respiratory rate、nasogastric reflux PH、packed cell volume、total protein、abdomcentesis total protein。

下面分别统计出数值属性的有效总数、平均值、标准差、最小值、二分位数、中位数、四分位数及最大值。

（1）rectal temperature：

```
count    299.000000
mean      38.134448
std        0.711684
min       35.400000
25%       37.800000
50%       38.100000
75%       38.500000
max       40.800000
Name: rectal temperature, dtype: float64
```

(2) pulse:

```
count    342.000000
mean      70.757310
std       28.089867
min       30.000000
25%       48.000000
50%       60.000000
75%       88.000000
max      184.000000
Name: pulse, dtype: float64
```

(3) respiratory rate:

```
count    297.000000
mean      30.521886
std       17.669651
min        8.000000
25%       18.000000
50%       28.000000
75%       36.000000
max       96.000000
Name: respiratory rate, dtype: float64
```

(4) nasogastric reflux PH:

```
count    69.000000
mean      4.962319
std       2.003901
min       1.000000
25%       3.500000
50%       5.400000
75%       6.500000
max       8.500000
Name: nasogastric reflux PH, dtype: float64
```

(5) packed cell volume:

```
count    331.000000
mean      45.656798
std       10.865663
min        4.000000
25%       37.250000
50%       44.000000
75%       52.000000
max       75.000000
Name:  packed cell volume, dtype: float64
```

（6）total protein：

```
count    325.000000
mean      24.771077
std       27.704880
min        3.300000
25%        6.500000
50%        7.500000
75%       58.000000
max       89.000000
Name: total protein, dtype: float64
```

（7）abdomcentesis total protein：

```
count    133.000000
mean       2.948120
std        1.927064
min        0.100000
25%        2.000000
50%        2.100000
75%        3.900000
max       10.100000
Name: abdomcentesis total protein, dtype: float64
```

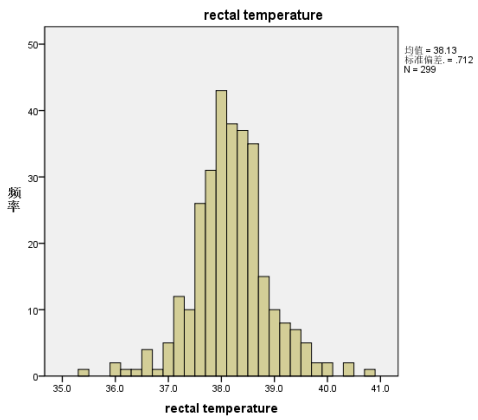
2. 数据可视化

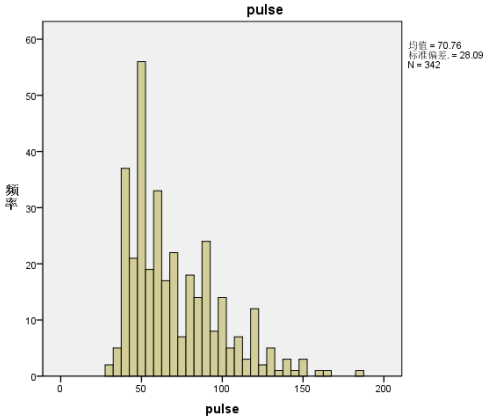
该部分内容通过 spss 工具完成。

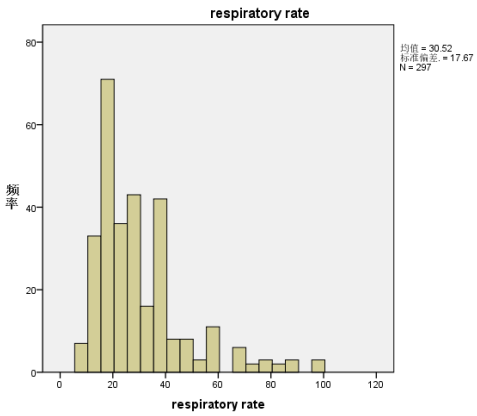
2.1 数值属性的直方图及 Q_Q 图

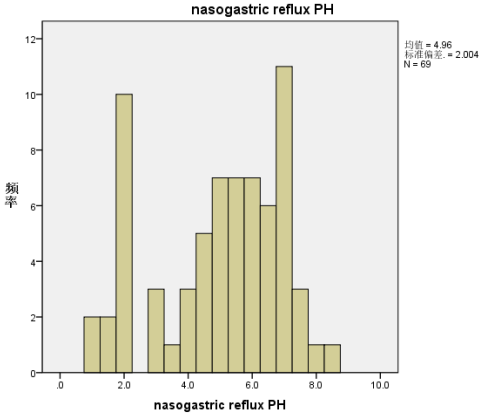
2.1.1 直方图

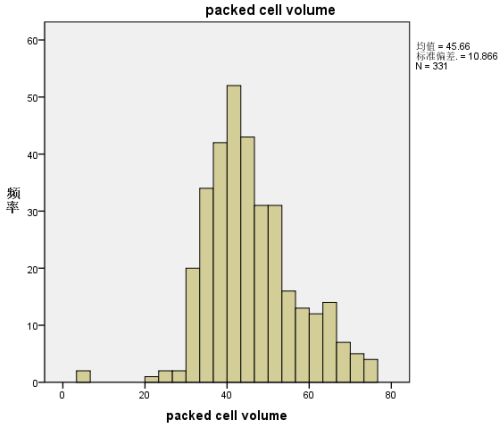
下面分别为数值数据的直方图：

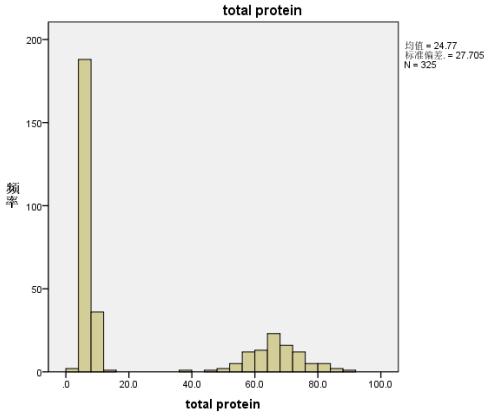


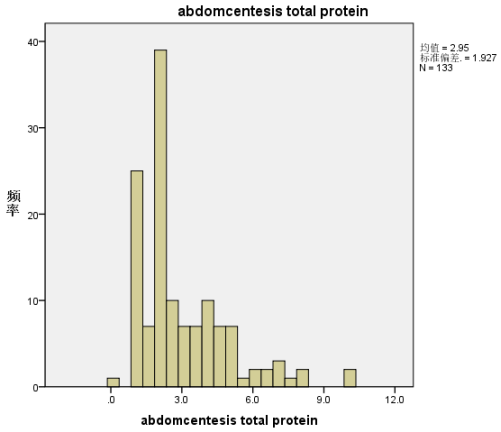






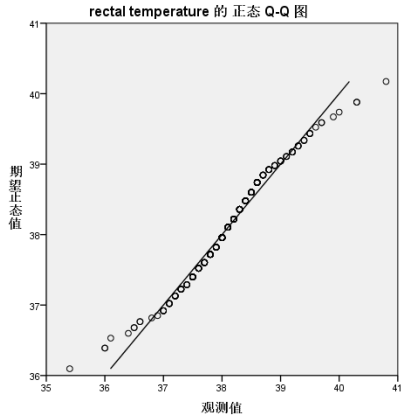


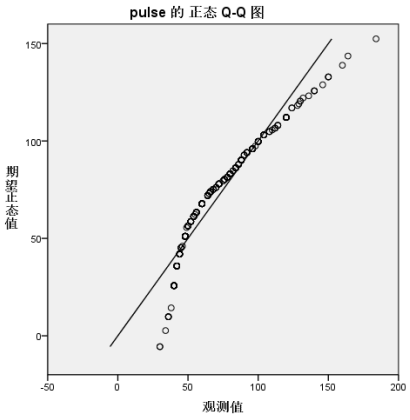


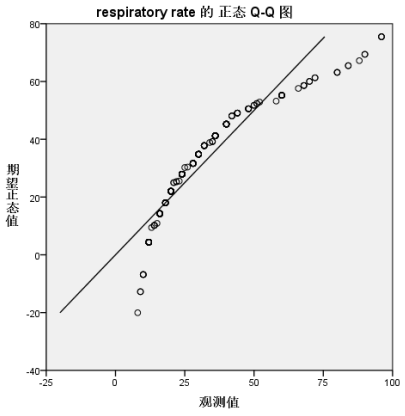


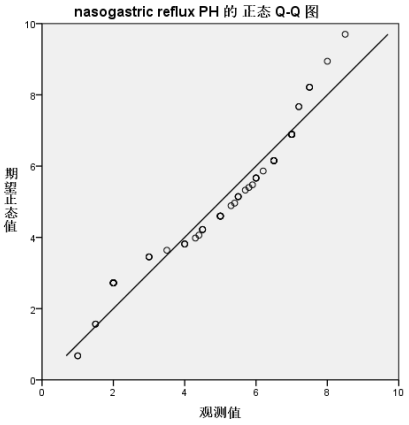
2.1.2 Q_Q 图

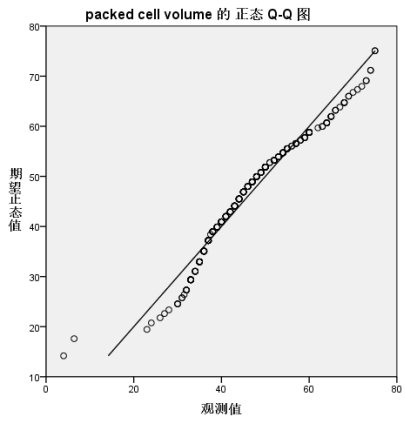
下面分别为数值数据的直方图：

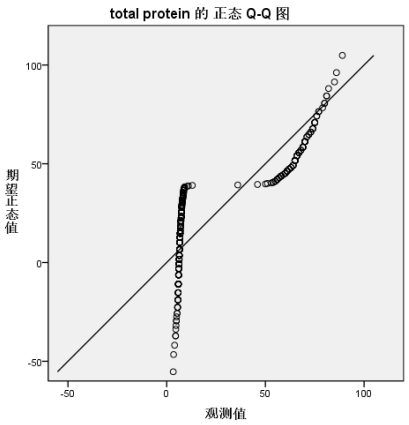

rectal temperature 的 正态 Q-Q 图
期望正态值
观测值

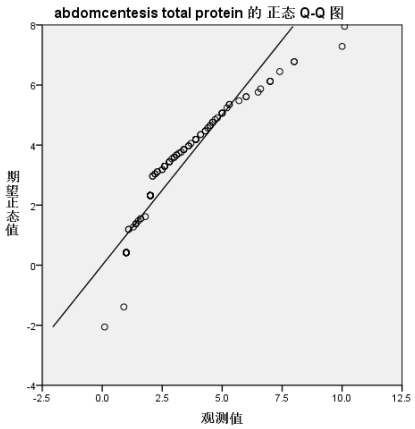

pulse 的 正态 Q-Q 图
期望正态值
观测值


respiratory rate 的 正态 Q-Q 图
期望正态值
观测值


nasogastric reflux PH 的 正态 Q-Q 图
期望正态值
观测值

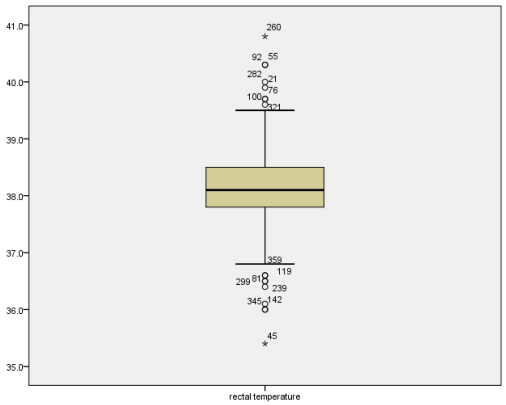

packed cell volume 的 正态 Q-Q 图
期望正态值
观测值

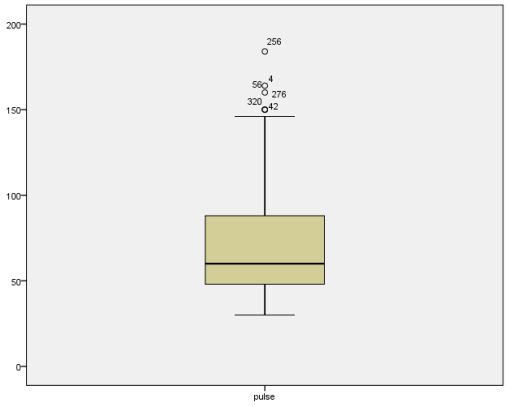

total protein 的 正态 Q-Q 图
期望正态值
观测值

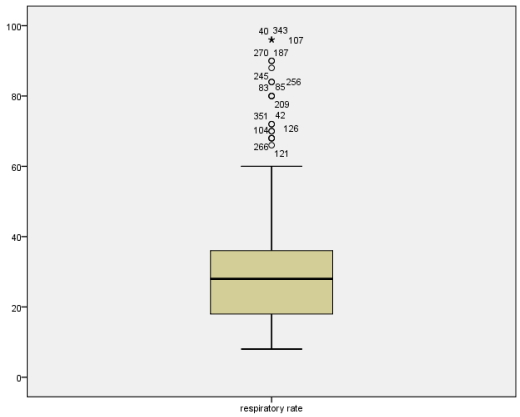


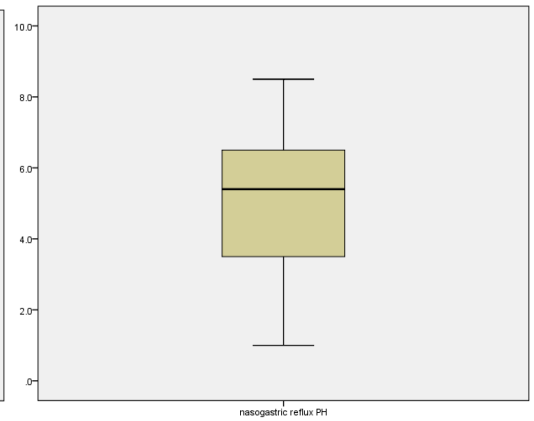
2.2 数值属性的盒图

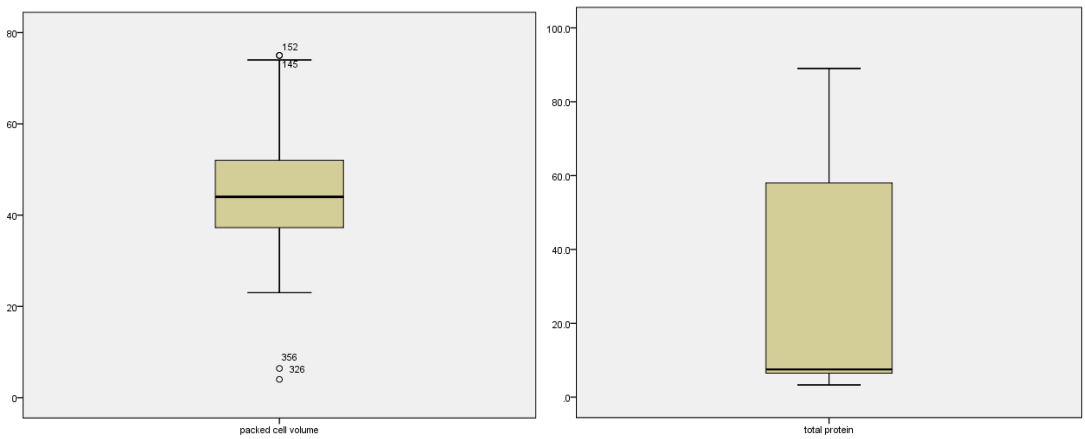
下面分别为数值数据的盒图：

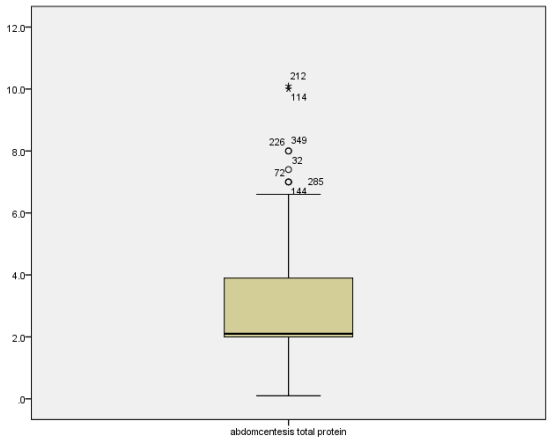












二、 数据缺失的处理

该部分内容先通过 python 对数据进行处理，后通过 spss 制作绘图

1. 将缺失部分剔除

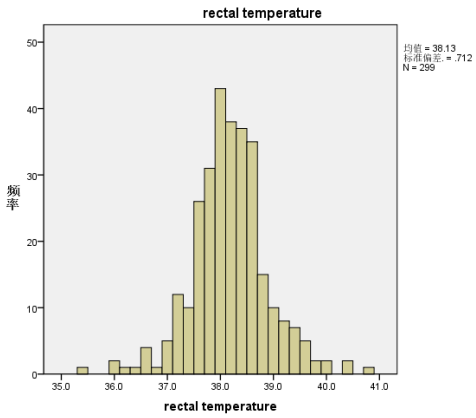
该部分图例已在上一部分展示，不做重复处理。

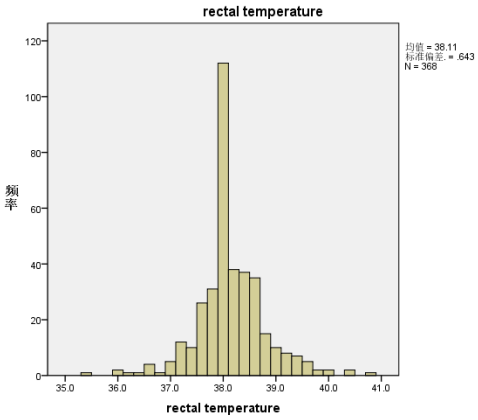
2. 用最高频率值来填补缺失值

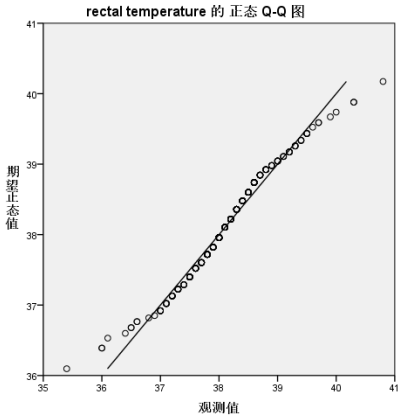
首先通过对每组数值属性进行词频统计，找出该组数值属性的最高频值，并用该值填补缺失值。

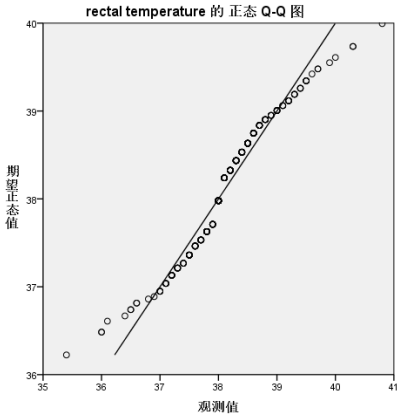
(1) rectal temperature：

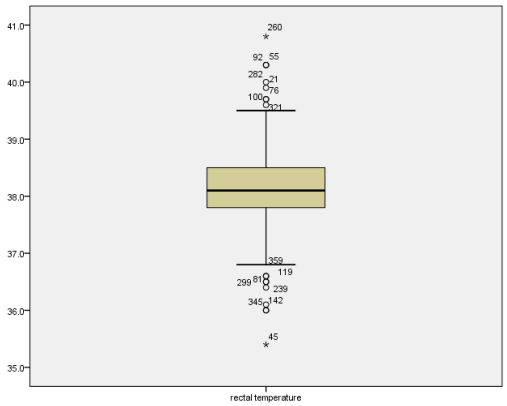
该属性的最高频值为 38.0，用该值填充缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

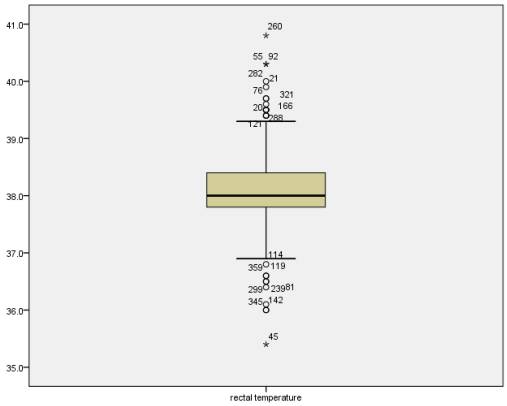






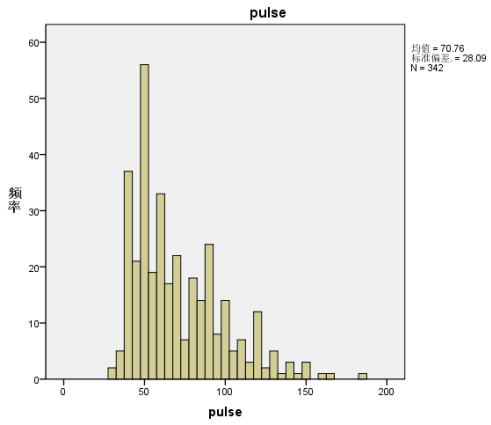


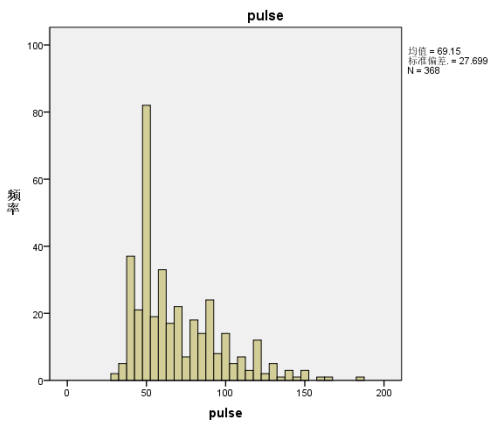


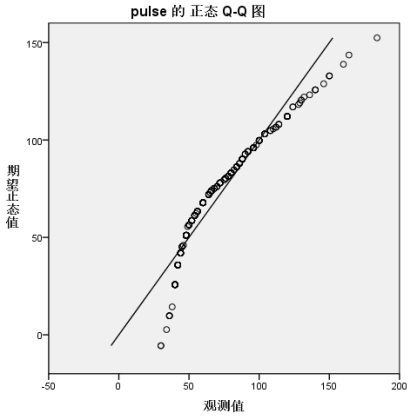


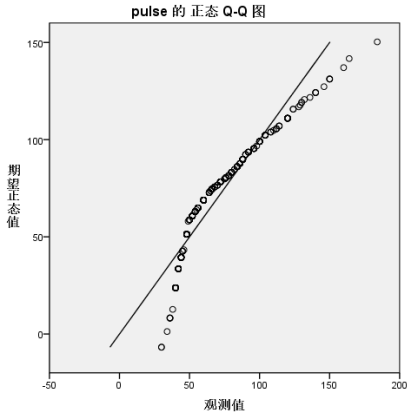
（2）pulse：

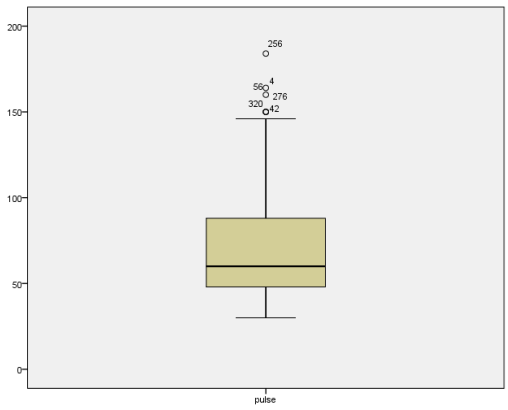
该属性的最高频值为 48，用该值填充缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

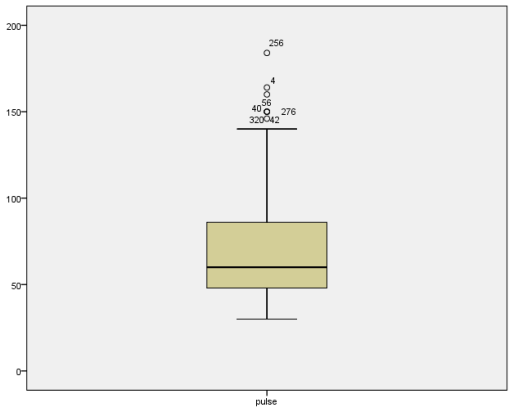






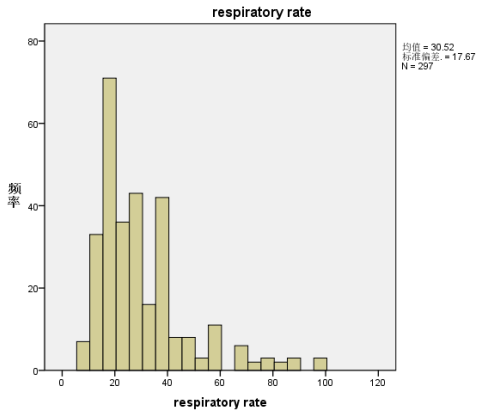


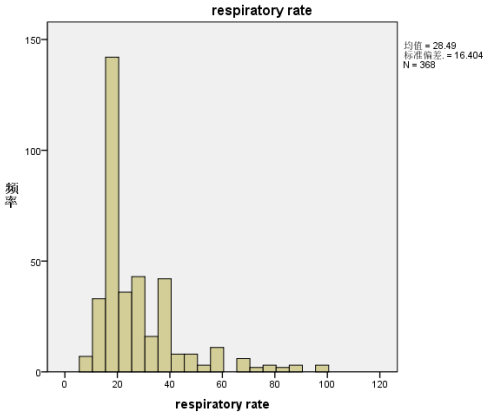


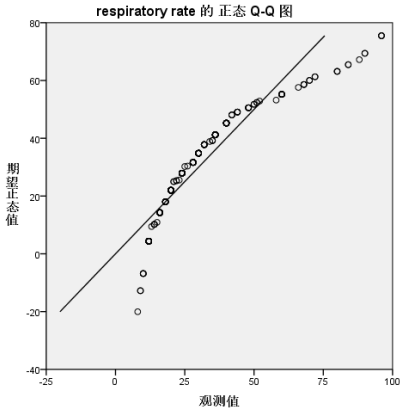


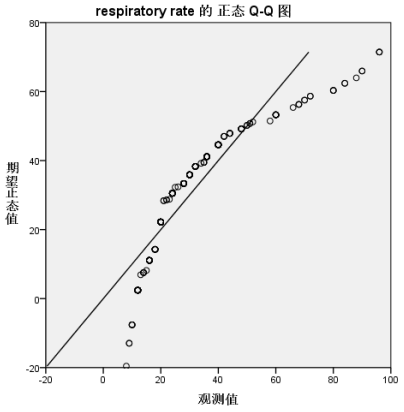
（3）respiratory rate：

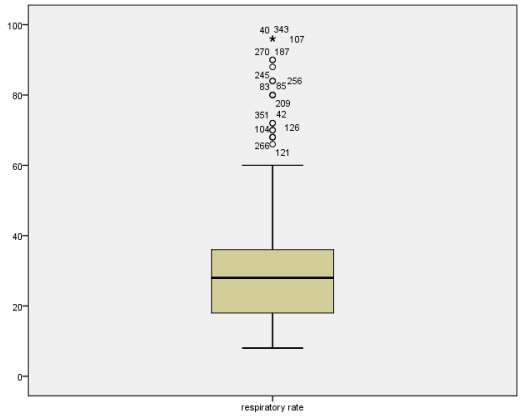
该属性的最高频值为 20.0，用该值填充缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

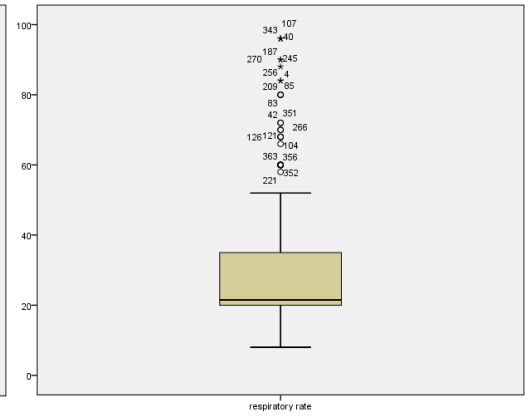






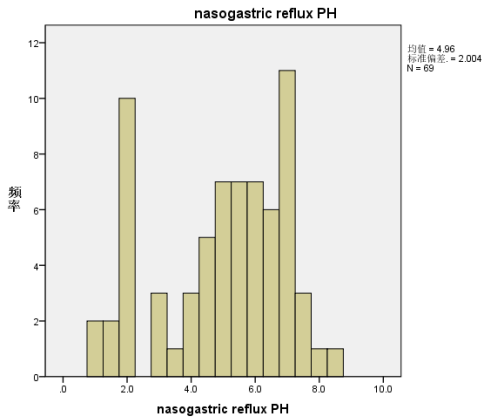


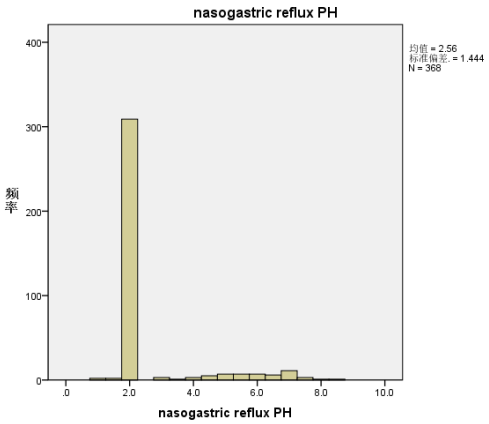


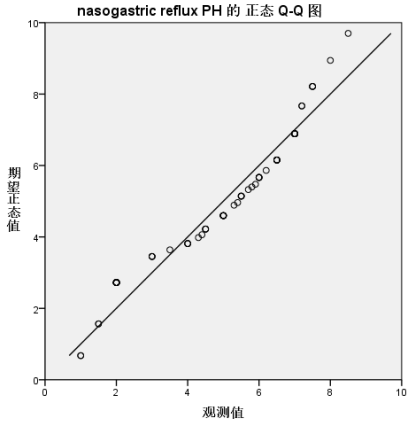


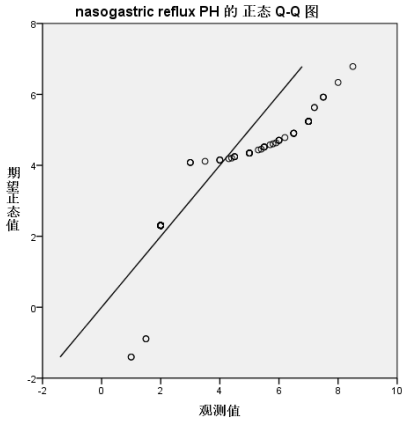
（4）nasogastric reflux PH：

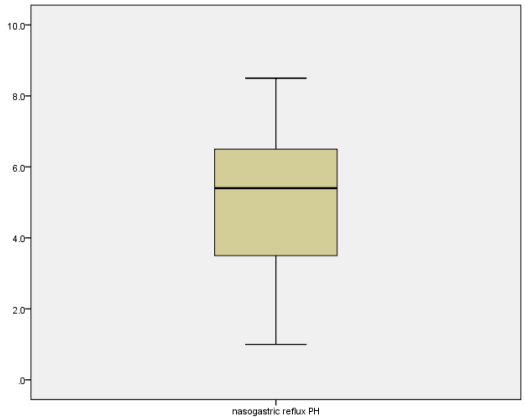
该属性的最高频值为 2.0，用该值填充缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

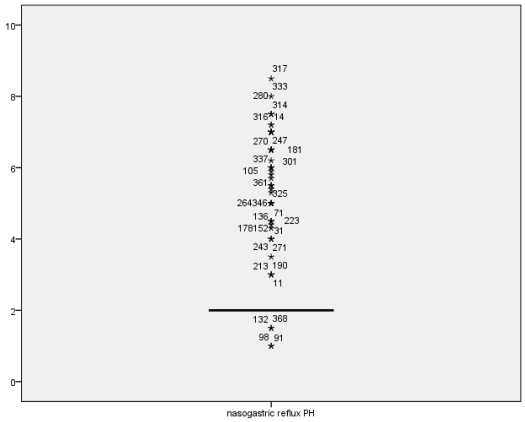






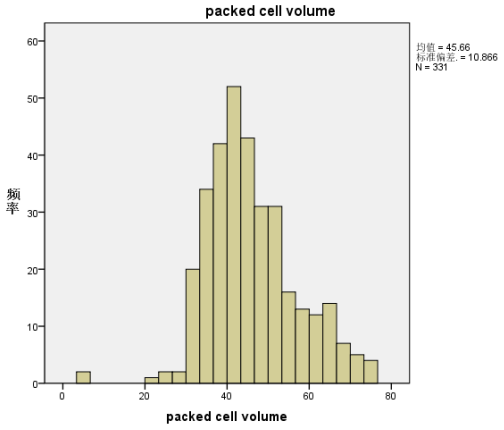


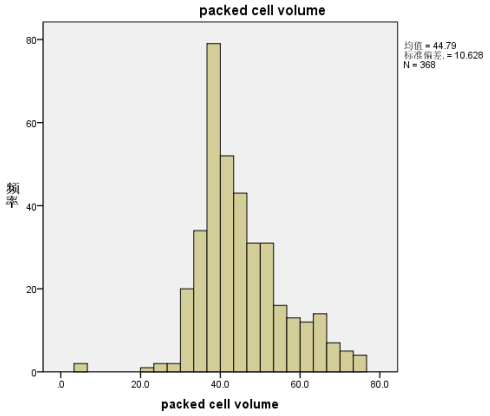


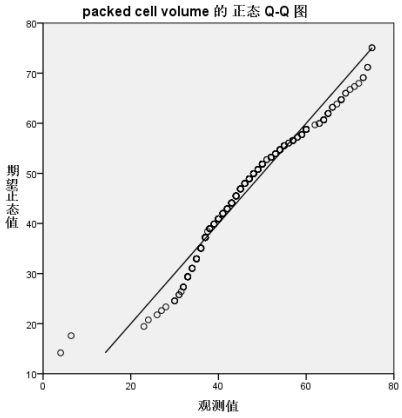


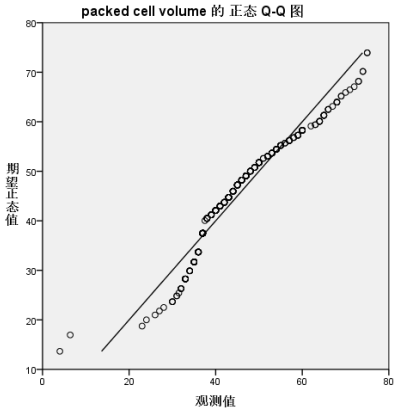
(5) packed cell volume：

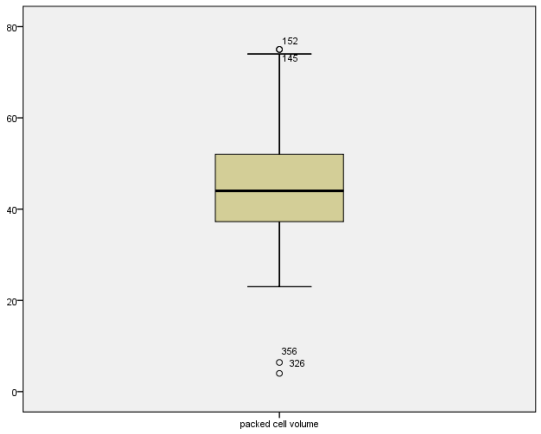
该属性的最高频值为 37.0，用该值填充缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

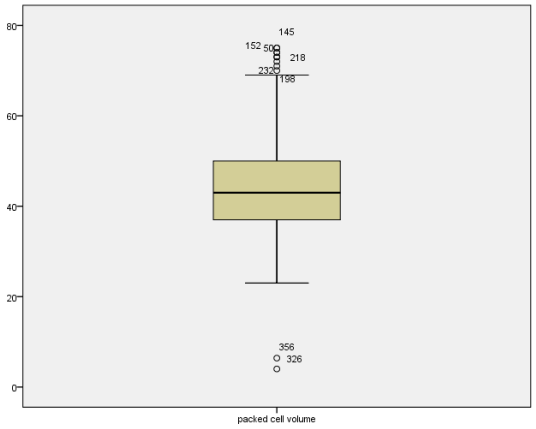






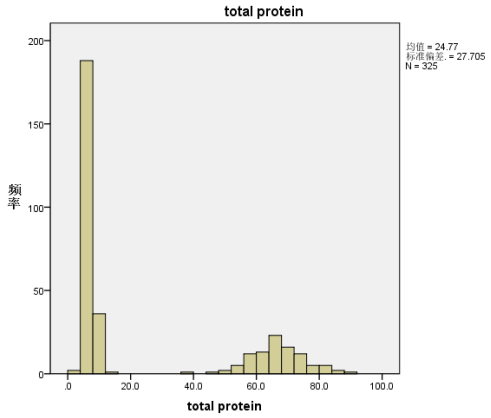


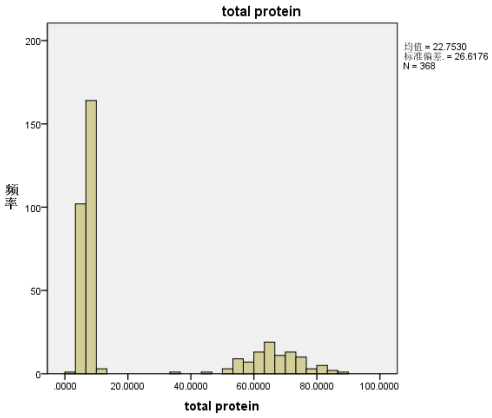


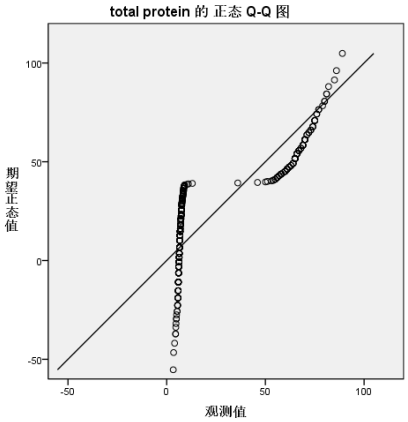


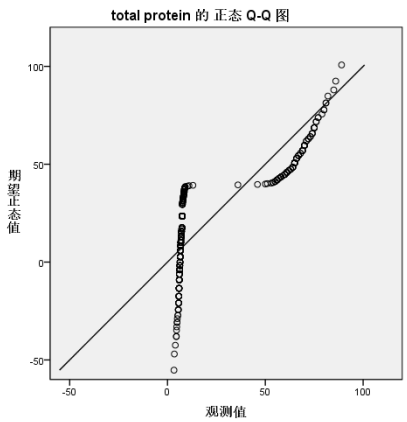
（6）total protein：

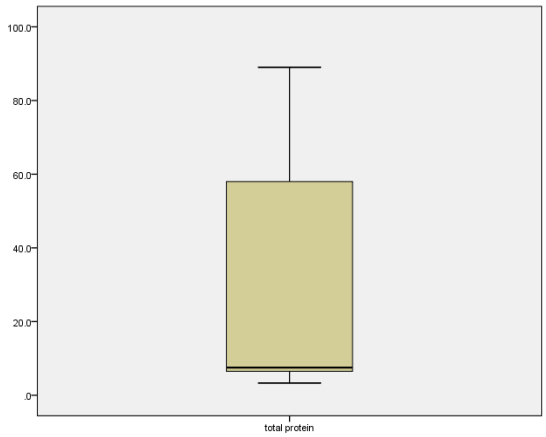
该属性的最高频值为 7.5，用该值填充缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

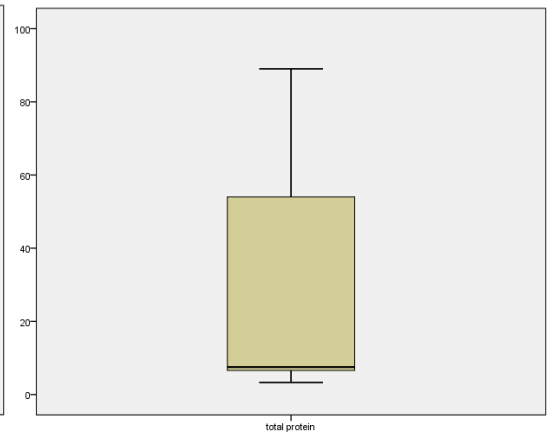






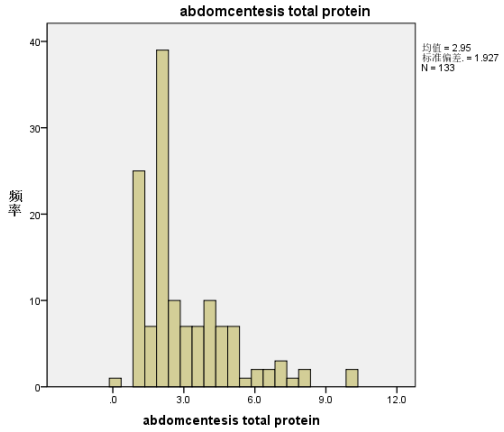


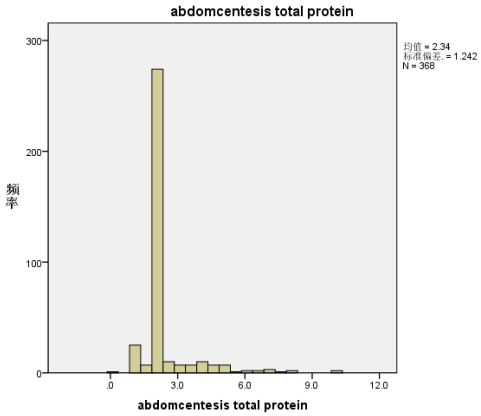


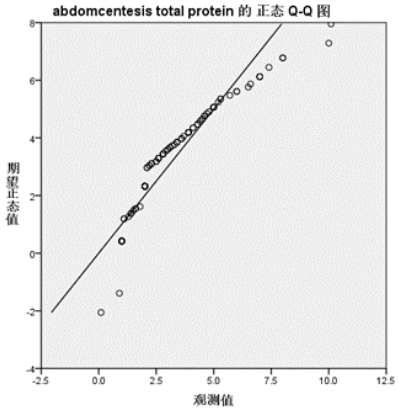


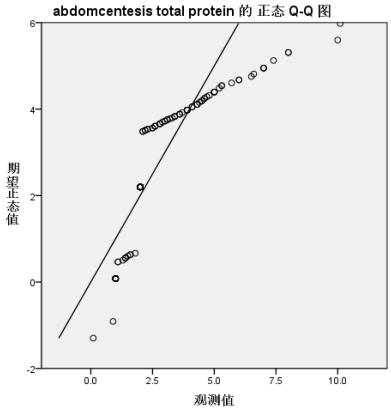
（7）abdomcentesis total protein：

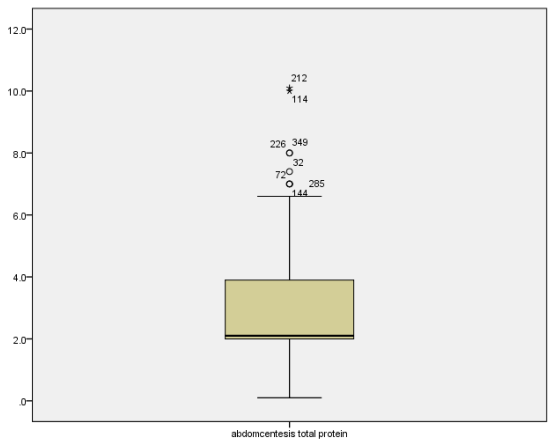
该属性的最高频值为 2.0，用该值填充缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

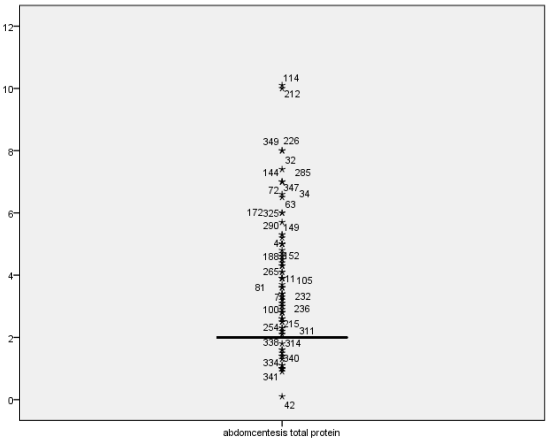








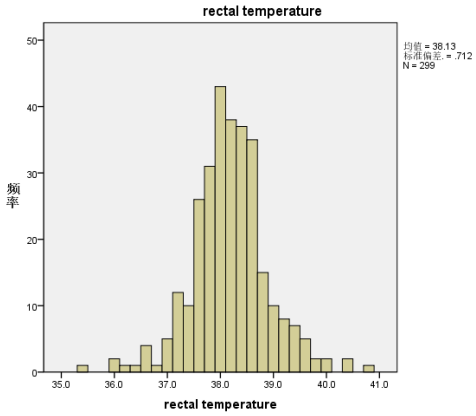


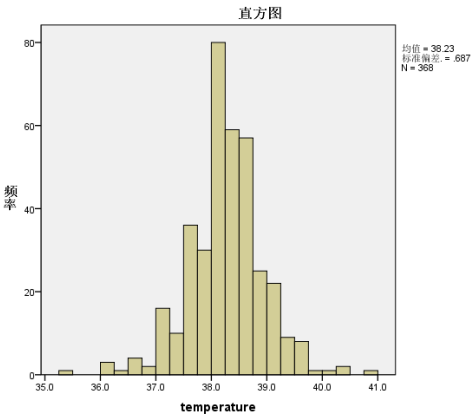


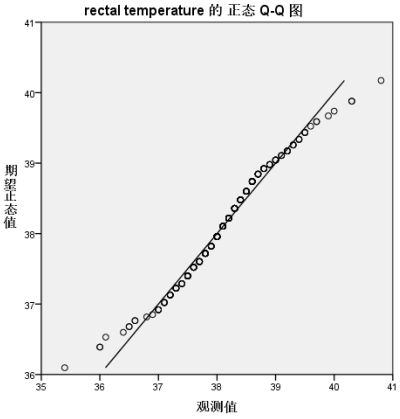
3.用属性的相关关系来填补缺失值

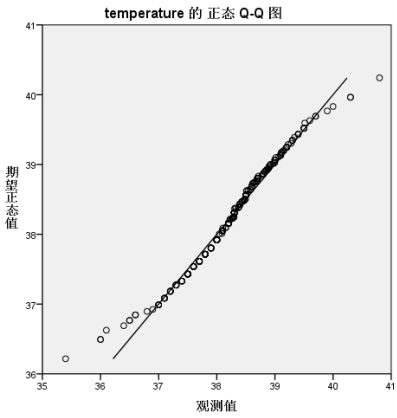
(1) rectal temperature：

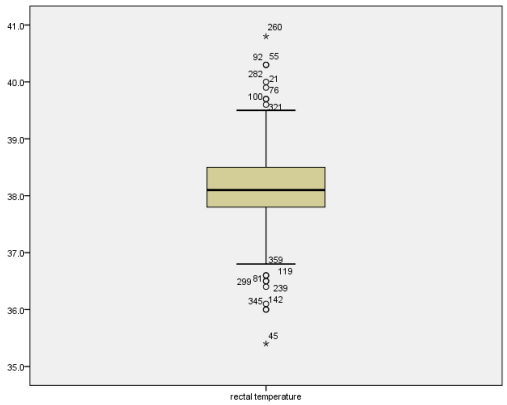
用属性的相关关系来填补缺失值后，与省略缺失值图的对比如下(左侧为省略缺失图)：

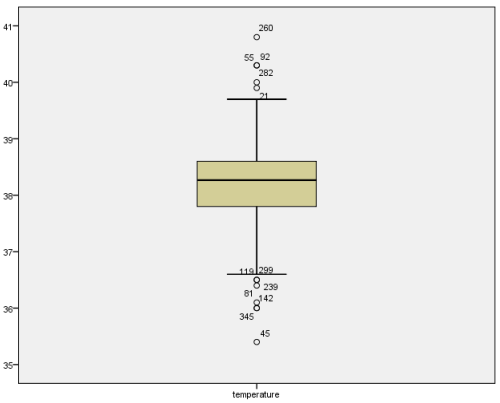






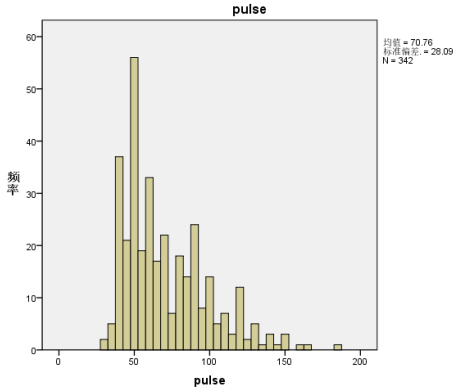


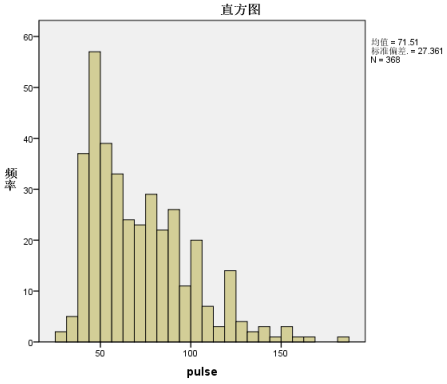


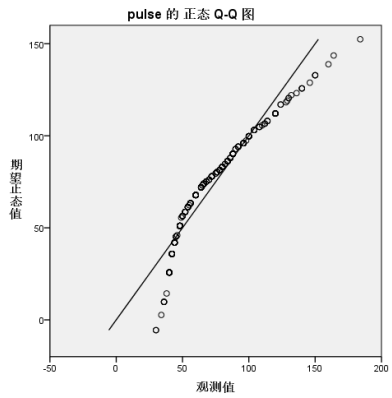


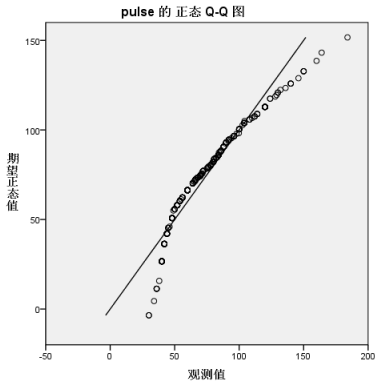
(2) pulse：

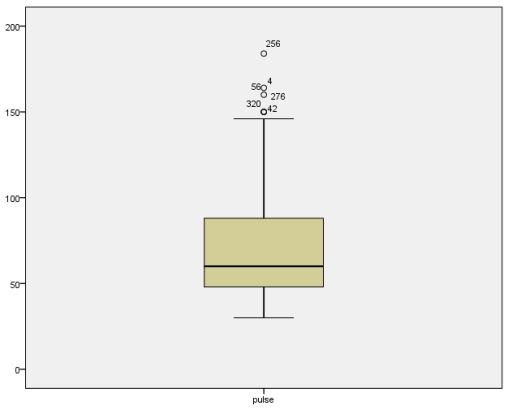
用属性的相关关系来填补缺失值后，与省略缺失值图的对比如下(左侧为省略缺失图)：

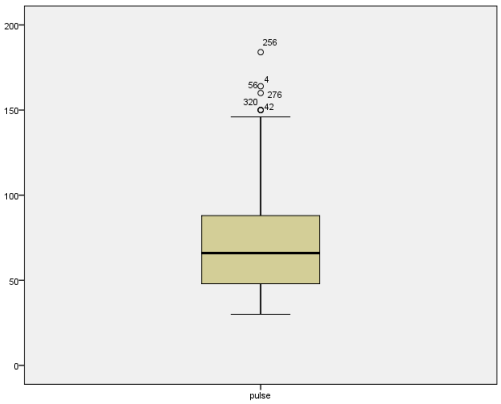






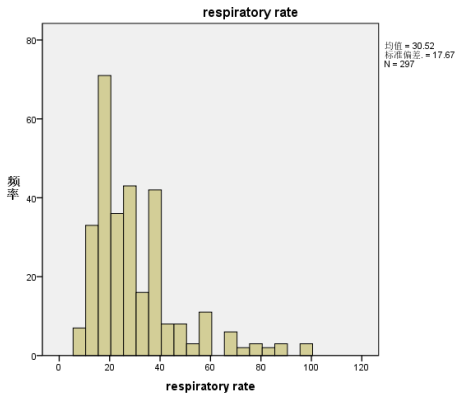


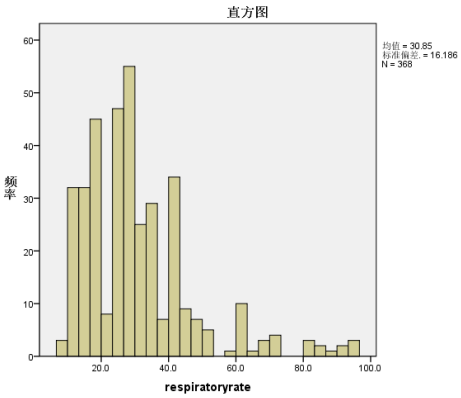


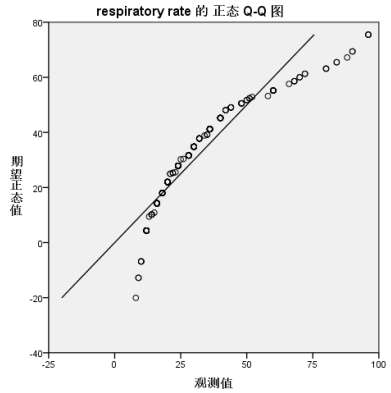


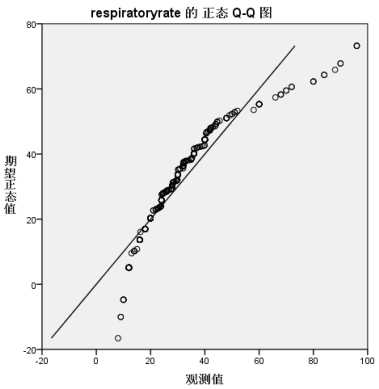
(3) respiratory rate：

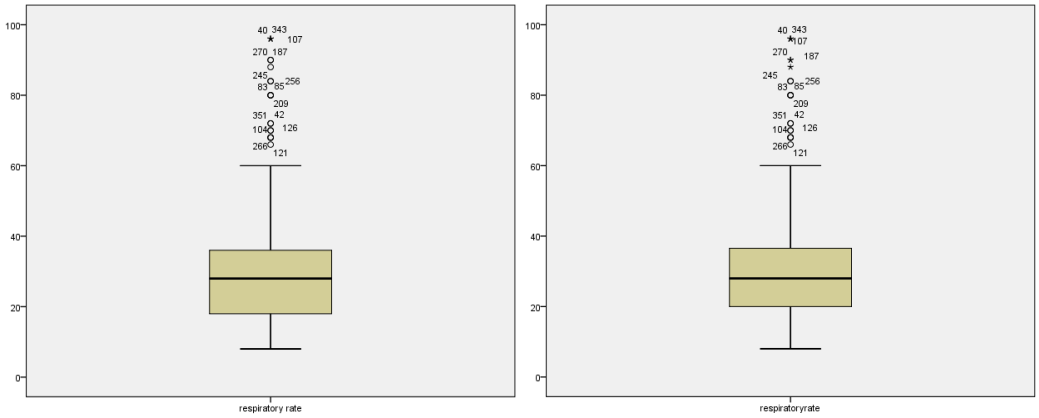
用属性的相关关系来填补缺失值后，与省略缺失值图的对比如下(左侧为省略缺失图)：





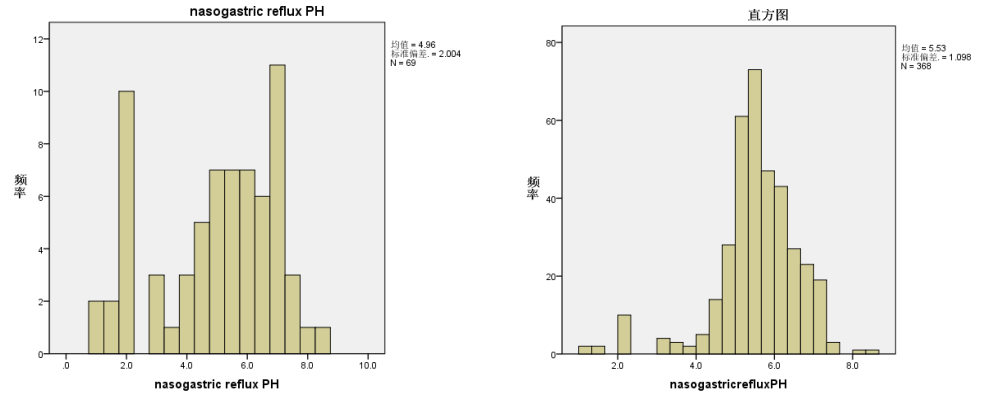


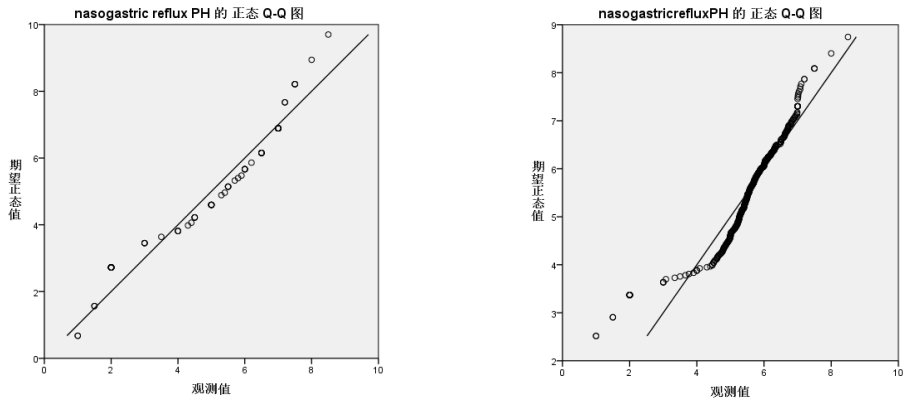


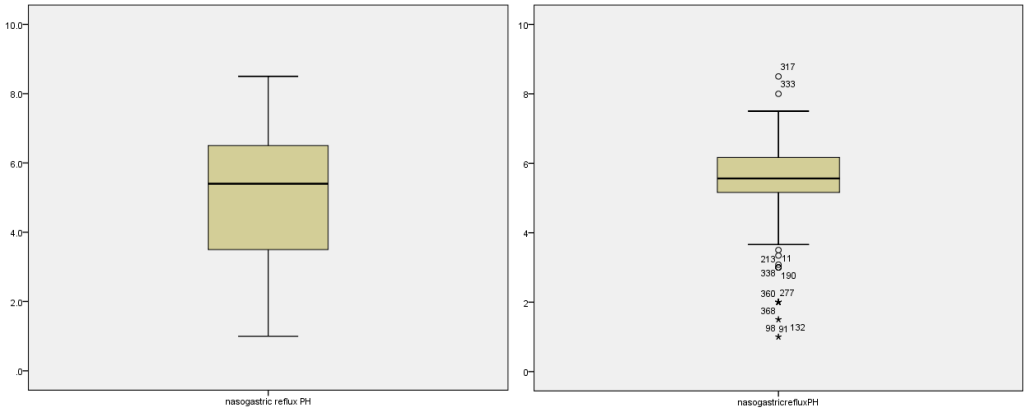


(4) nasogastric reflux PH：

用属性的相关关系来填补缺失值后，与省略缺失值图的对比如下(左侧为省略缺失图)：

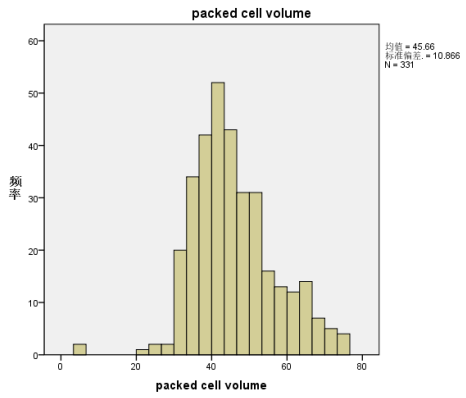


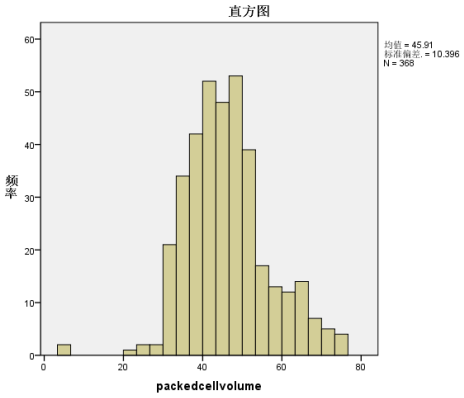


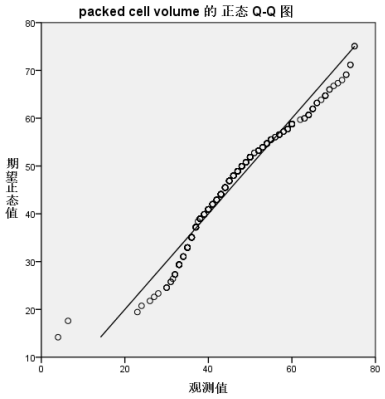


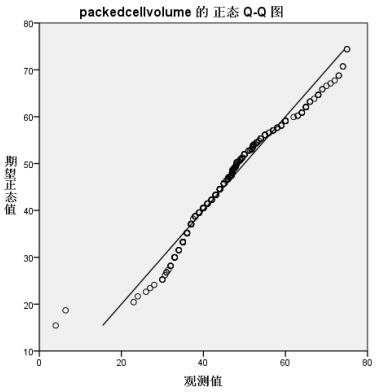
(5) packed cell volume：

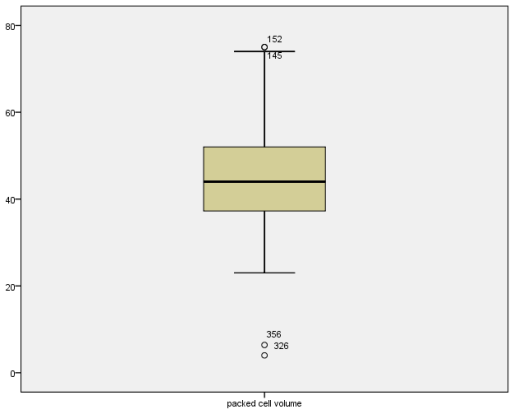
用属性的相关关系来填补缺失值后，与省略缺失值图的对比如下(左侧为省略缺失图)：

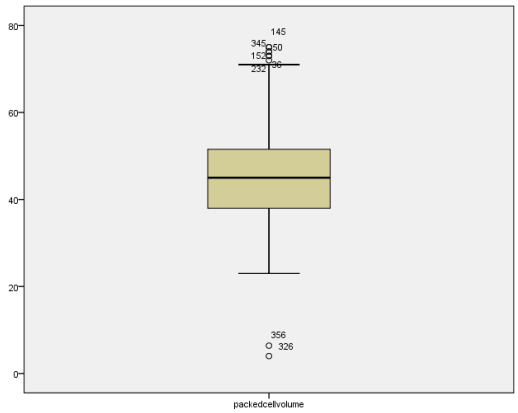






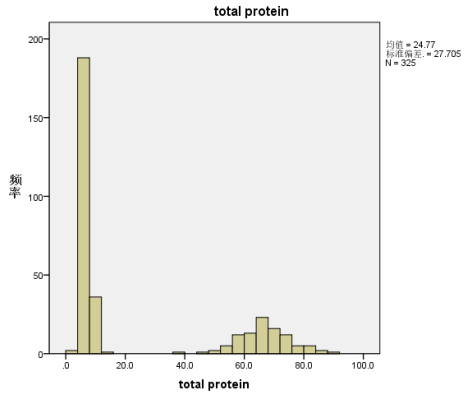


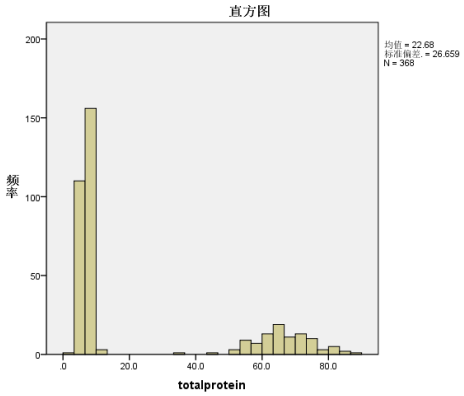


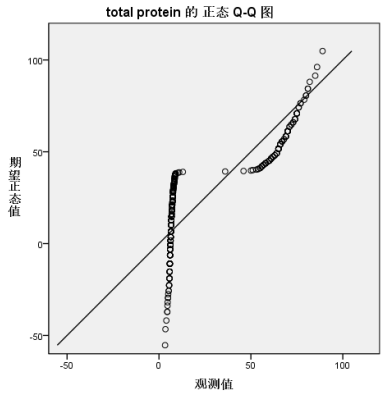


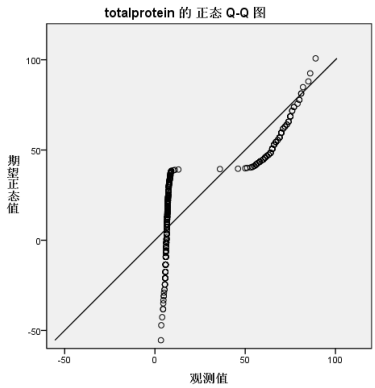
(6) total protein：

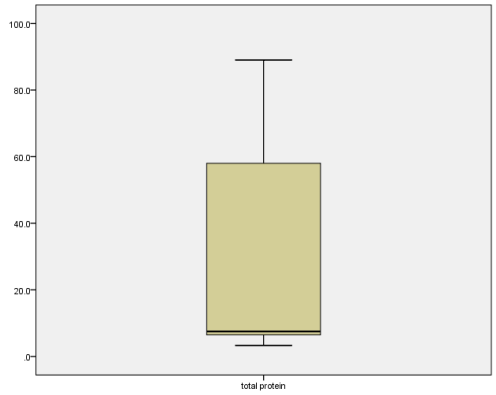
用属性的相关关系来填补缺失值后，与省略缺失值图的对比如下(左侧为省略缺失图)：





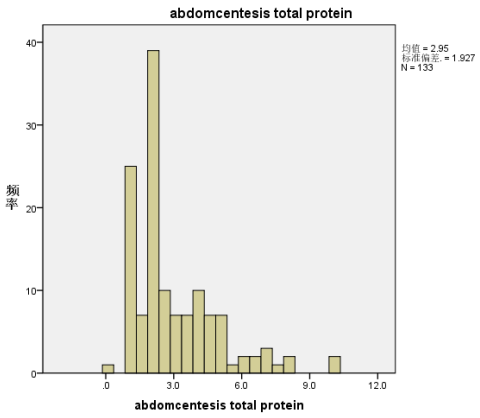


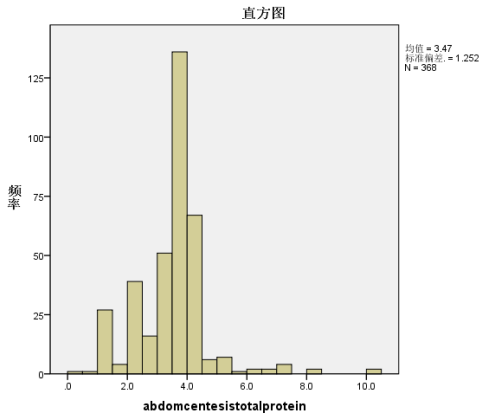


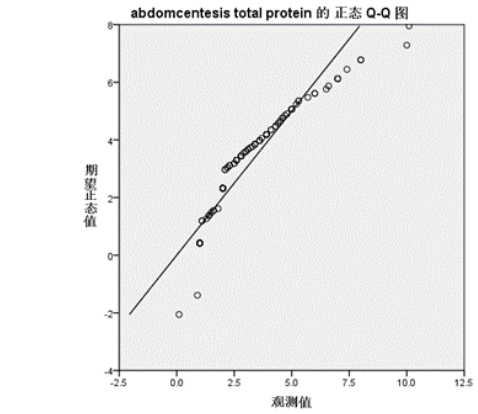


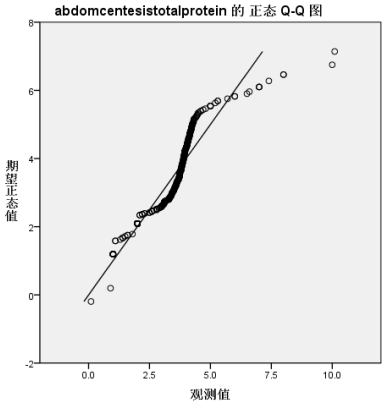
(7) abdomcentesis total protein：

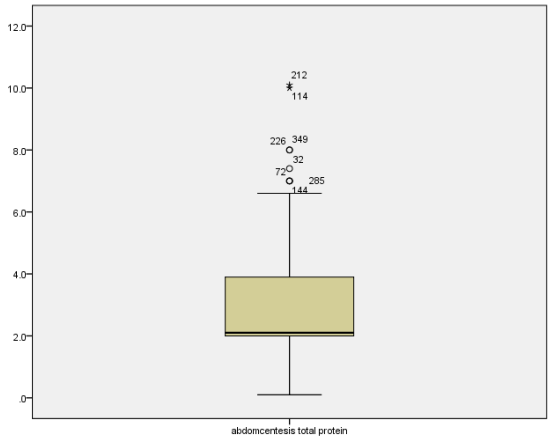
用属性的相关关系来填补缺失值后，与省略缺失值图的对比如下(左侧为省略缺失图)：

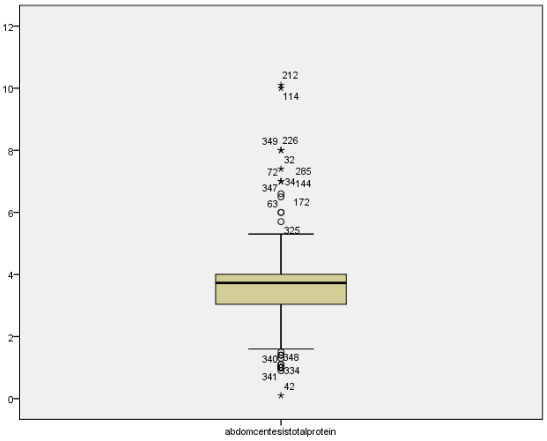








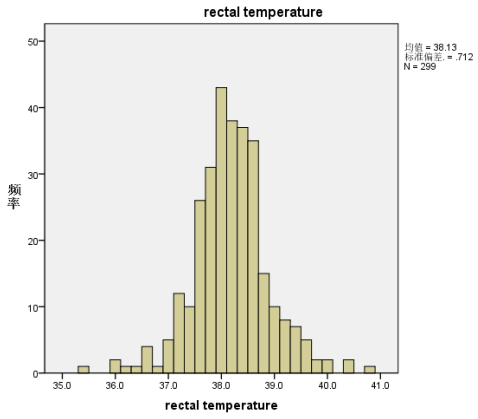


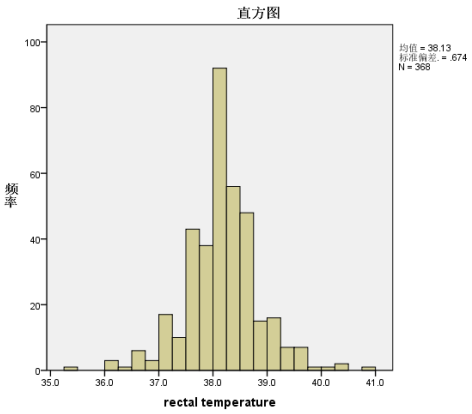


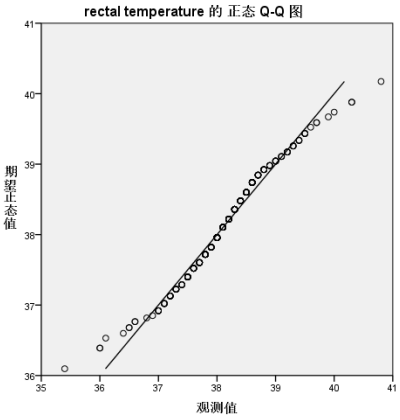
4. 通过数据对象之间的相似性来填补缺失值

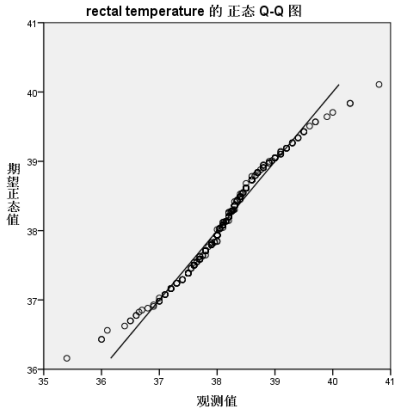
(1) rectal temperature：

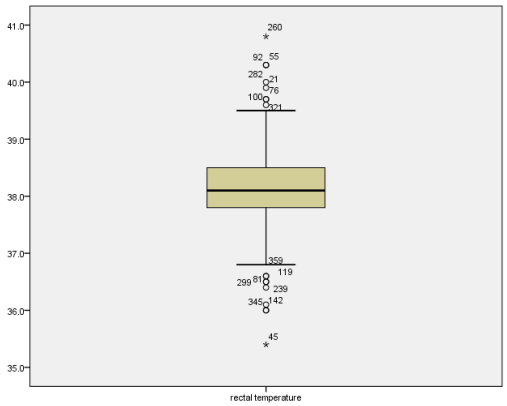
通过数据对象之间的相似性来填补缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

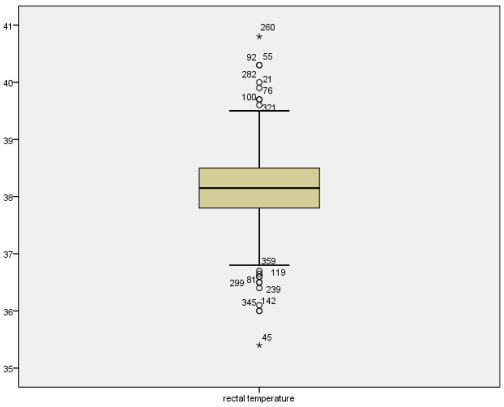






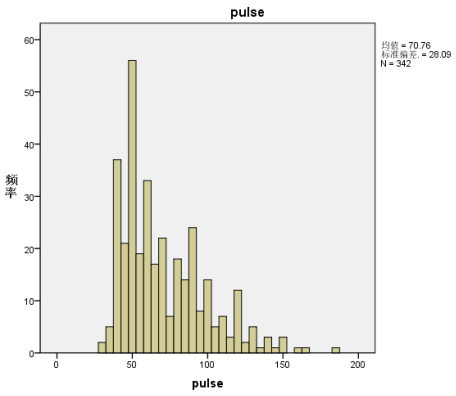


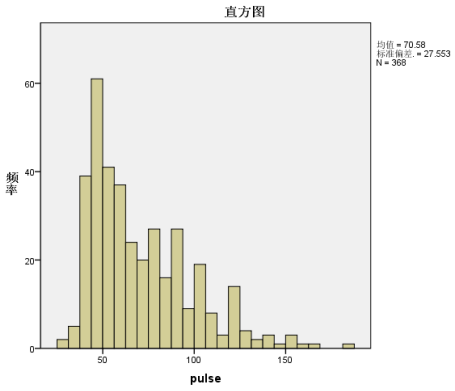


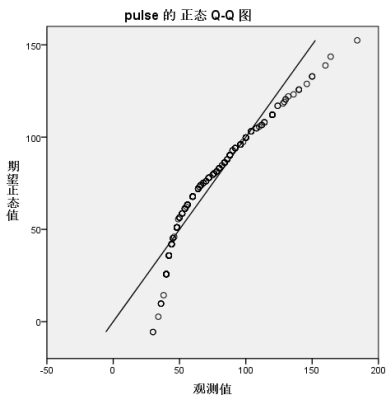


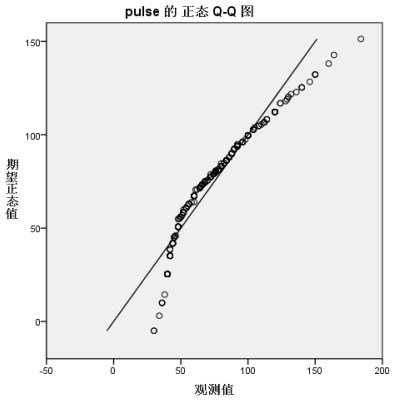
（2）pulse：

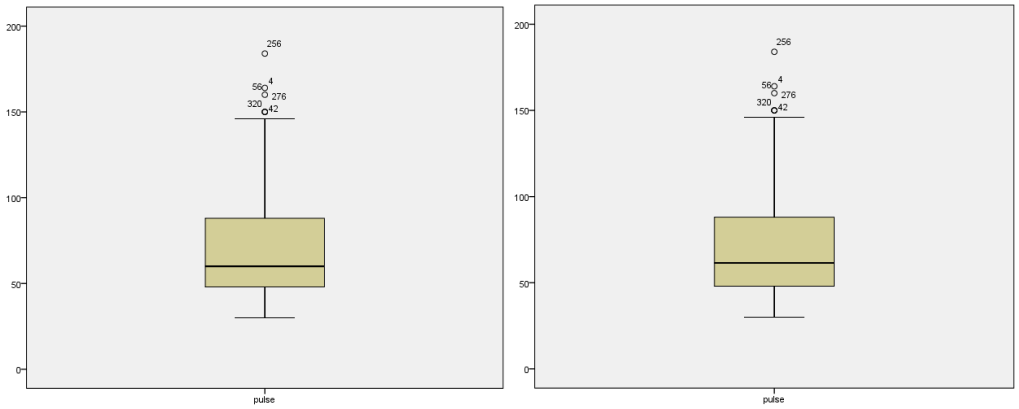
通过数据对象之间的相似性来填补缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：





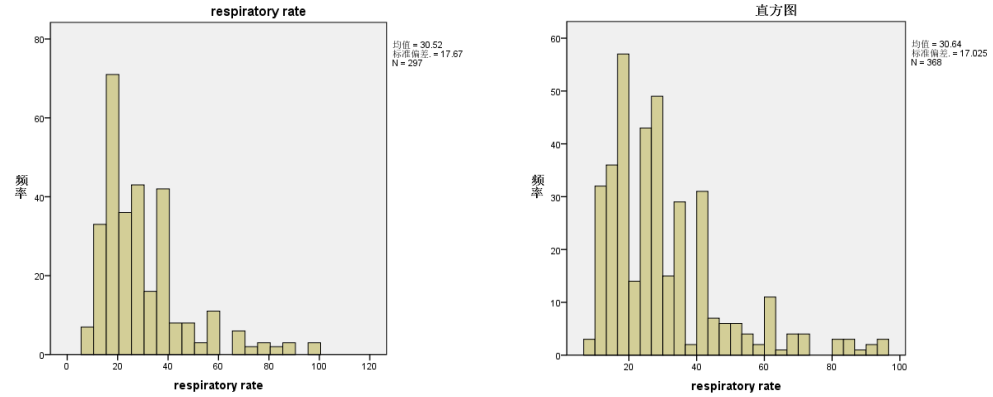


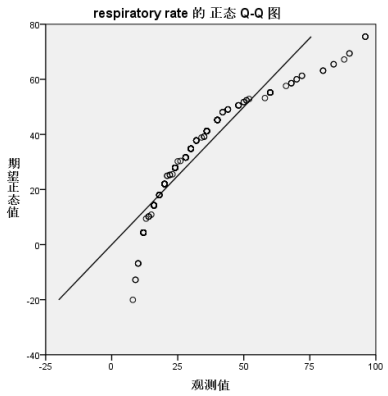


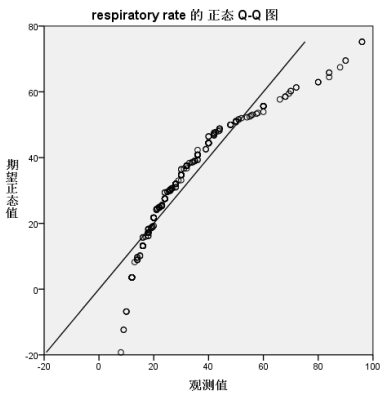


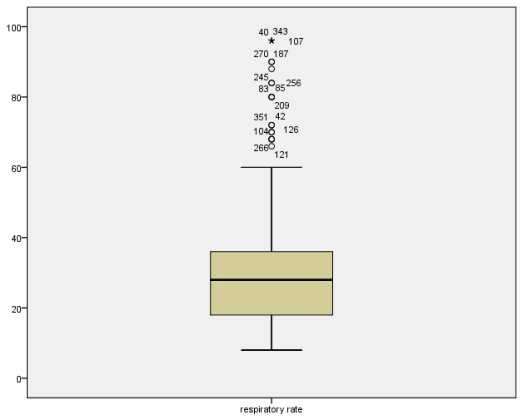
(3) respiratory rate：

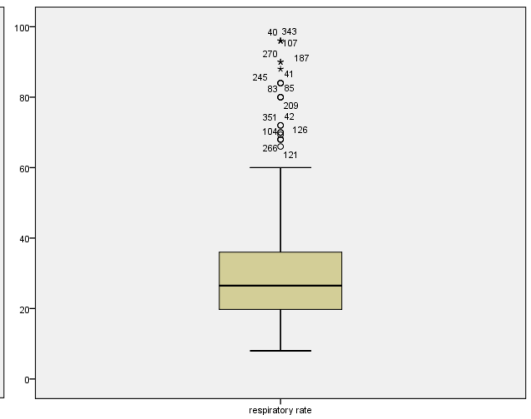
通过数据对象之间的相似性来填补缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：





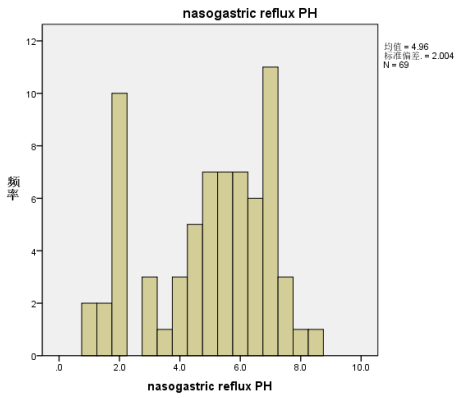


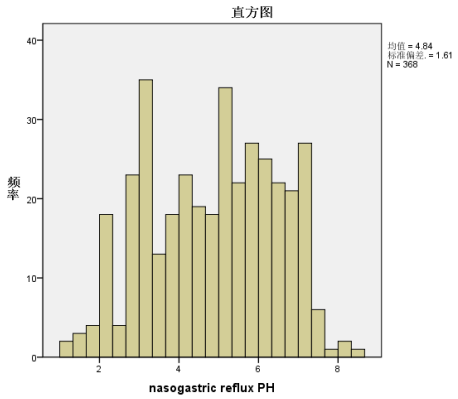


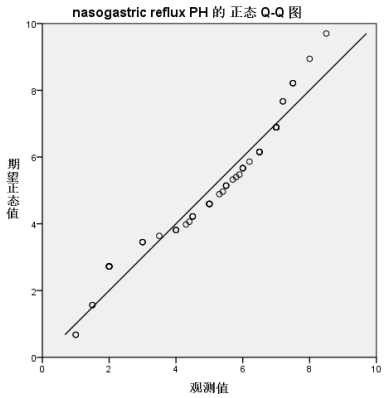


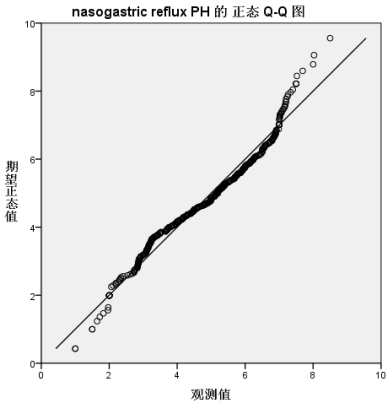
(4) nasogastric reflux PH：

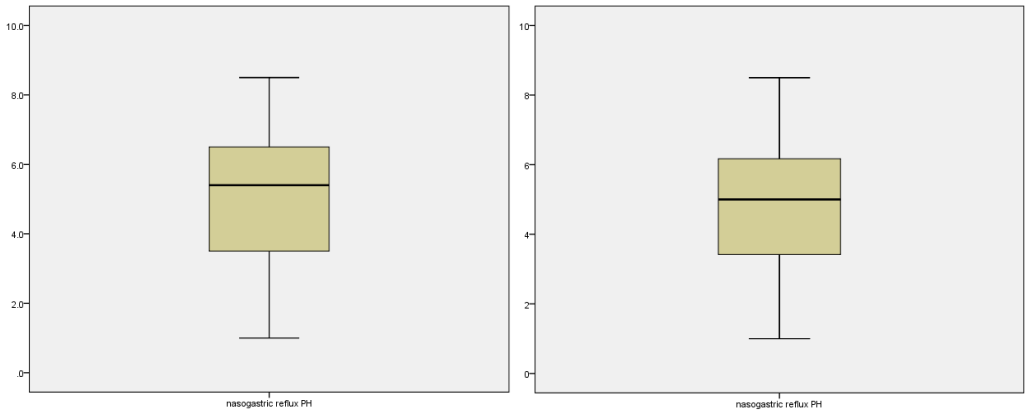
通过数据对象之间的相似性来填补缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：





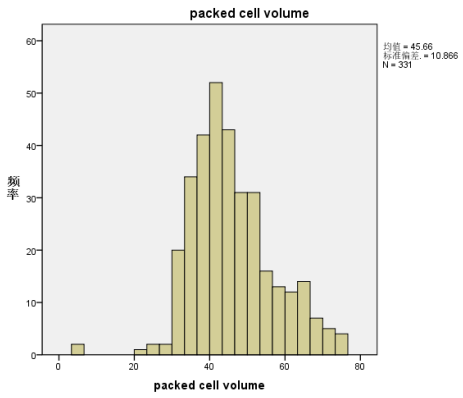


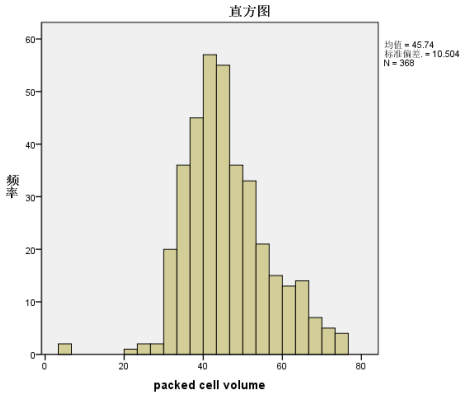


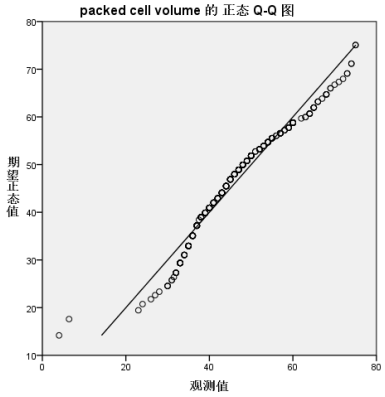


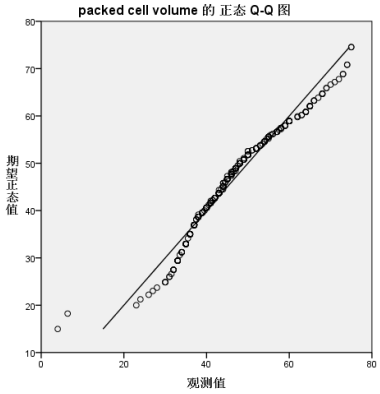
(5) packed cell volume：

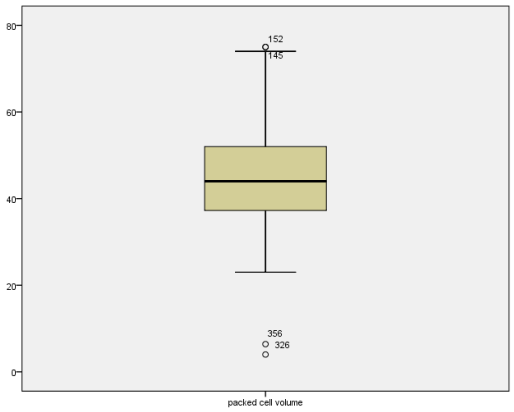
通过数据对象之间的相似性来填补缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

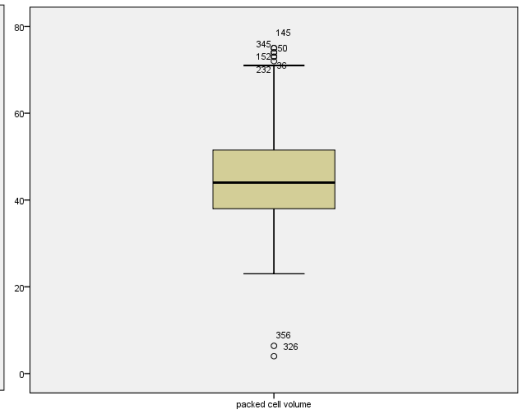






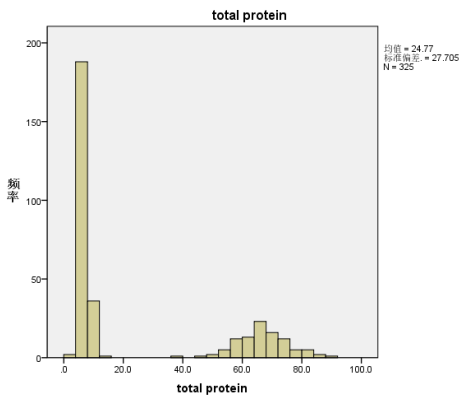


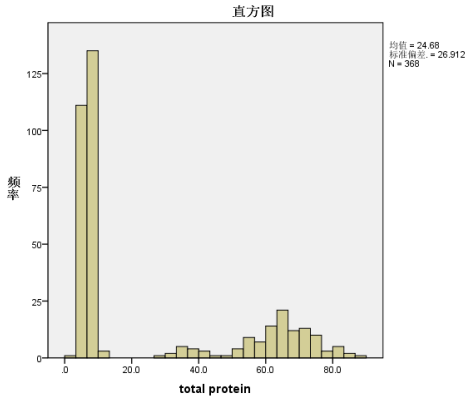


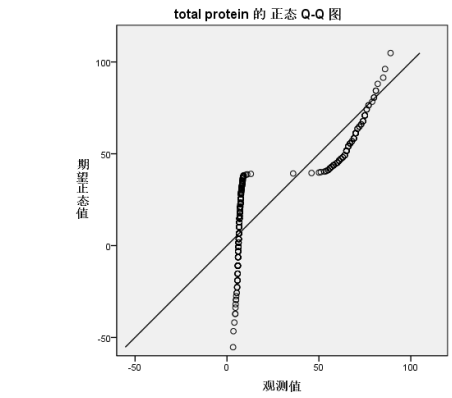


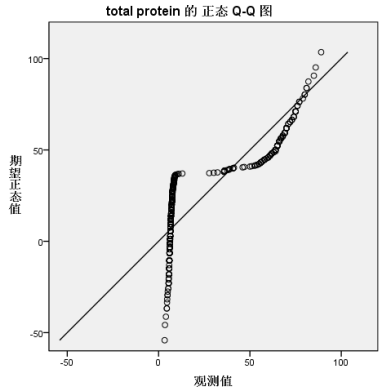
（6）total protein：

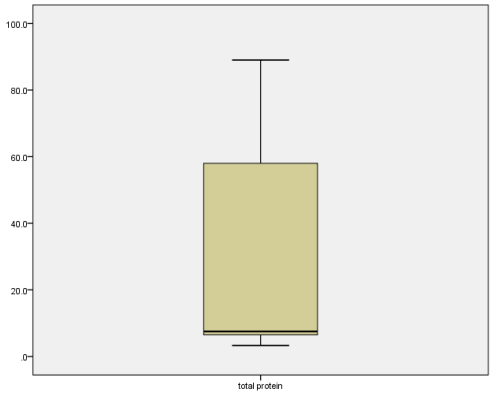
通过数据对象之间的相似性来填补缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

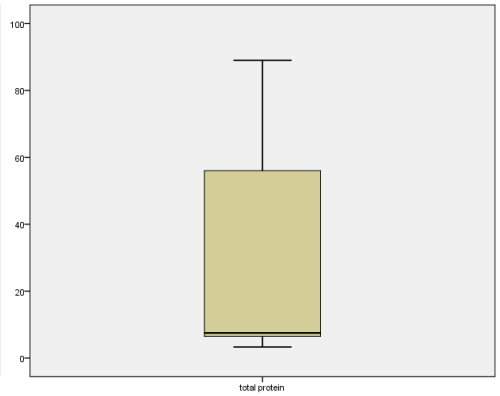






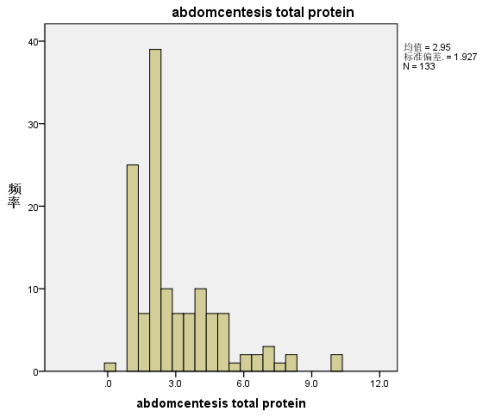


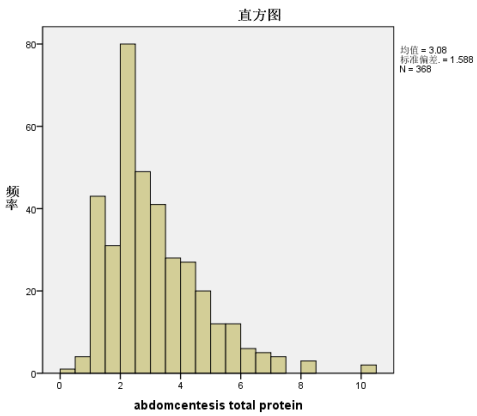


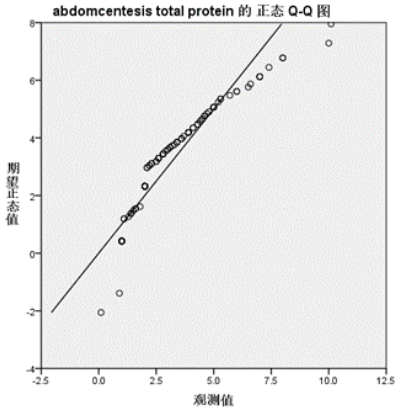


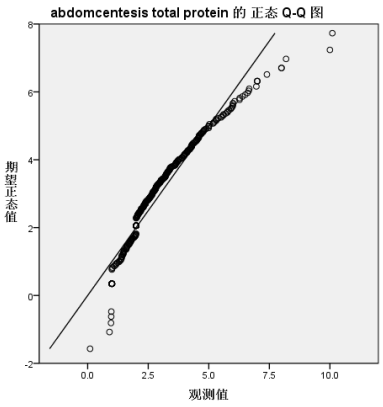
(7) abdomcentesis total protein：

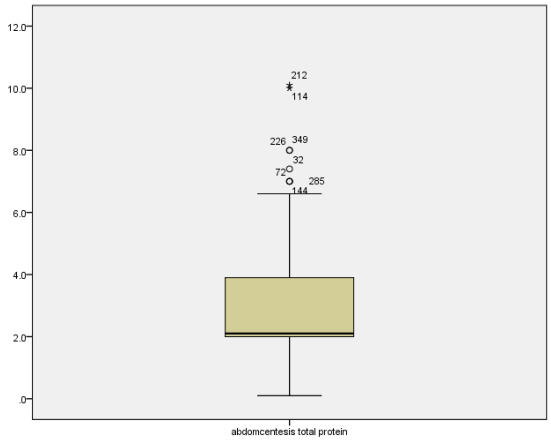
通过数据对象之间的相似性来填补缺失值后，与省略缺失值图的对比如下（左侧为省略缺失图）：

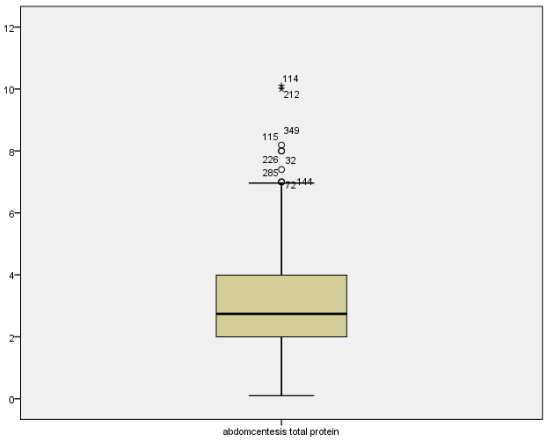









12.0
10.0
8.0
6.0
4.0
2.0
.0
212
114
226
349
32
72
285
144
abdomcentesis total protein


12
10
8
6
4
2
0
114
212
115
349
226
32
285
72
144
abdomcentesis total protein