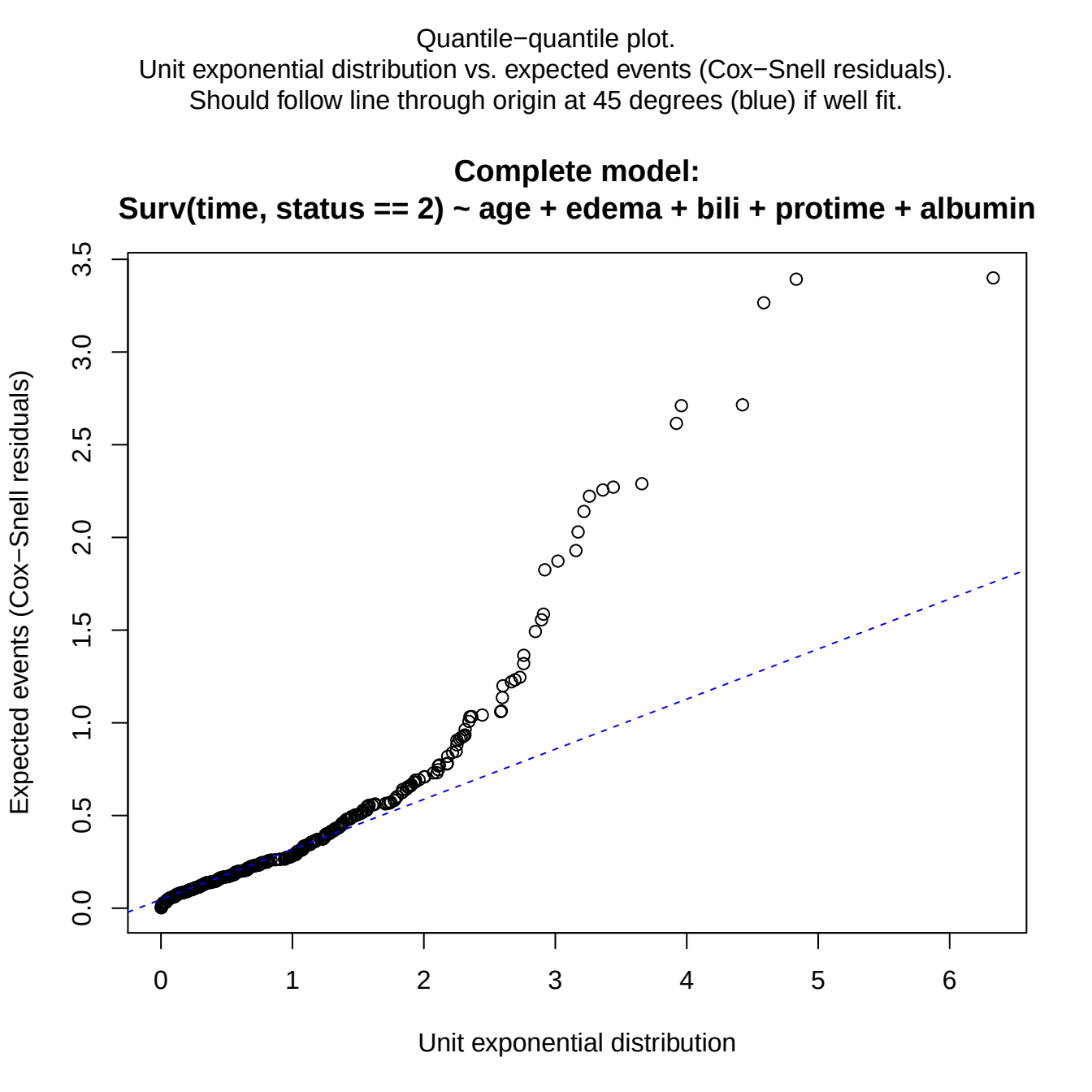
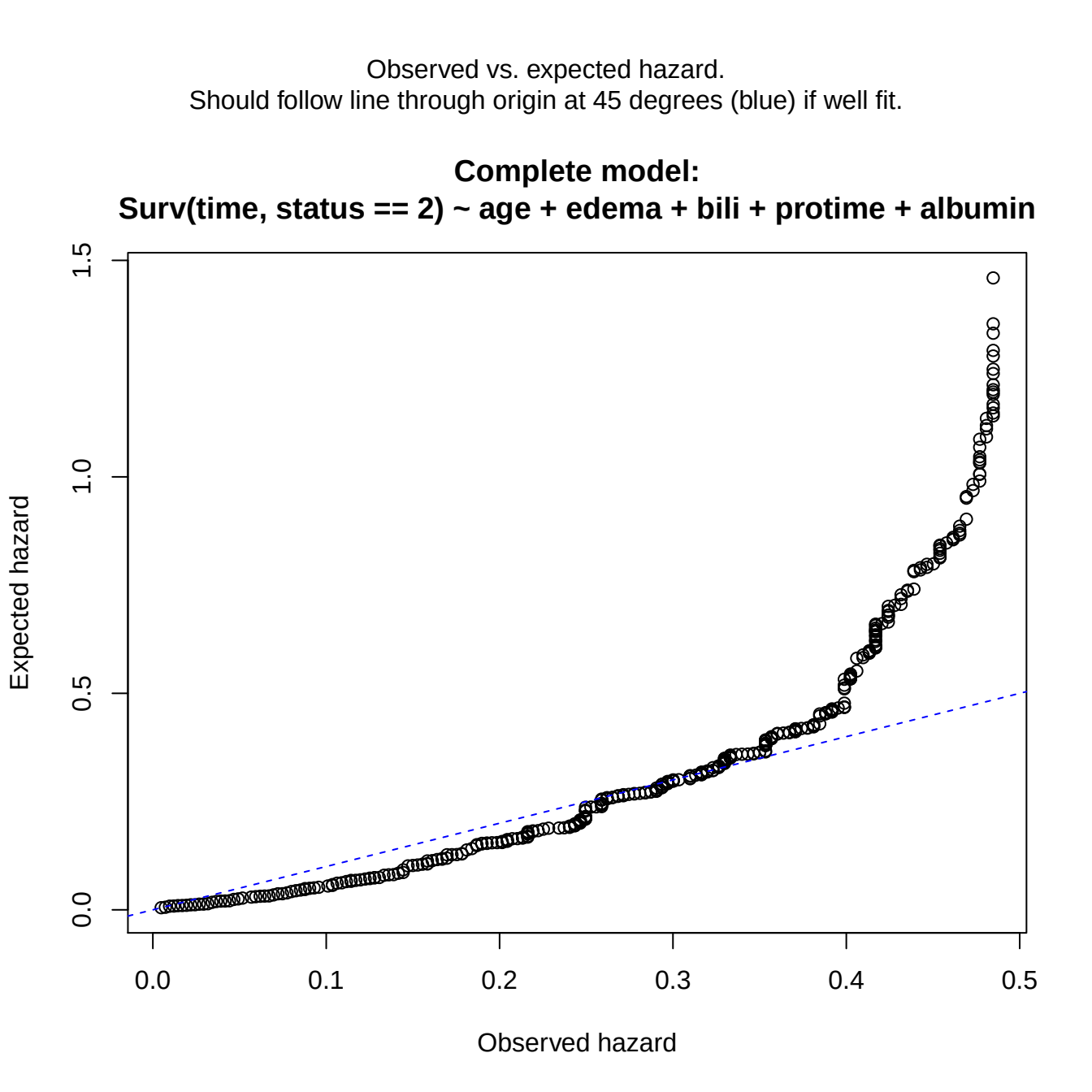
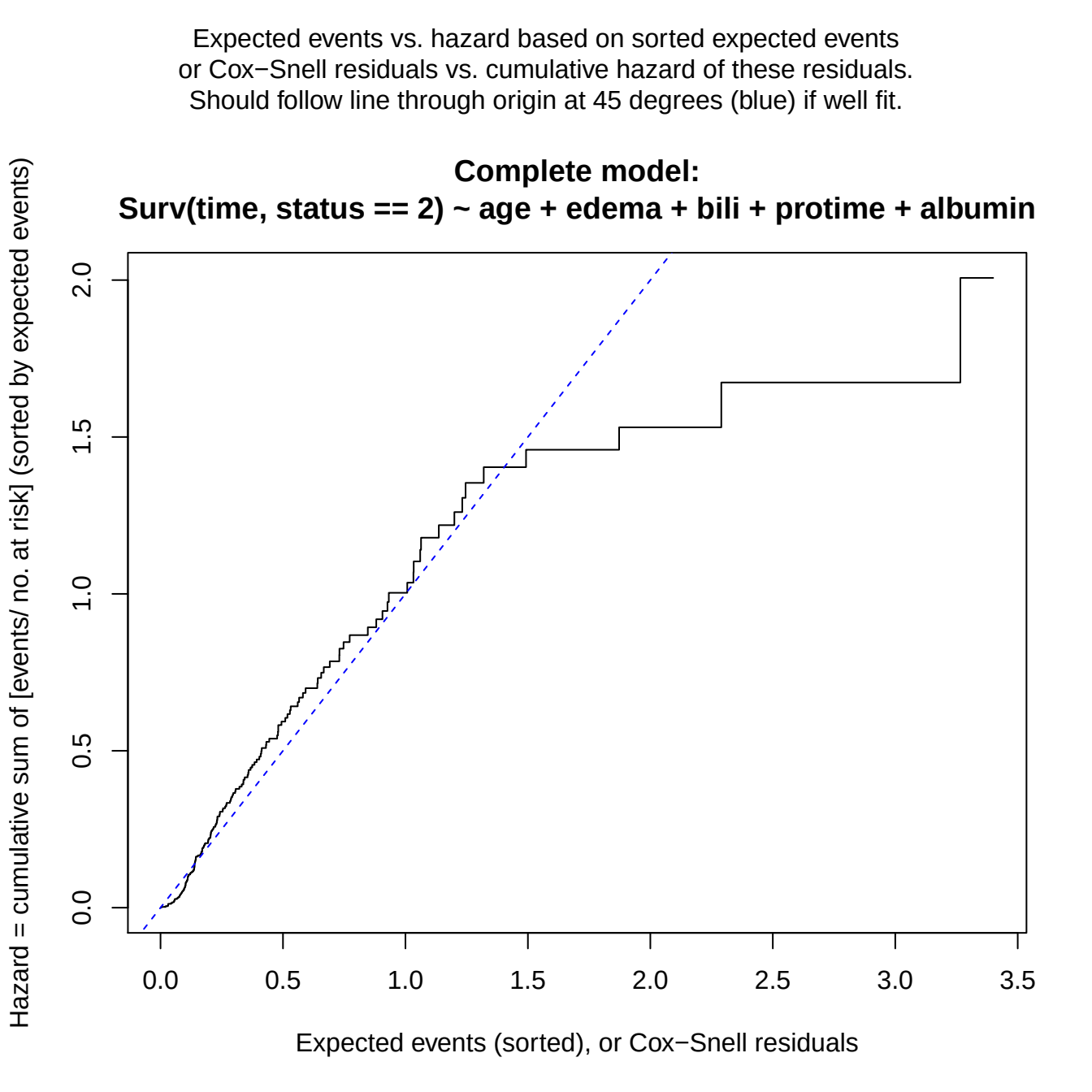
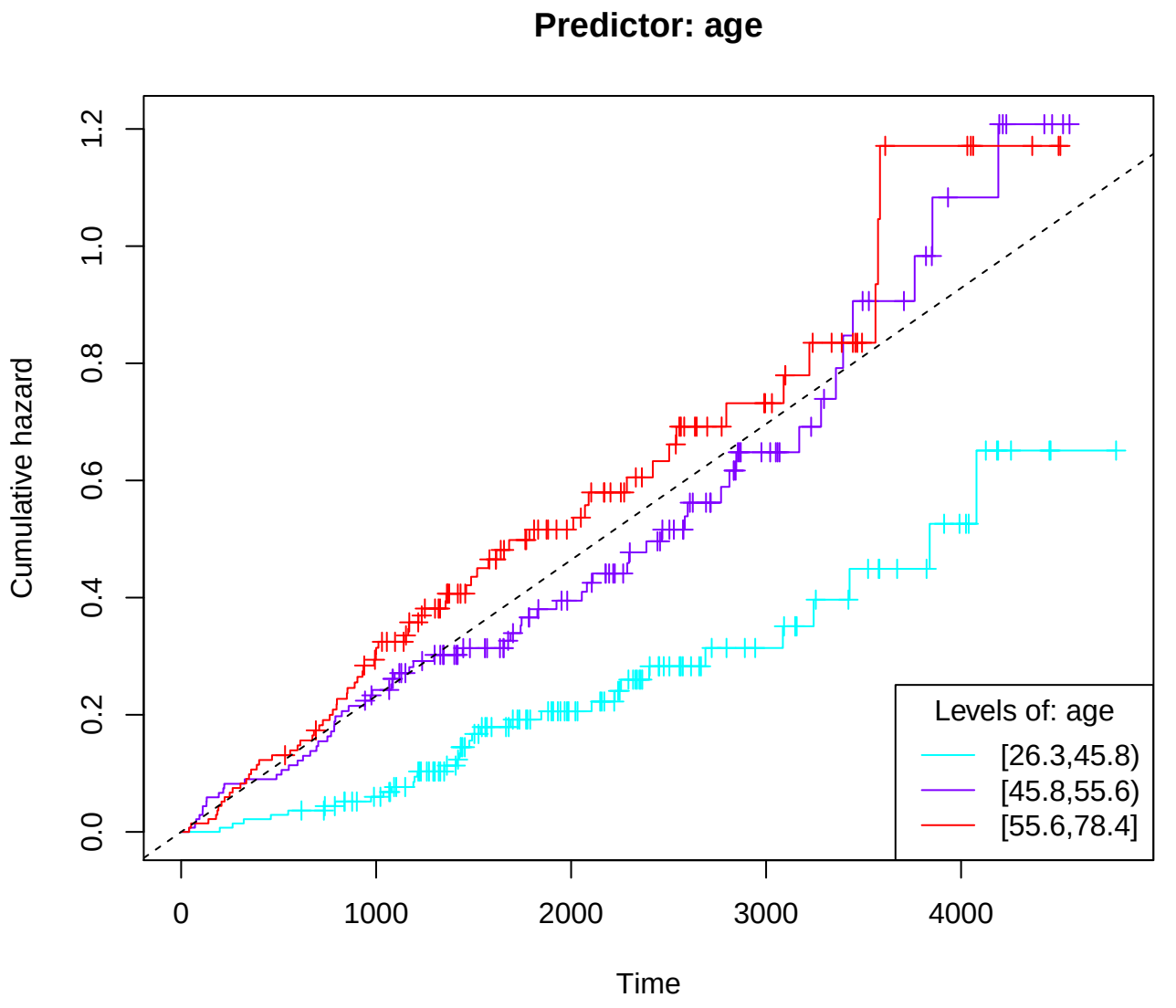

Quantile−quantile plot.
Unit exponential distribution vs. expected events (Cox−Snell residuals).
Should follow line through origin at 45 degrees (blue) if well fit.
Complete model:
Surv(time, status == 2) ~ age + edema + bili + protime + albumin
Expected events (Cox−Snell residuals)
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
0
1
2
3
4
5
6
Unit exponential distribution

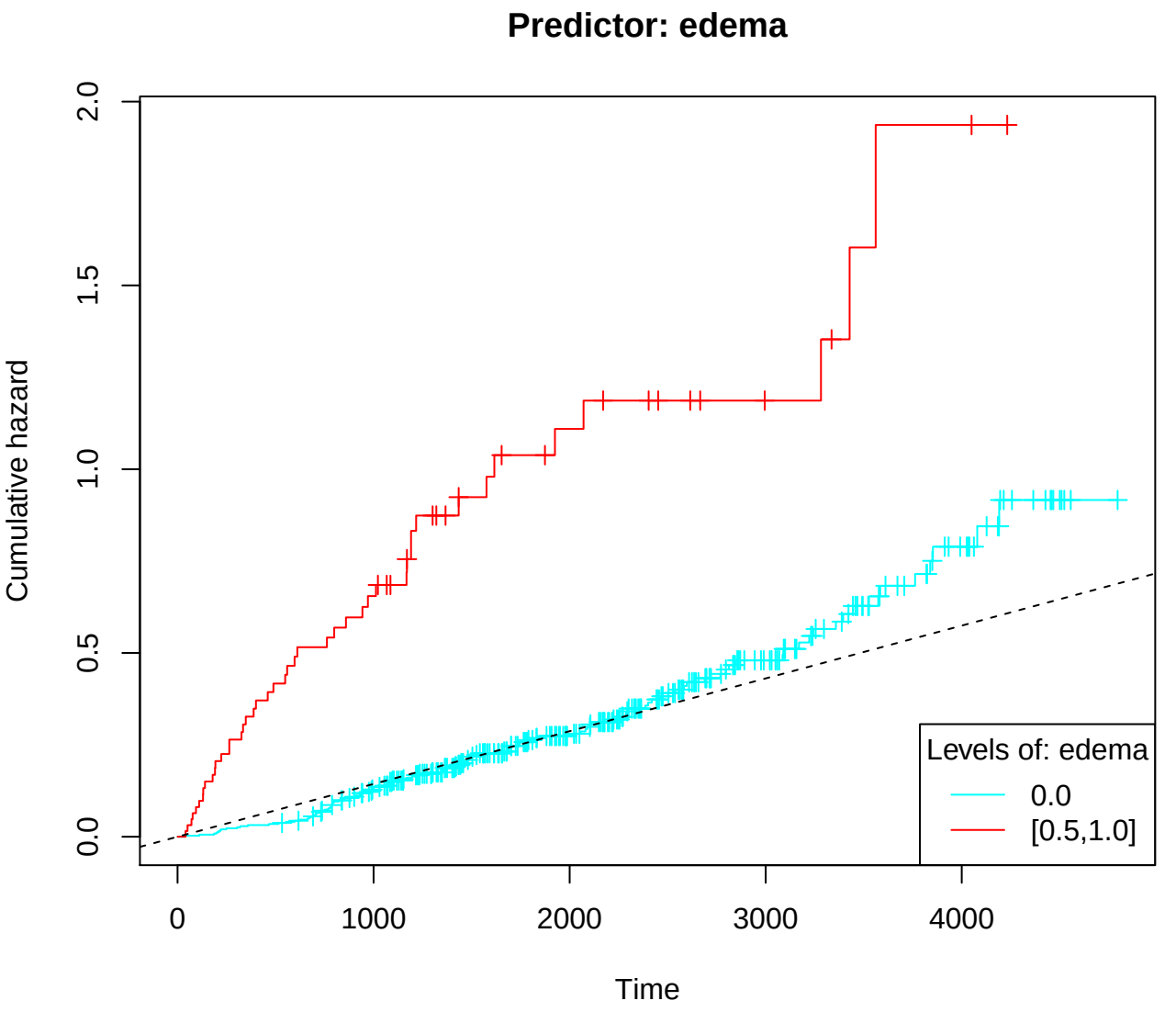

Observed vs. expected hazard.
Should follow line through origin at 45 degrees (blue) if well fit.
Complete model:
Surv(time, status == 2) ~ age + edema + bili + protime + albumin
Expected hazard
0.0
0.5
1.0
1.5
0.0
0.1
0.2
0.3
0.4
0.5
Observed hazard


Expected events vs. hazard based on sorted expected events
or Cox−Snell residuals vs. cumulative hazard of these residuals.
Should follow line through origin at 45 degrees (blue) if well fit.
Complete model:
Surv(time, status == 2) ~ age + edema + bili + protime + albumin
Hazard = cumulative sum of [events/ no. at risk] (sorted by expected events)
0.0
0.5
1.0
1.5
2.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
Expected events (sorted), or Cox−Snell residuals

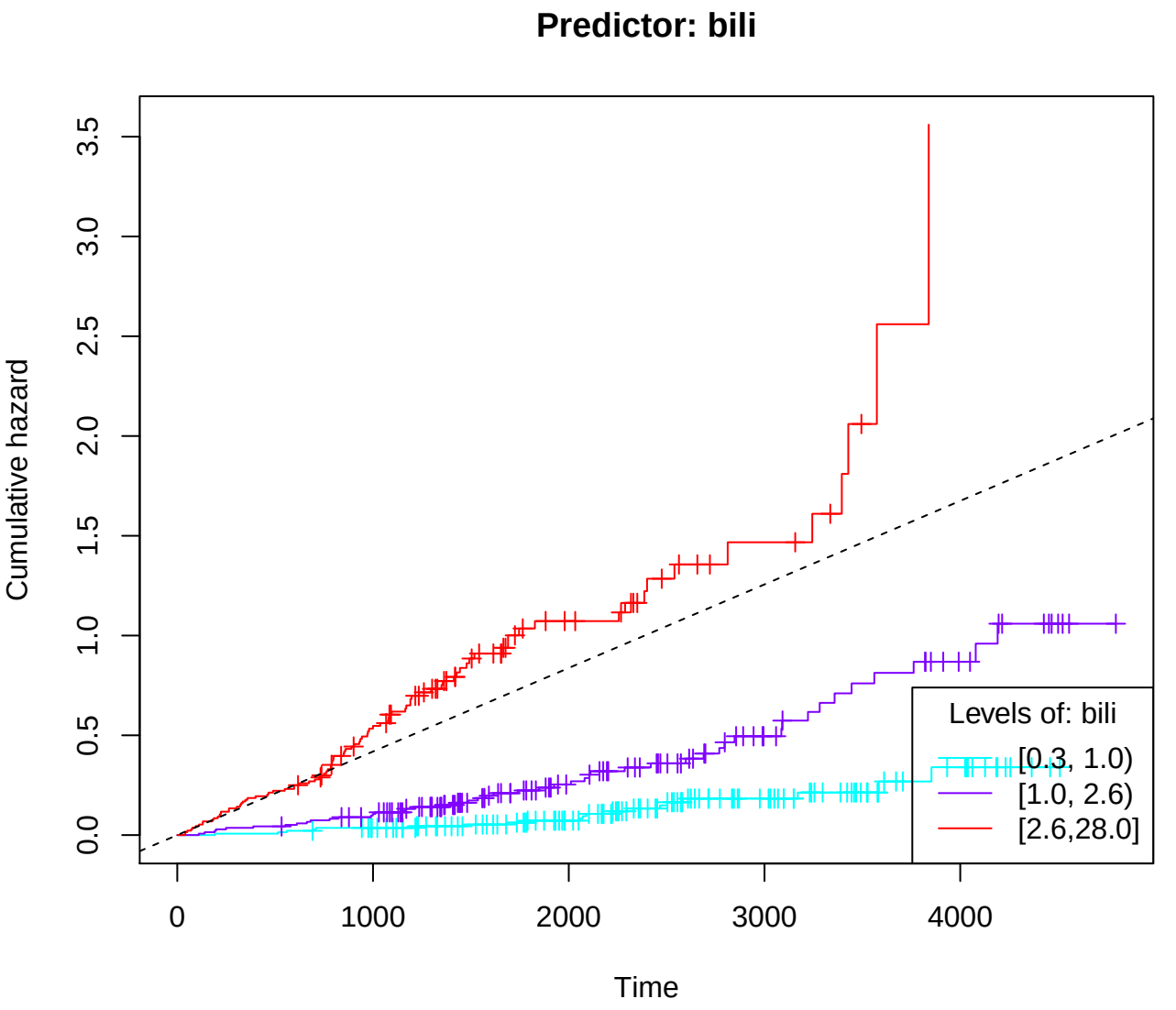
Time vs. hazard, per predictor.
If hazards proportional then curves should be constant multiples of a baseline.
Reference (black) line is 45 degrees.



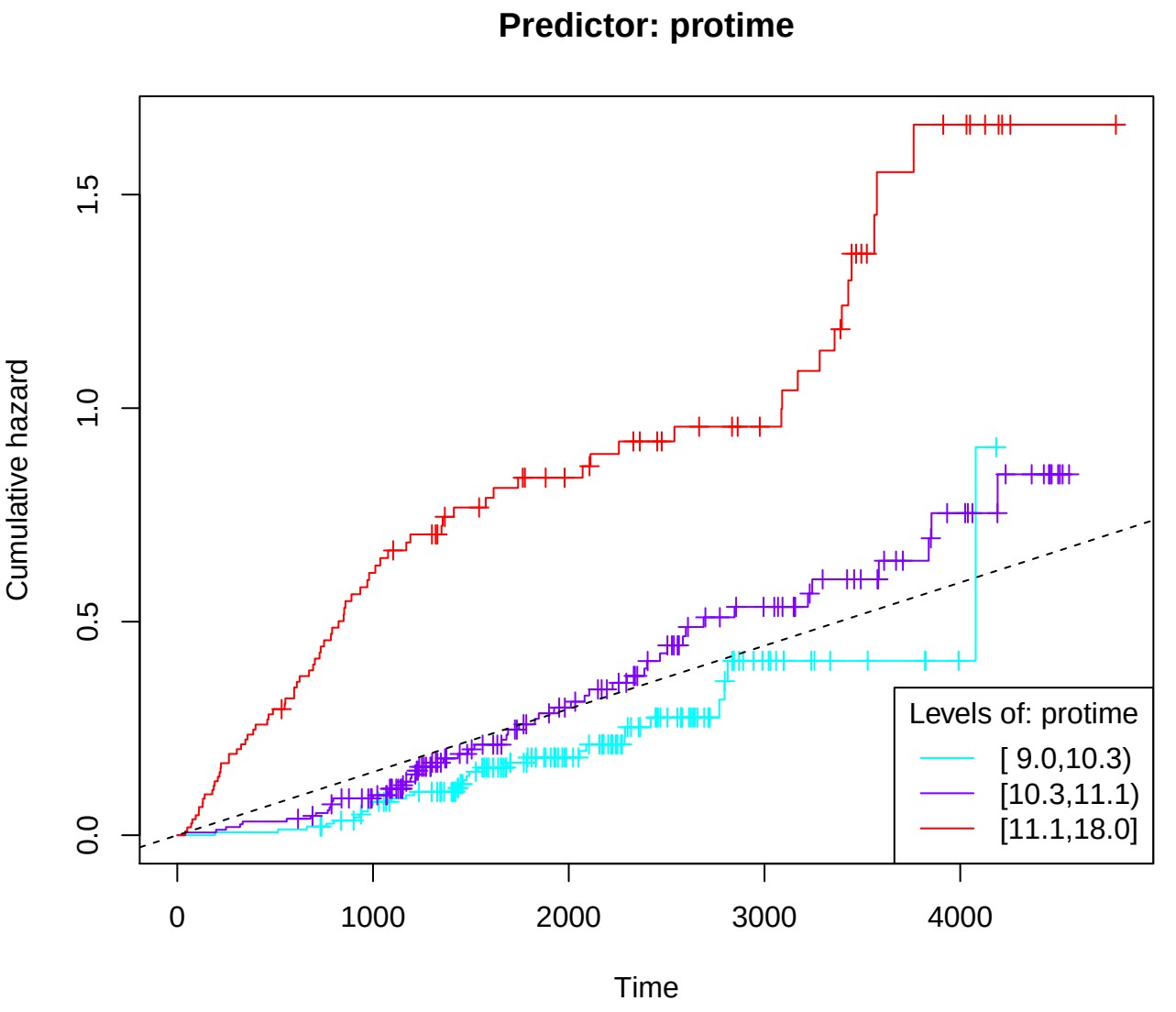
Time vs. hazard, per predictor.
If hazards proportional then curves should be constant multiples of a baseline.
Reference (black) line is 45 degrees.



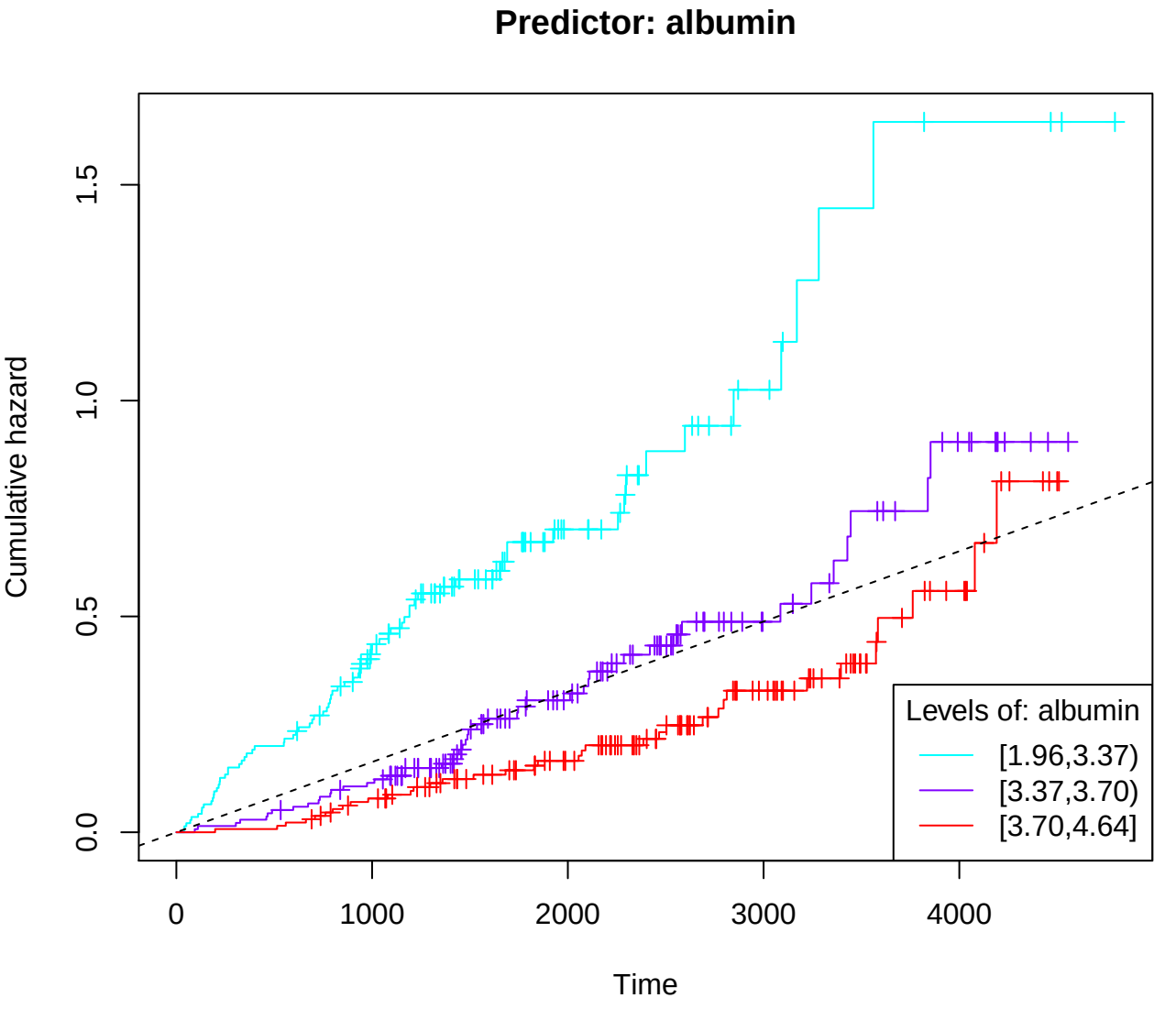
Time vs. hazard, per predictor.
If hazards proportional then curves should be constant multiples of a baseline.
Reference (black) line is 45 degrees.

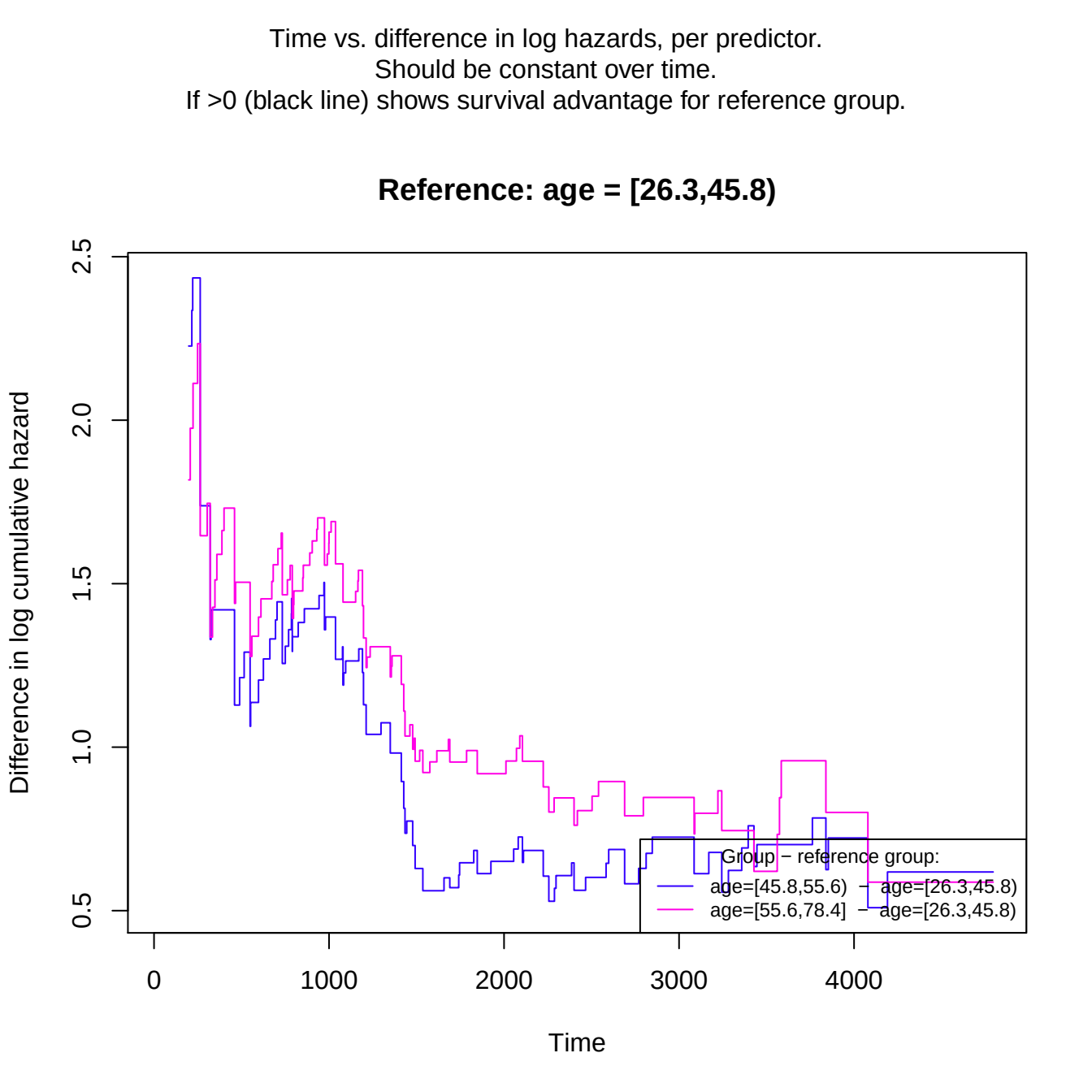


Time vs. hazard, per predictor.
If hazards proportional then curves should be constant multiples of a baseline.
Reference (black) line is 45 degrees.

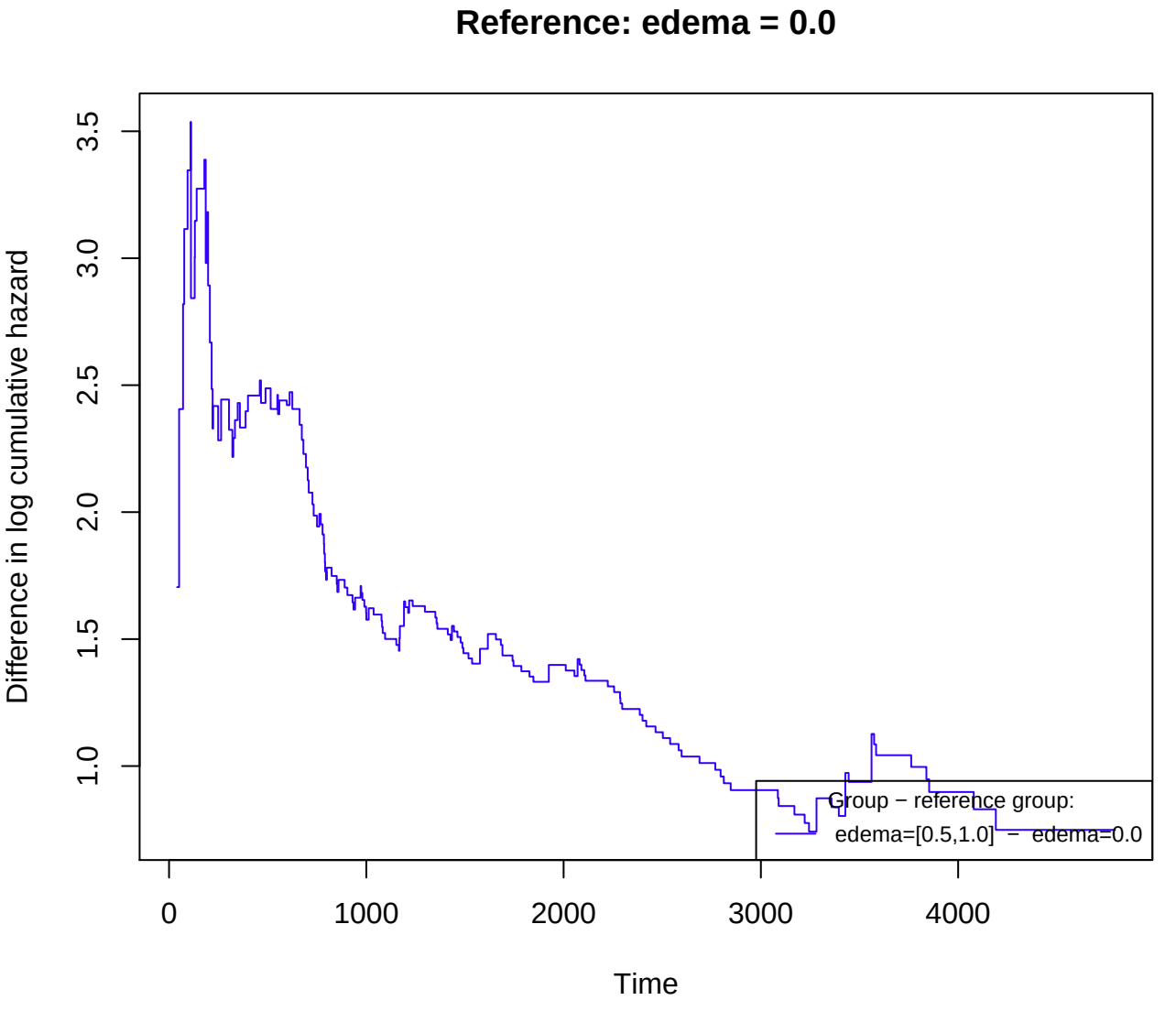


Time vs. hazard, per predictor.
If hazards proportional then curves should be constant multiples of a baseline.
Reference (black) line is 45 degrees.

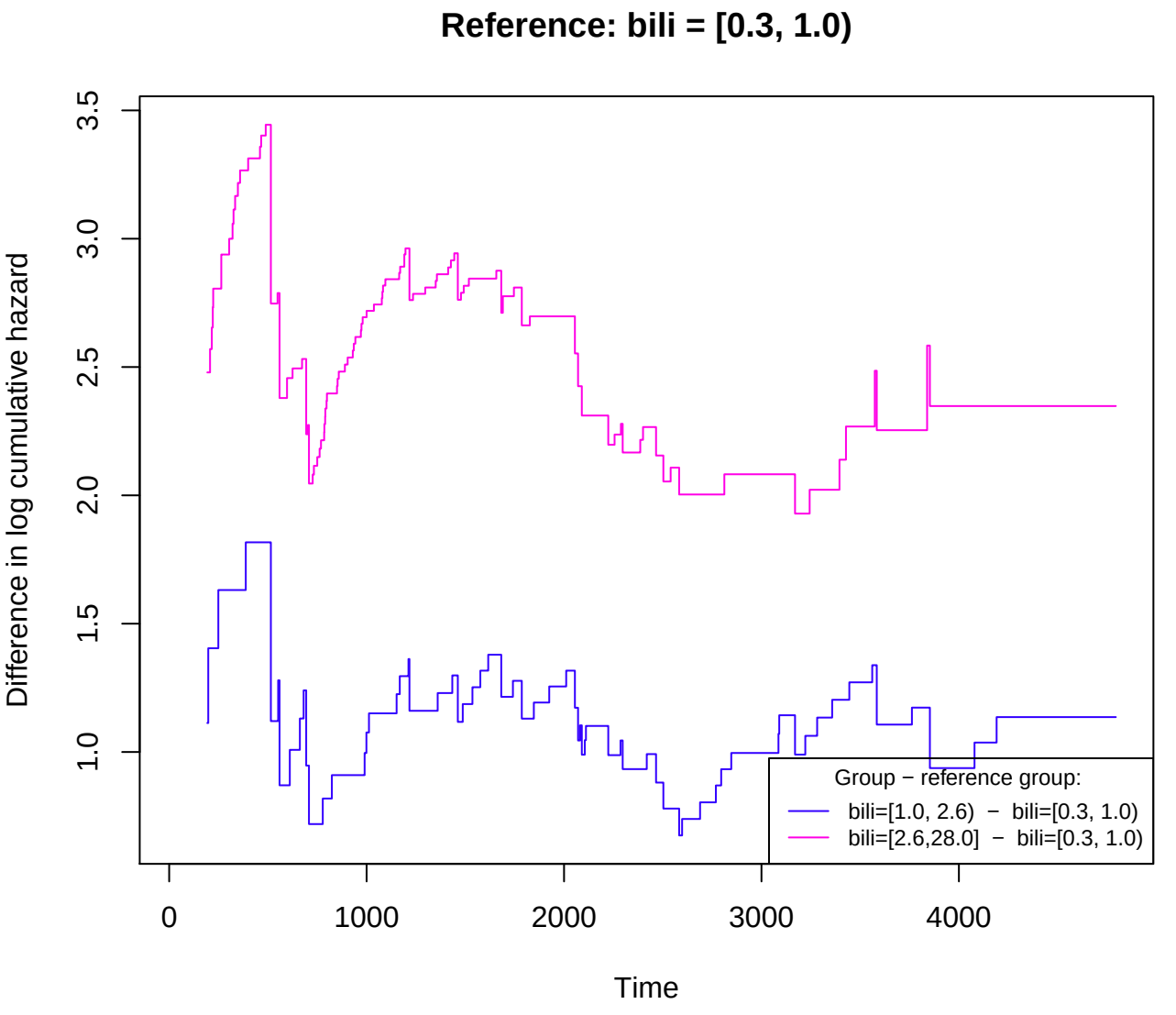


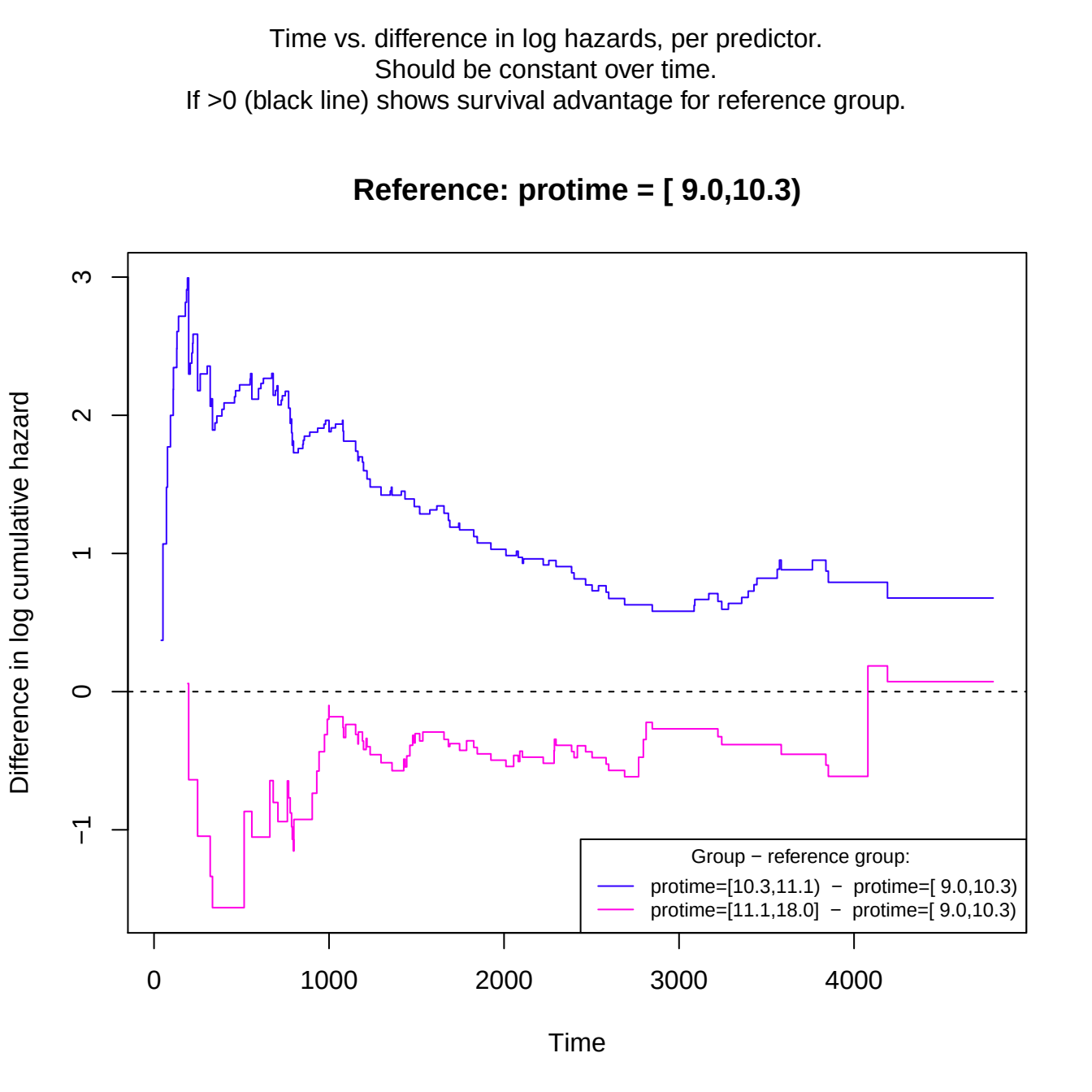

Time vs. difference in log hazards, per predictor.
Should be constant over time.
If >0 (black line) shows survival advantage for reference group.
Reference: age = [26.3,45.8)
Difference in log cumulative hazard
0.5
1.0
1.5
2.0
2.5
0
1000
2000
3000
4000
Time
Group − reference group:
age=[45.8,55.6) − age=[26.3,45.8)
age=[55.6,78.4] − age=[26.3,45.8)

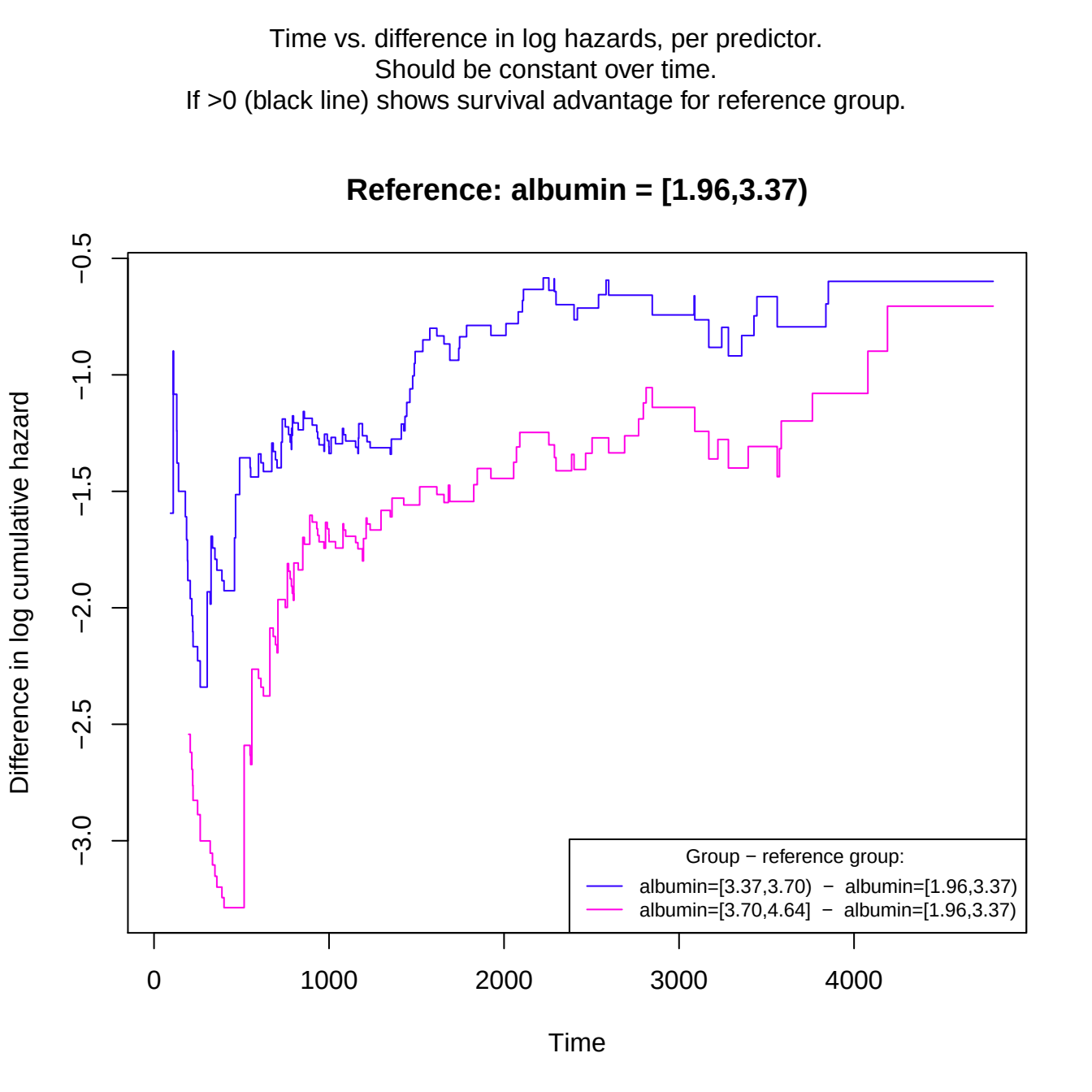
Time vs. difference in log hazards, per predictor.
Should be constant over time.
If >0 (black line) shows survival advantage for reference group.



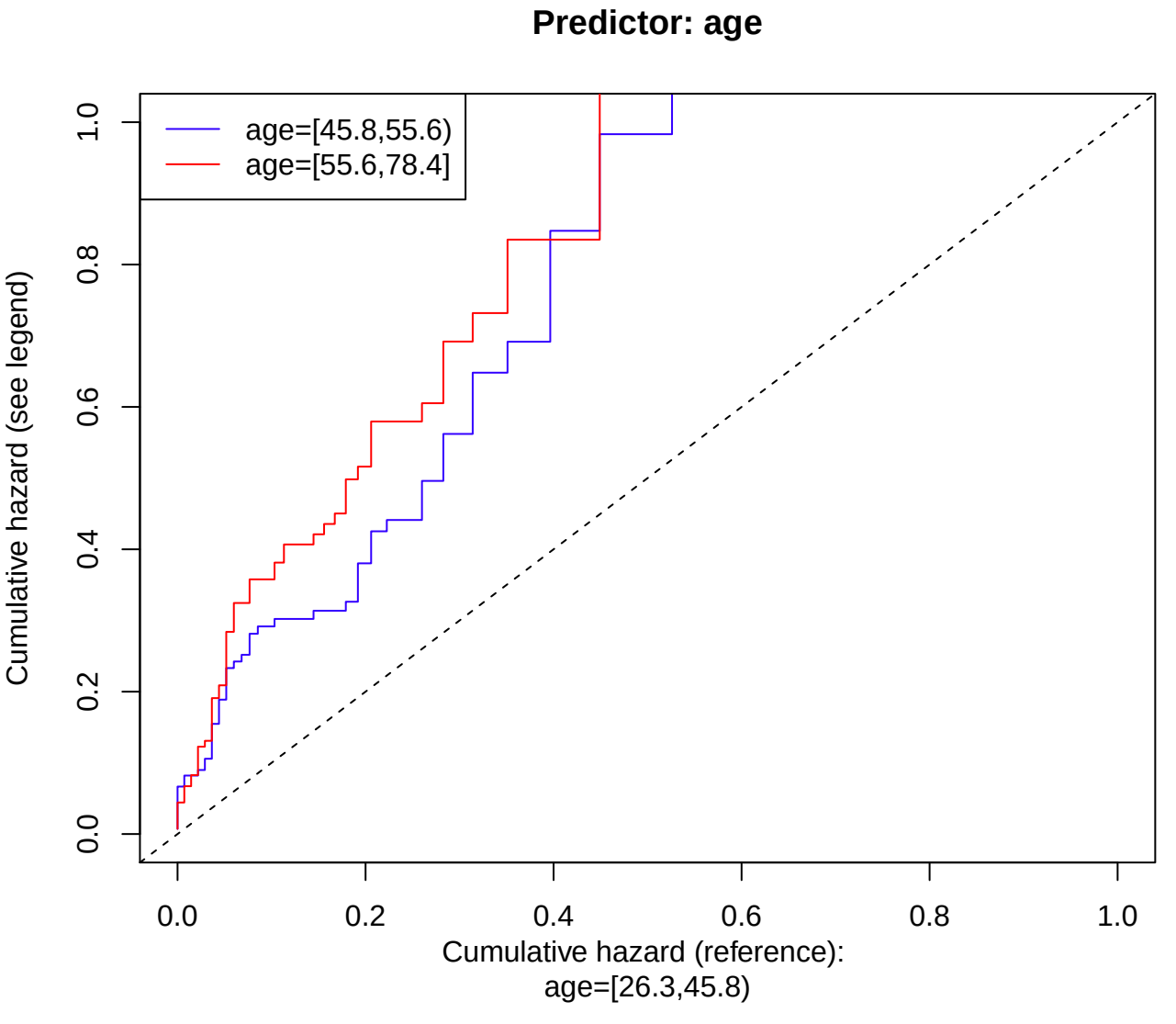
Time vs. difference in log hazards, per predictor.
Should be constant over time.
If >0 (black line) shows survival advantage for reference group.



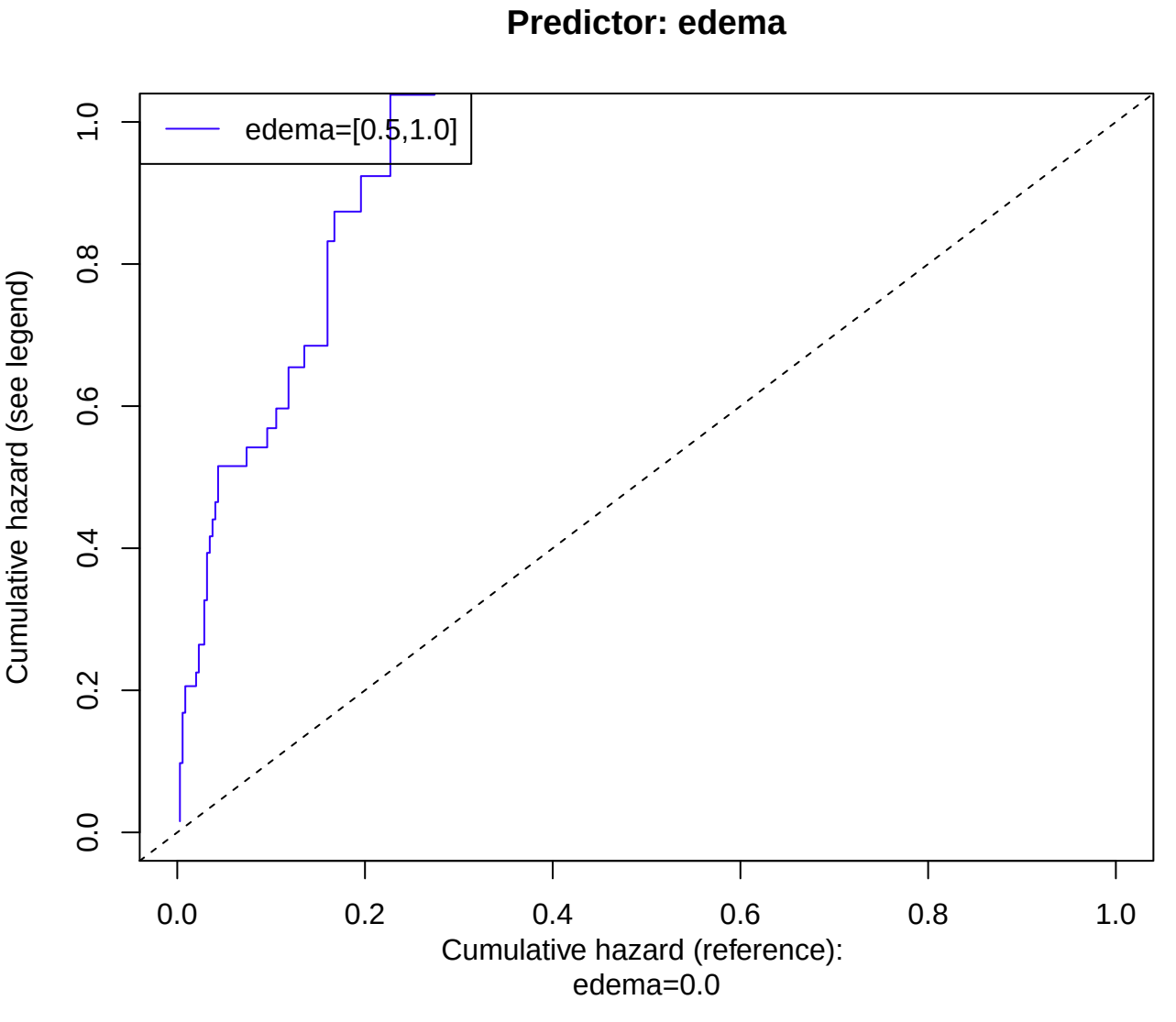

Time vs. difference in log hazards, per predictor.
Should be constant over time.
If >0 (black line) shows survival advantage for reference group.
Reference: protime = [9.0,10.3)
Difference in log cumulative hazard
3
2
1
0
−1
0
1000
2000
3000
4000
Time
Group − reference group:
protime=[10.3,11.1) − protime=[9.0,10.3)
protime=[11.1,18.0] − protime=[9.0,10.3)


Time vs. difference in log hazards, per predictor.
Should be constant over time.
If >0 (black line) shows survival advantage for reference group.
Reference: albumin = [1.96,3.37)
Difference in log cumulative hazard
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
0
1000
2000
3000
4000
Time
Group − reference group:
albumin=[3.37,3.70) − albumin=[1.96,3.37)
albumin=[3.70,4.64] − albumin=[1.96,3.37)

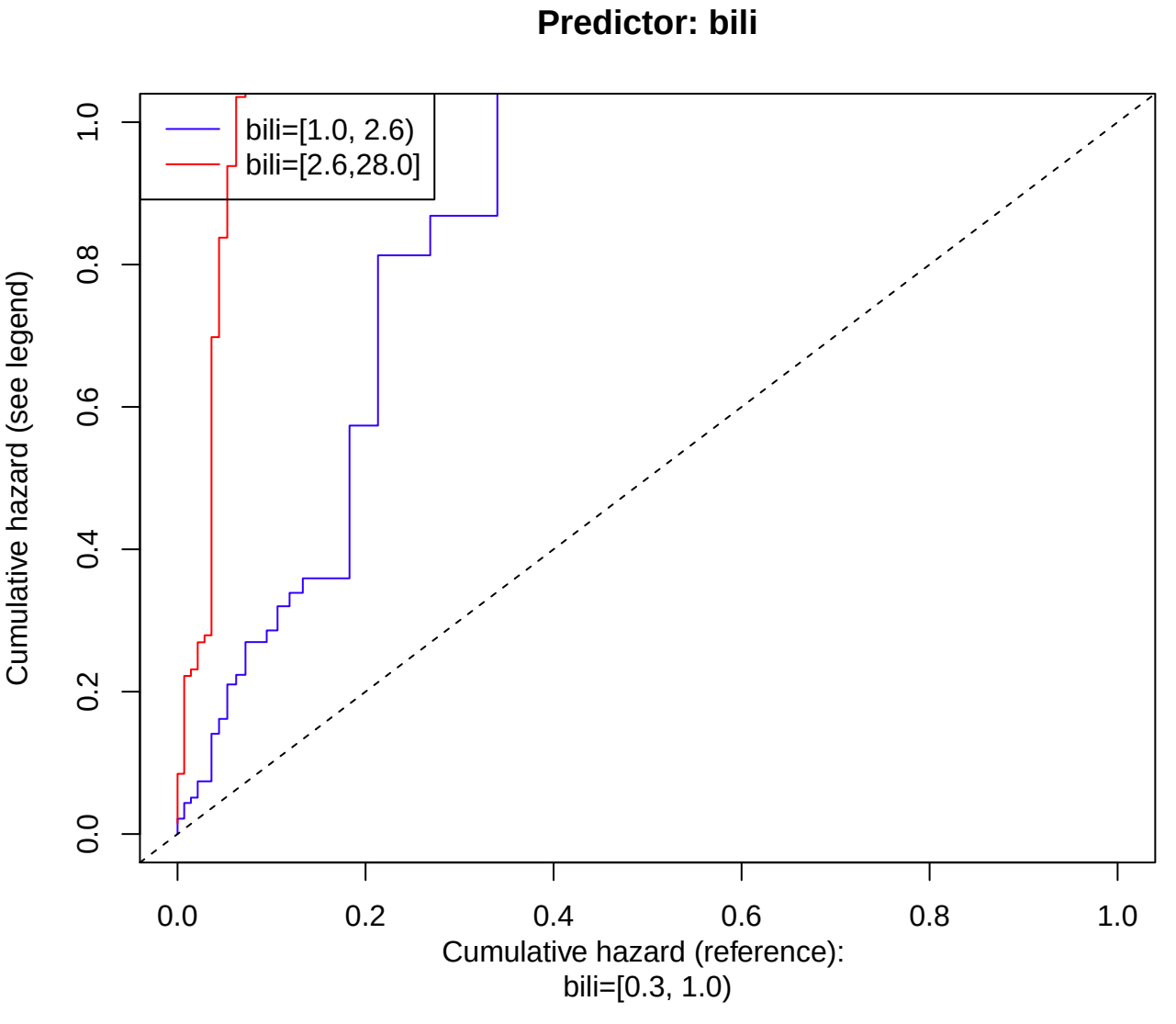
Cumulative hazard vs. reference group. Should be linear plot through origin.
If convex (towards top left) shows ratio of hazards is increasing over time.
Reference line (black) is at 45 degrees.



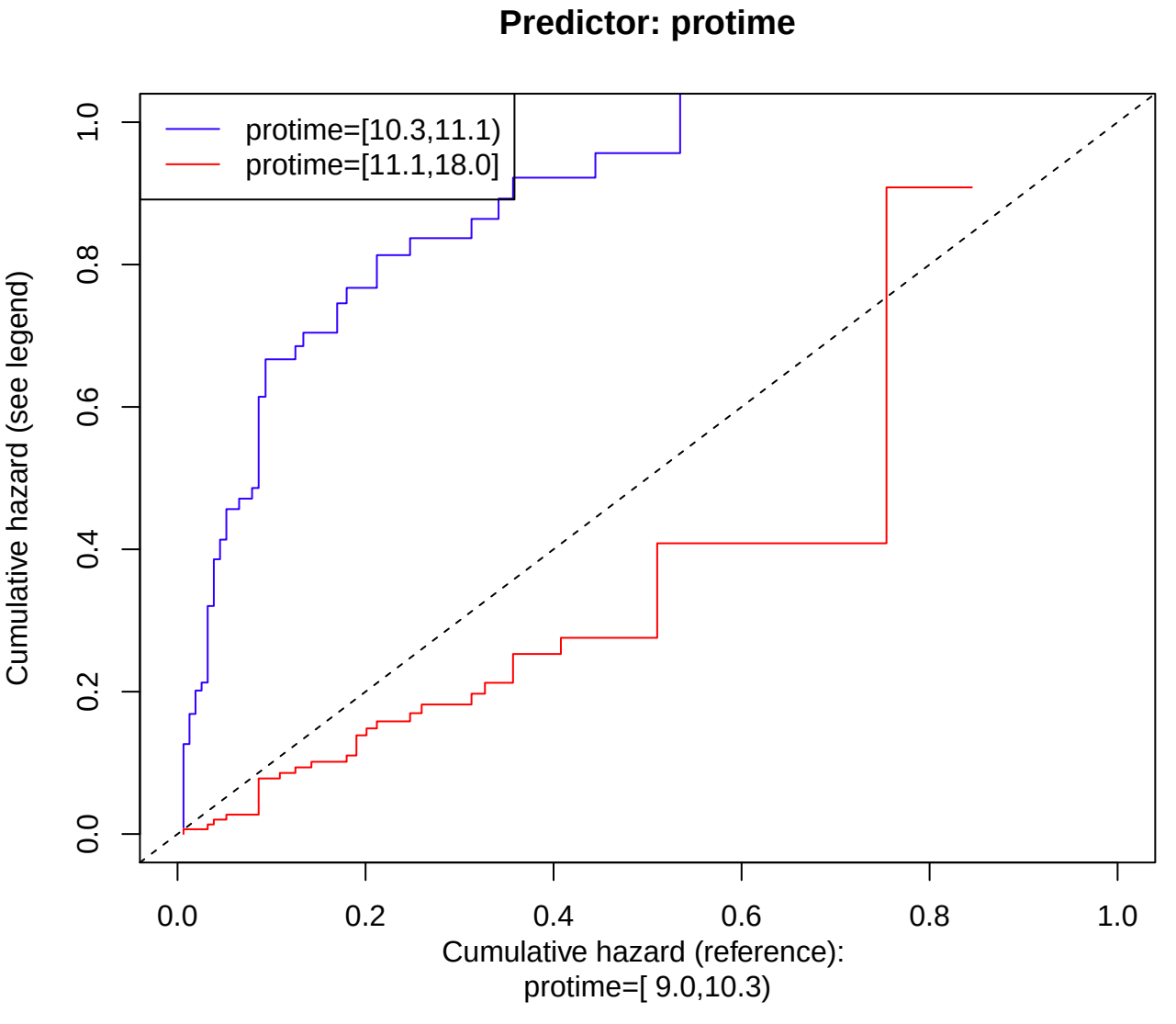
Cumulative hazard vs. reference group. Should be linear plot through origin.
If convex (towards top left) shows ratio of hazards is increasing over time.
Reference line (black) is at 45 degrees.



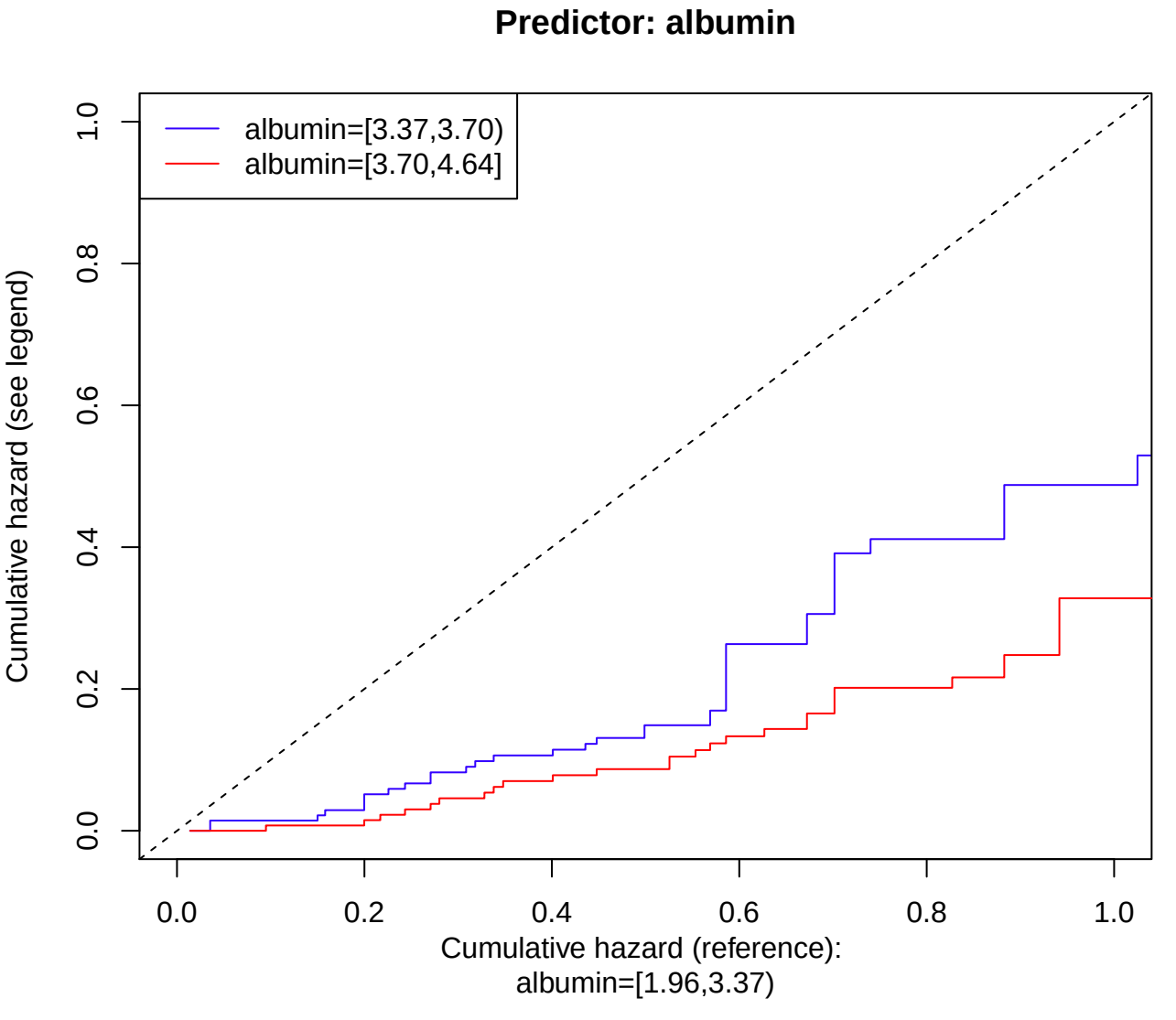
Cumulative hazard vs. reference group. Should be linear plot through origin.
If convex (towards top left) shows ratio of hazards is increasing over time.
Reference line (black) is at 45 degrees.

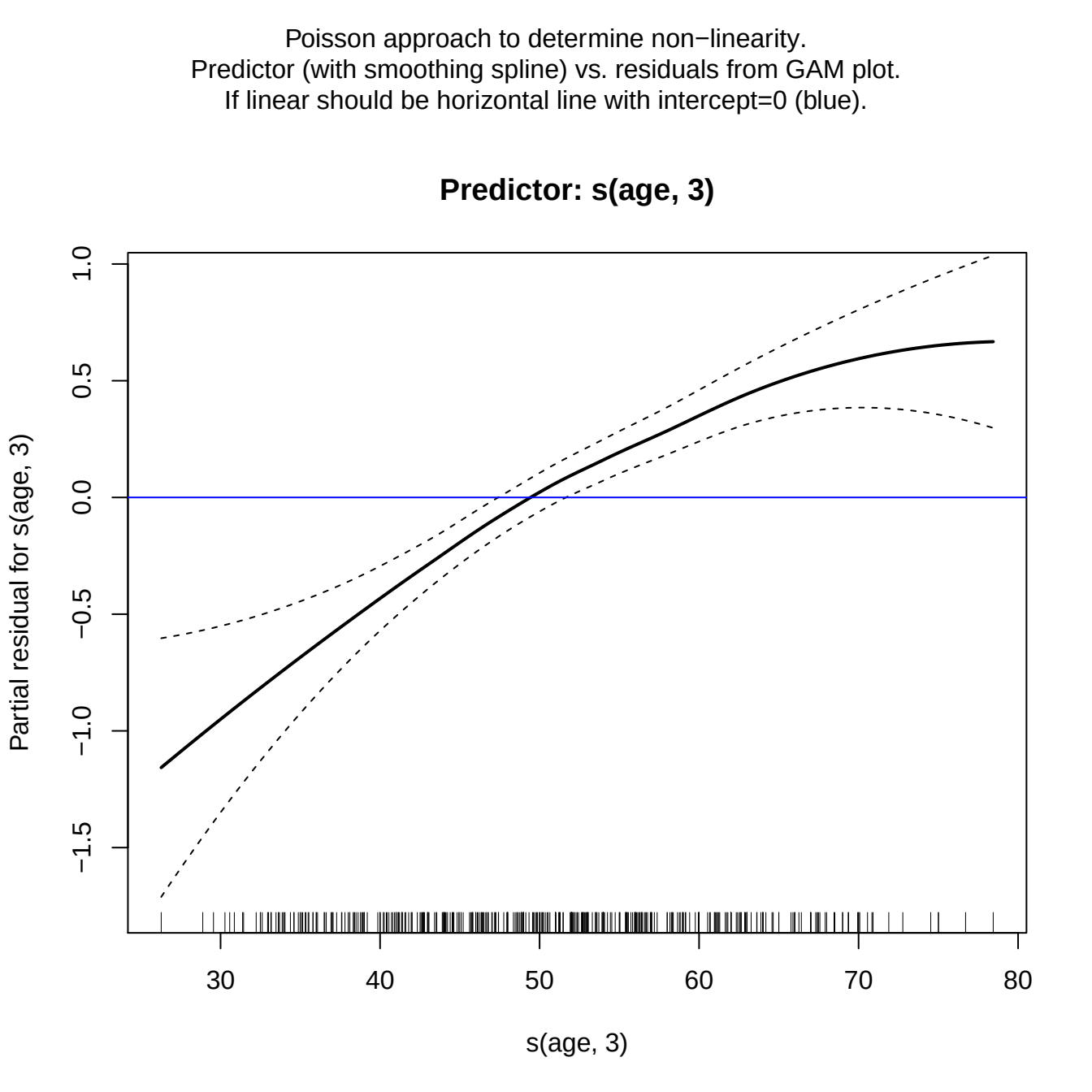


Cumulative hazard vs. reference group. Should be linear plot through origin.
If convex (towards top left) shows ratio of hazards is increasing over time.
Reference line (black) is at 45 degrees.

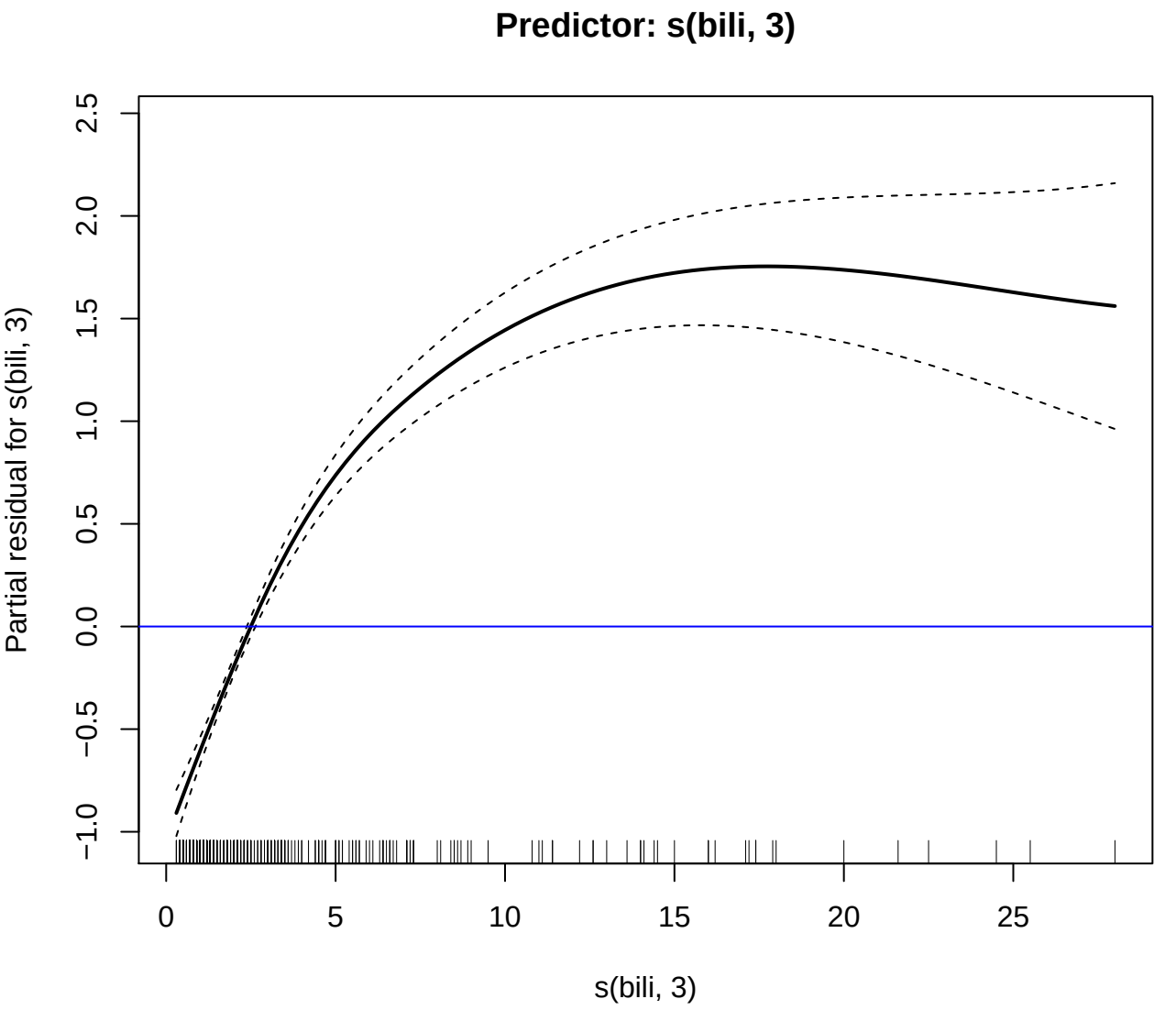


Cumulative hazard vs. reference group. Should be linear plot through origin.
If convex (towards top left) shows ratio of hazards is increasing over time.
Reference line (black) is at 45 degrees.

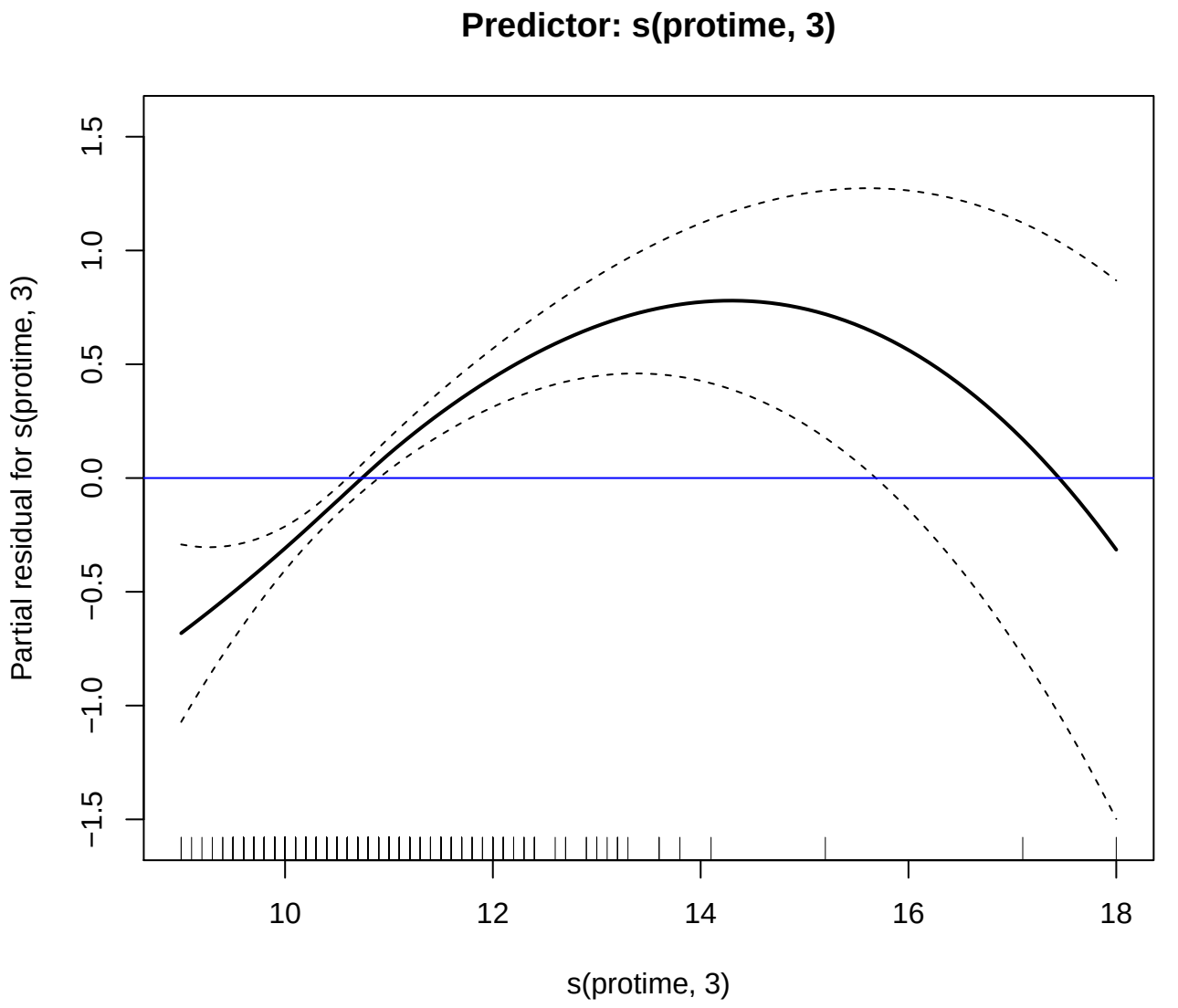



Poisson approach to determine non−linearity.
Predictor (with smoothing spline) vs. residuals from GAM plot.
If linear should be horizontal line with intercept=0 (blue).
Predictor: s(age, 3)
Partial residual for s(age, 3)
1.0
0.5
0.0
−0.5
−1.0
−1.5
30
40
50
60
70
80
s(age, 3)

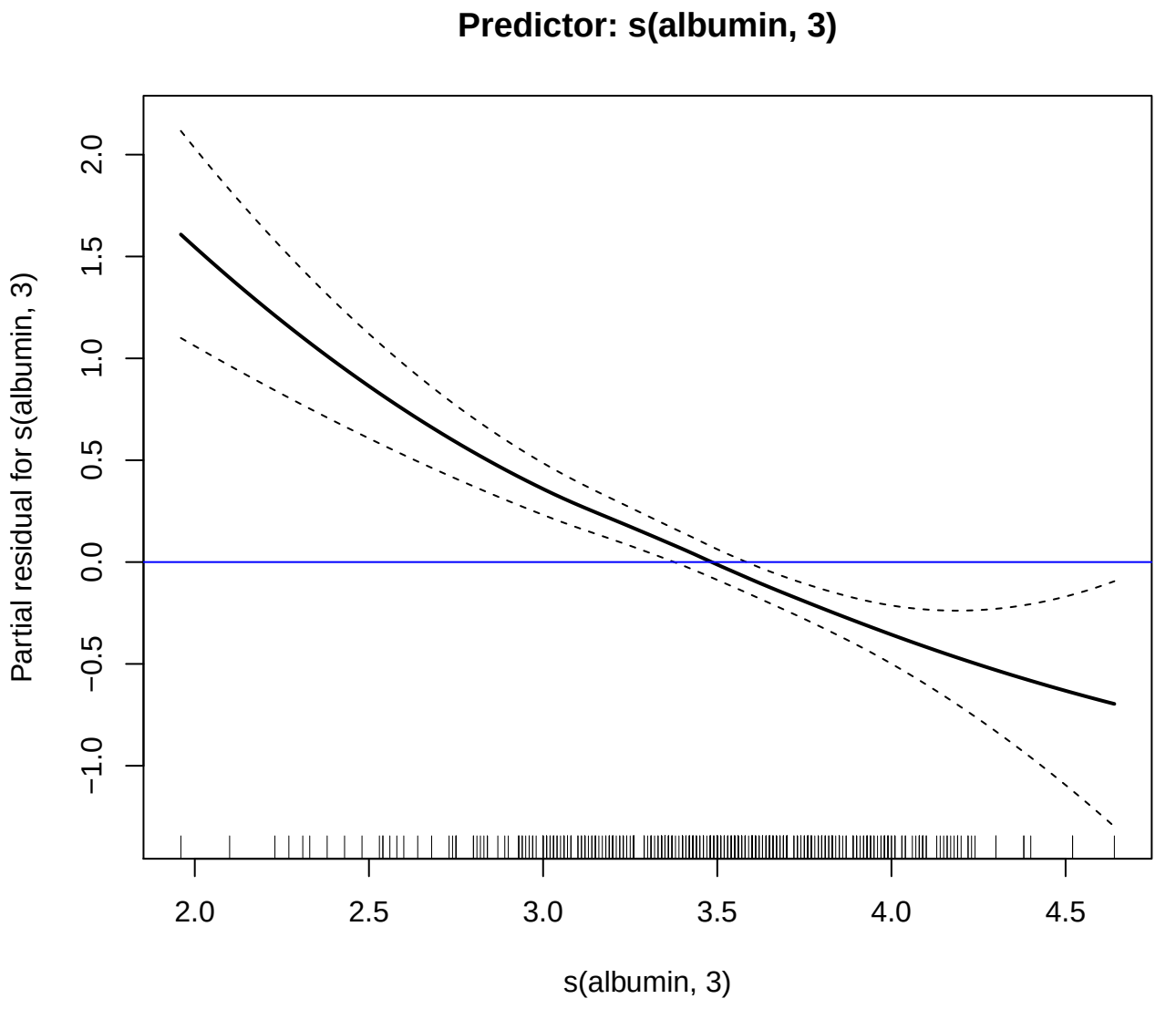
Poisson approach to determine non−linearity.
Predictor (with smoothing spline) vs. residuals from GAM plot.
If linear should be horizontal line with intercept=0 (blue).



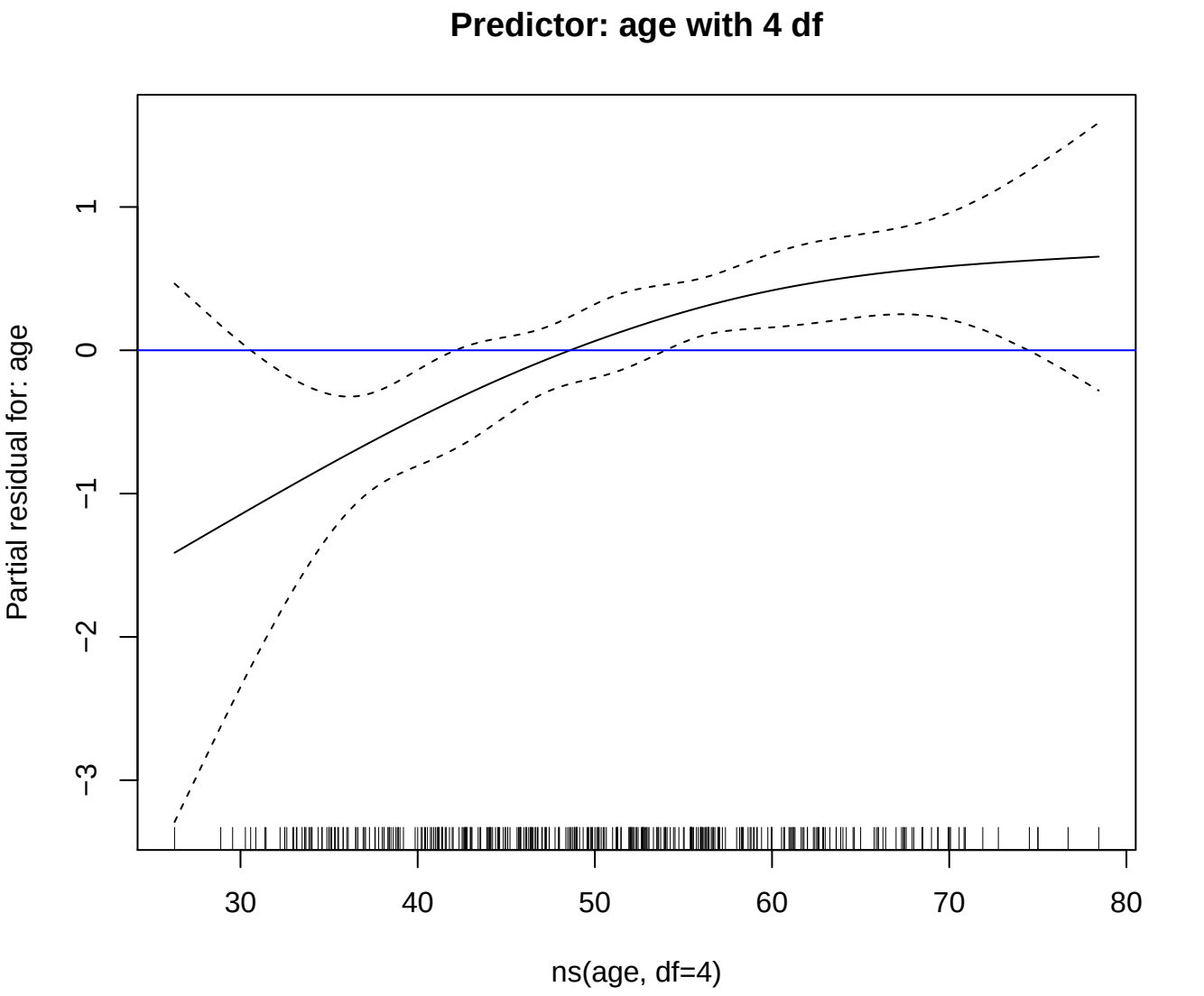
Poisson approach to determine non−linearity.
Predictor (with smoothing spline) vs. residuals from GAM plot.
If linear should be horizontal line with intercept=0 (blue).



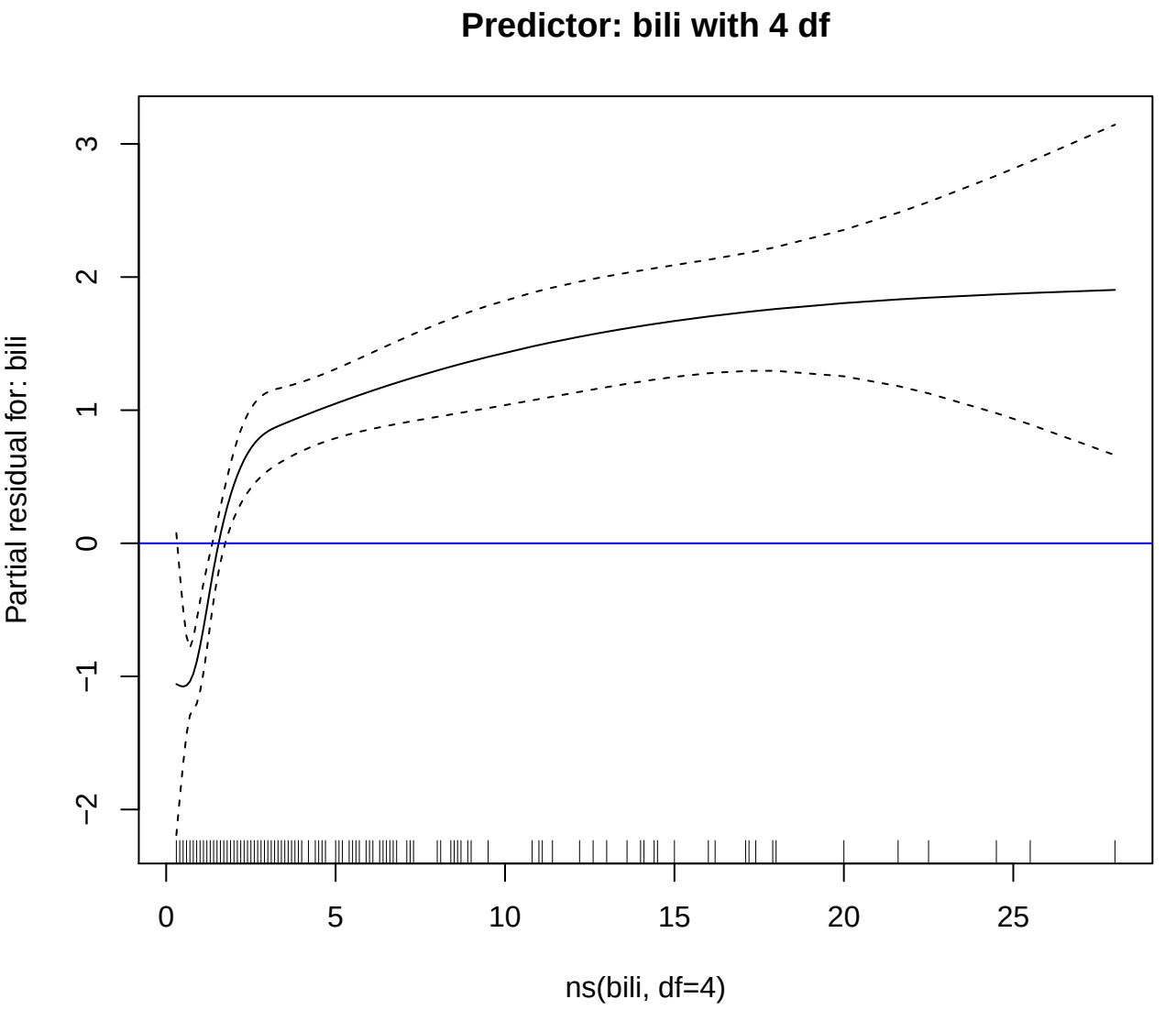
Poisson approach to determine non−linearity.
Predictor (with smoothing spline) vs. residuals from GAM plot.
If linear should be horizontal line with intercept=0 (blue).

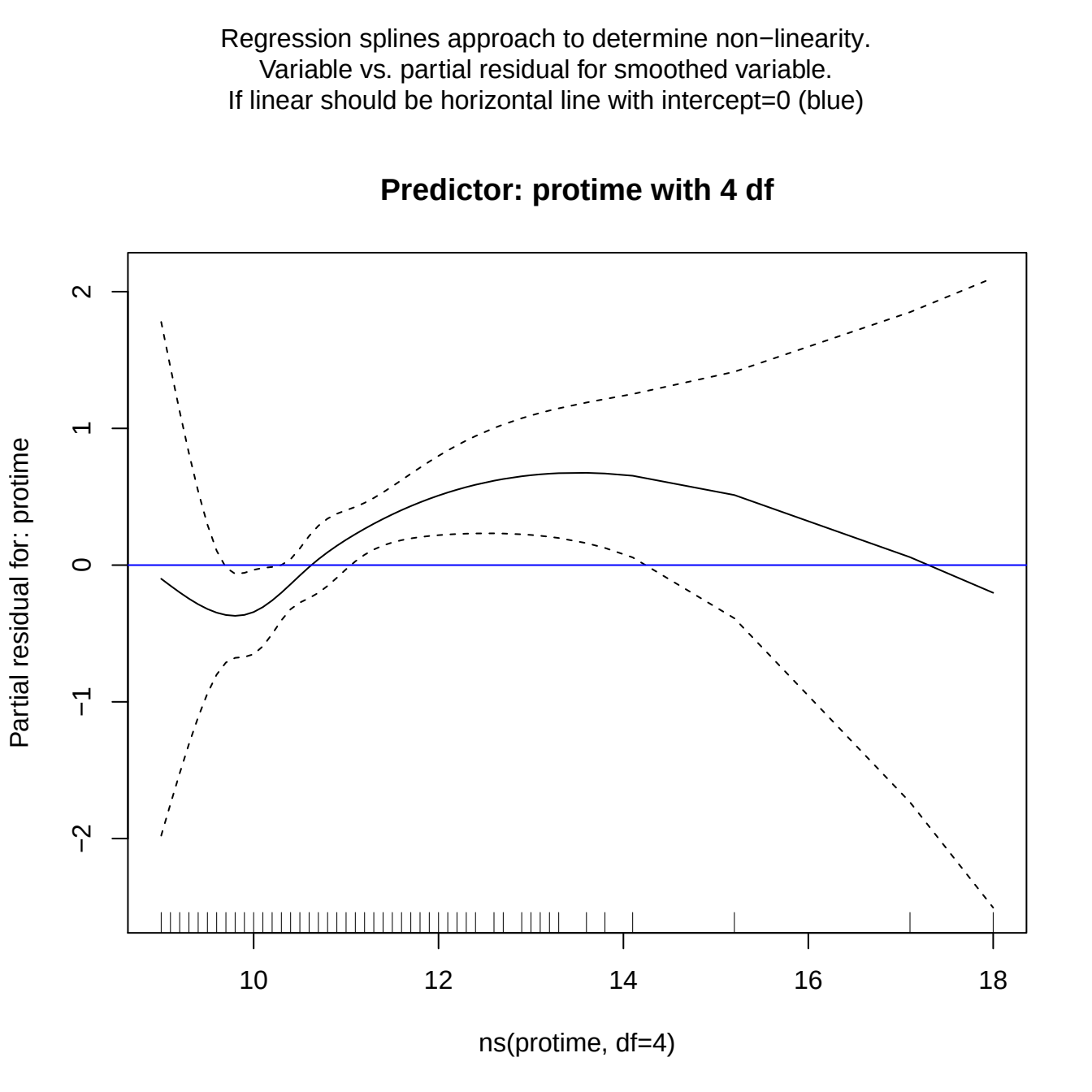


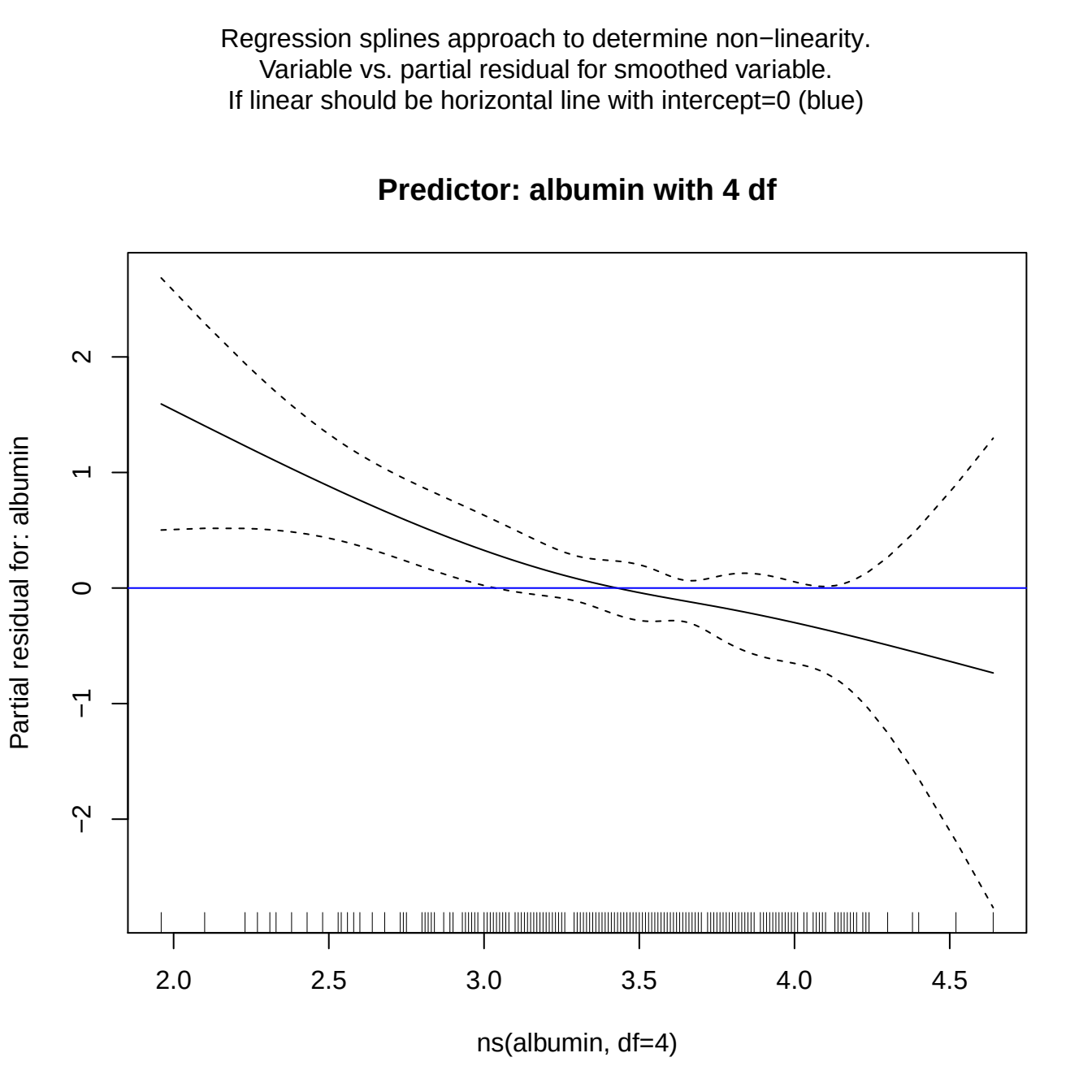
Regression splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)

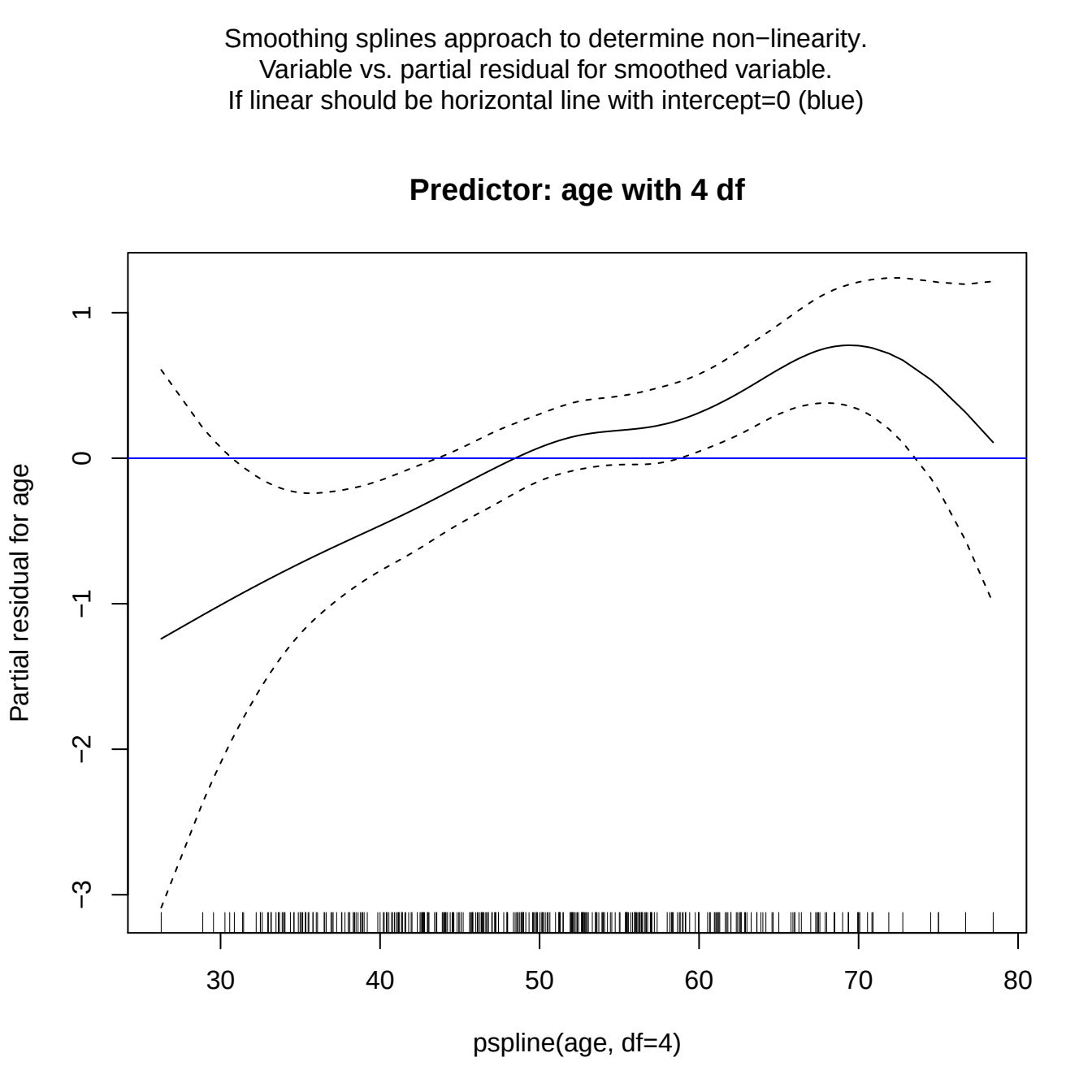


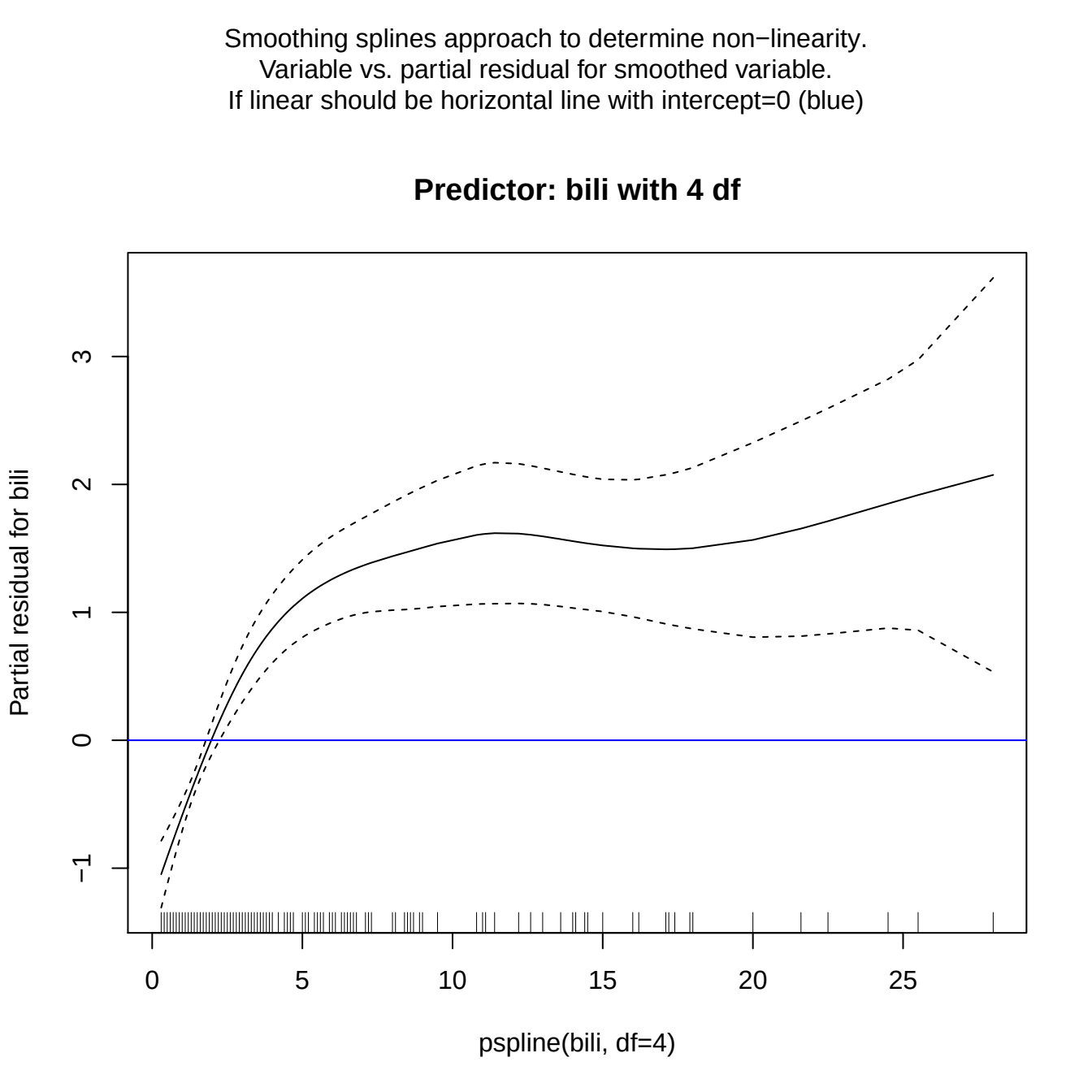
Regression splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)

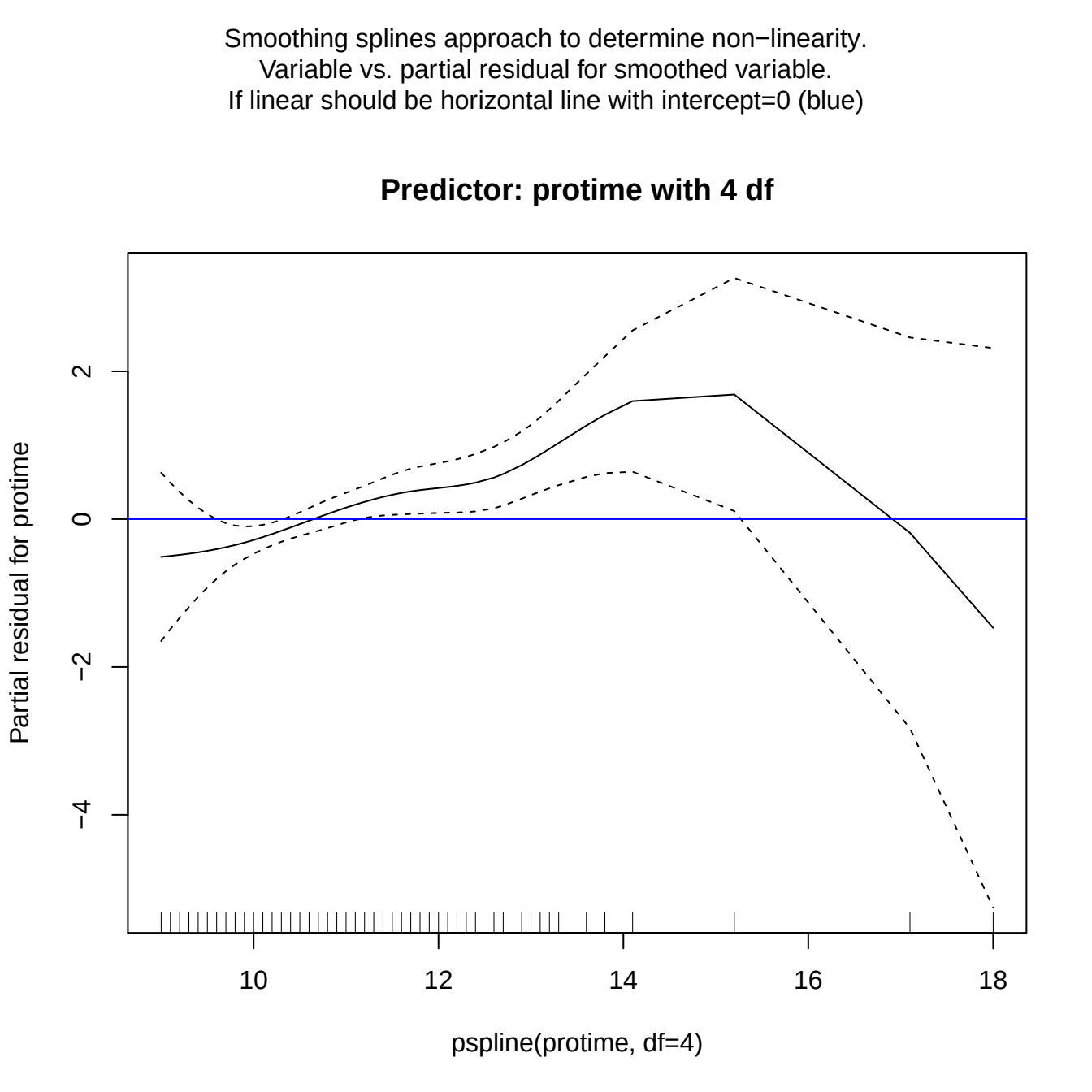



Regression splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)
Predictor: protime with 4 df
Partial residual for: protime
2
1
0
−1
−2
10
12
14
16
18
ns(protime, df=4)

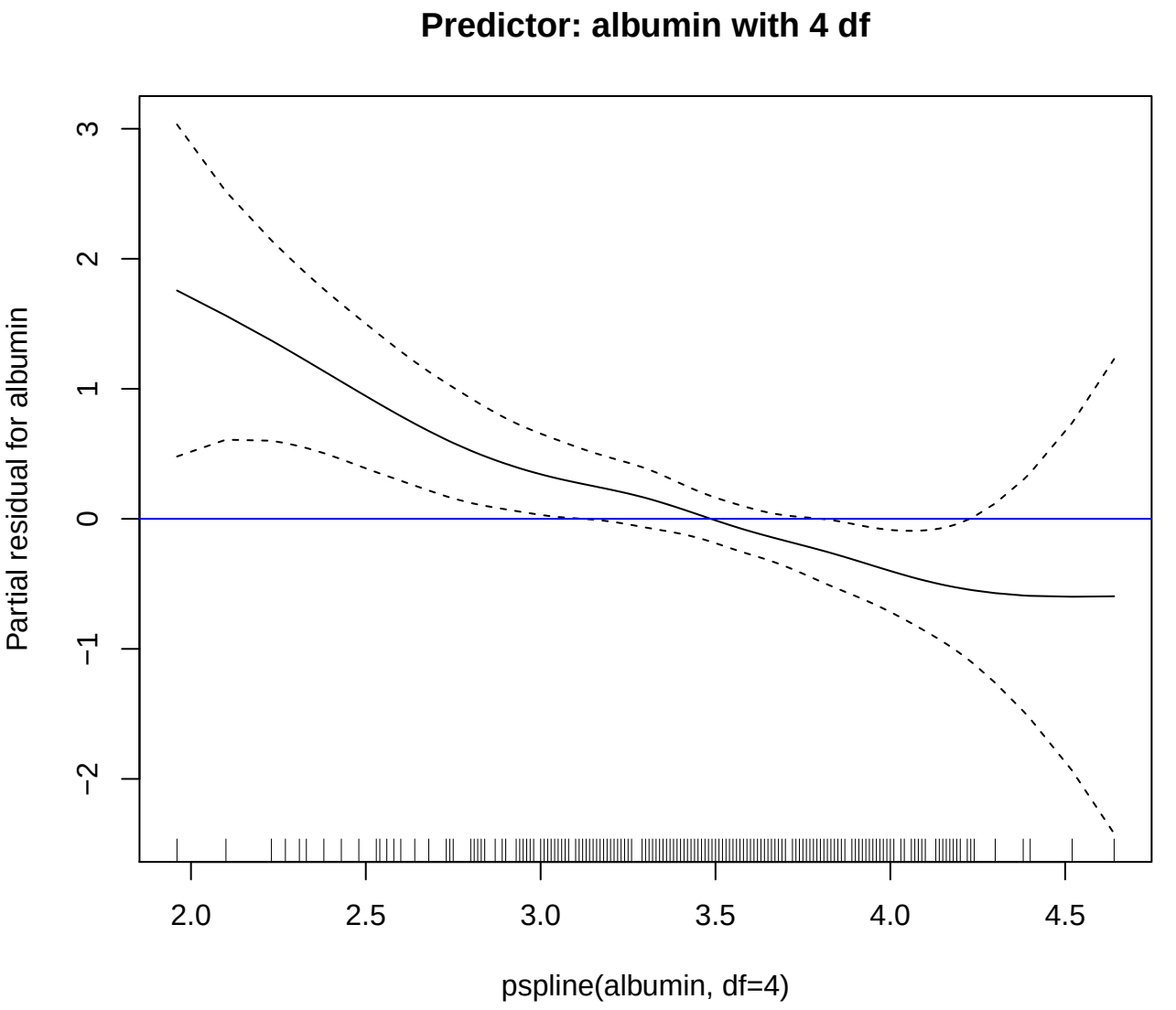

Regression splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)
Predictor: albumin with 4 df
Partial residual for: albumin
2
1
0
−1
−2
2.0
2.5
3.0
3.5
4.0
4.5
ns(albumin, df=4)


Smoothing splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)
Predictor: age with 4 df
Partial residual for age
1
0
−1
−2
−3
30
40
50
60
70
80
pspline(age, df=4)

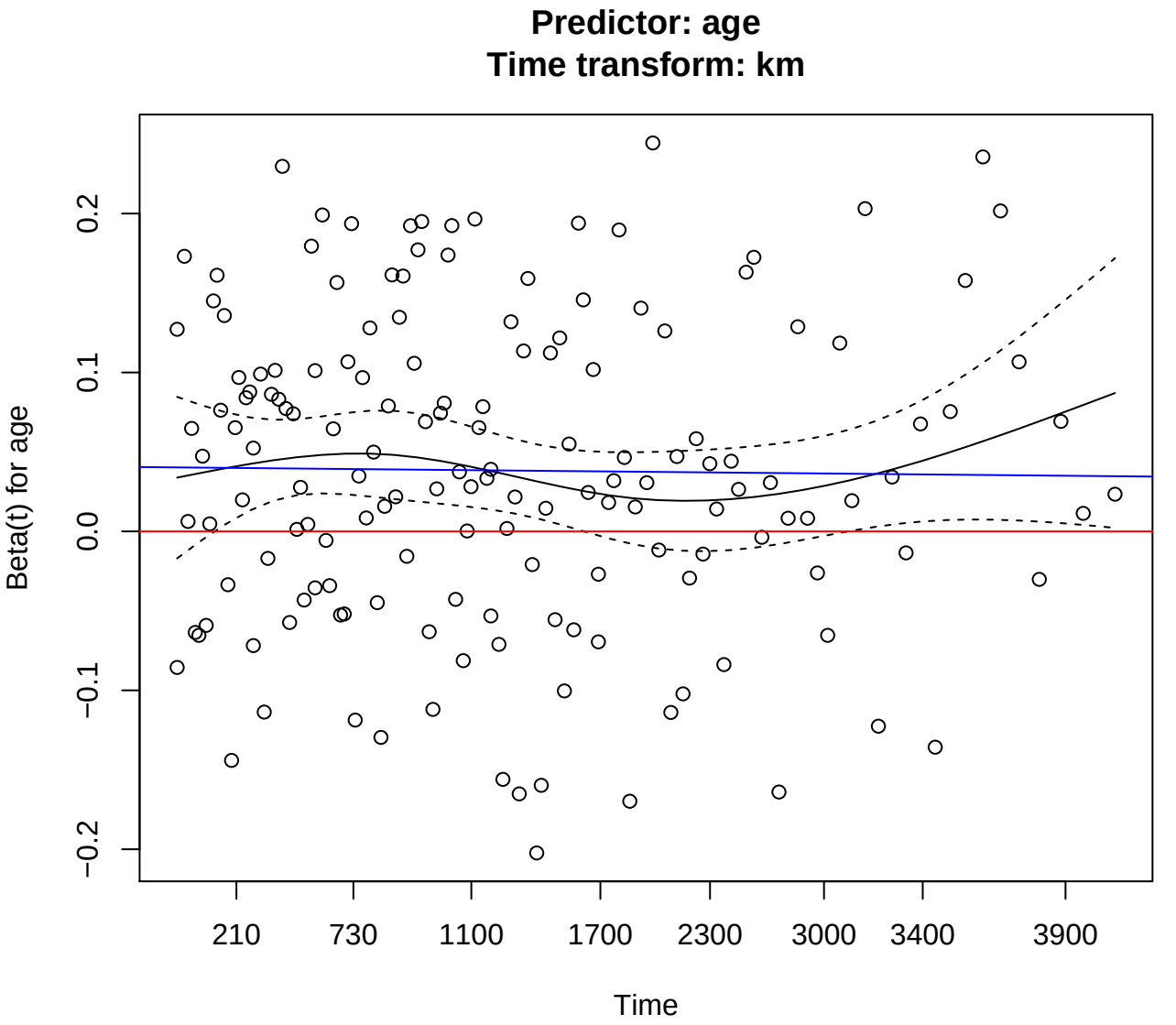

Smoothing splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)
Predictor: bili with 4 df
Partial residual for bili
−1
0
1
2
3
0
5
10
15
20
25
pspline(bili, df=4)

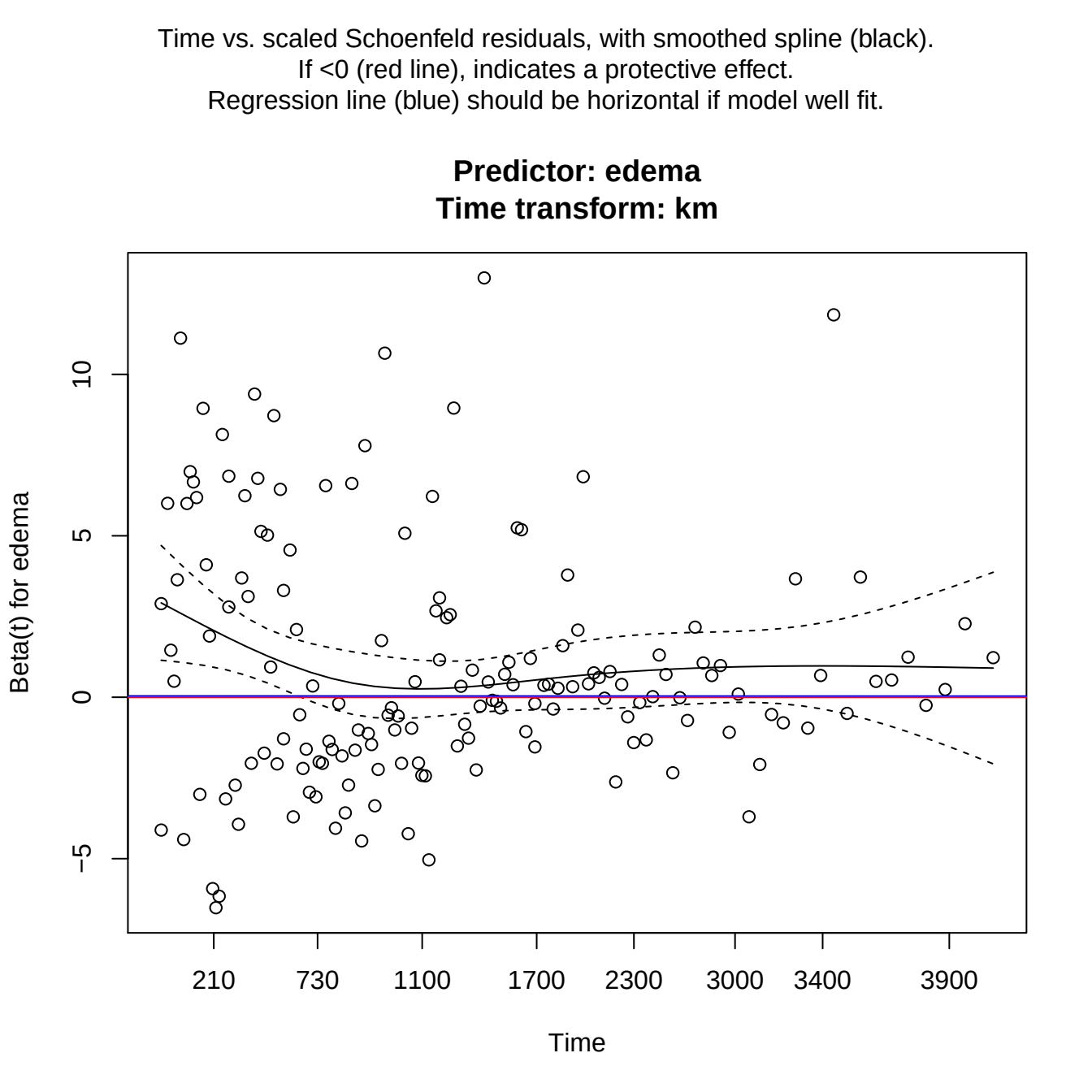

Smoothing splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)
Predictor: protime with 4 df
Partial residual for protime
2
0
−2
−4
10
12
14
16
18
pspline(protime, df=4)

Smoothing splines approach to determine non−linearity.
Variable vs. partial residual for smoothed variable.
If linear should be horizontal line with intercept=0 (blue)

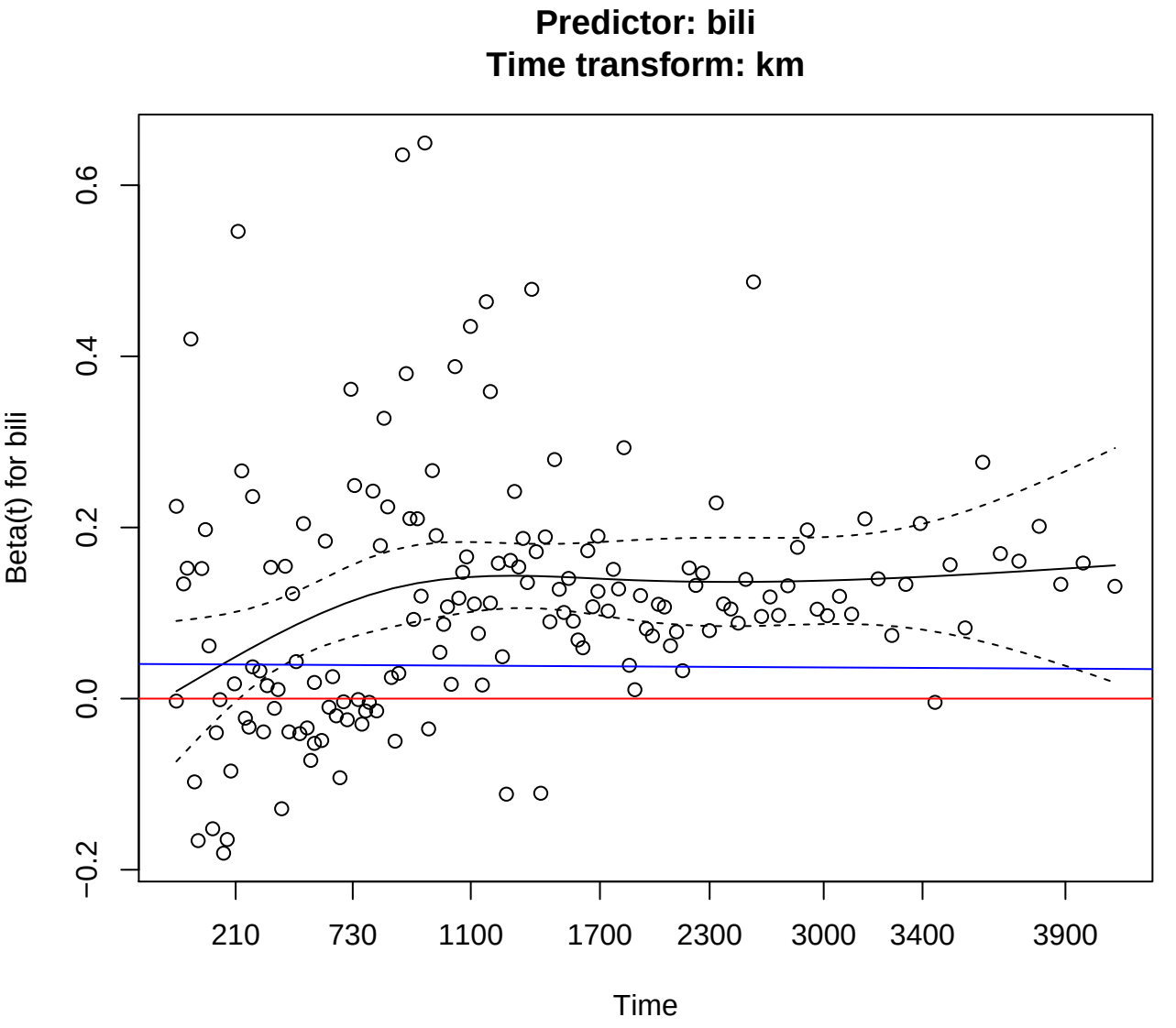


Time vs. scaled Schoenfeld residuals, with smoothed spline (black).
If <0 (red line), indicates a protective effect.
Regression line (blue) should be horizontal if model well fit.

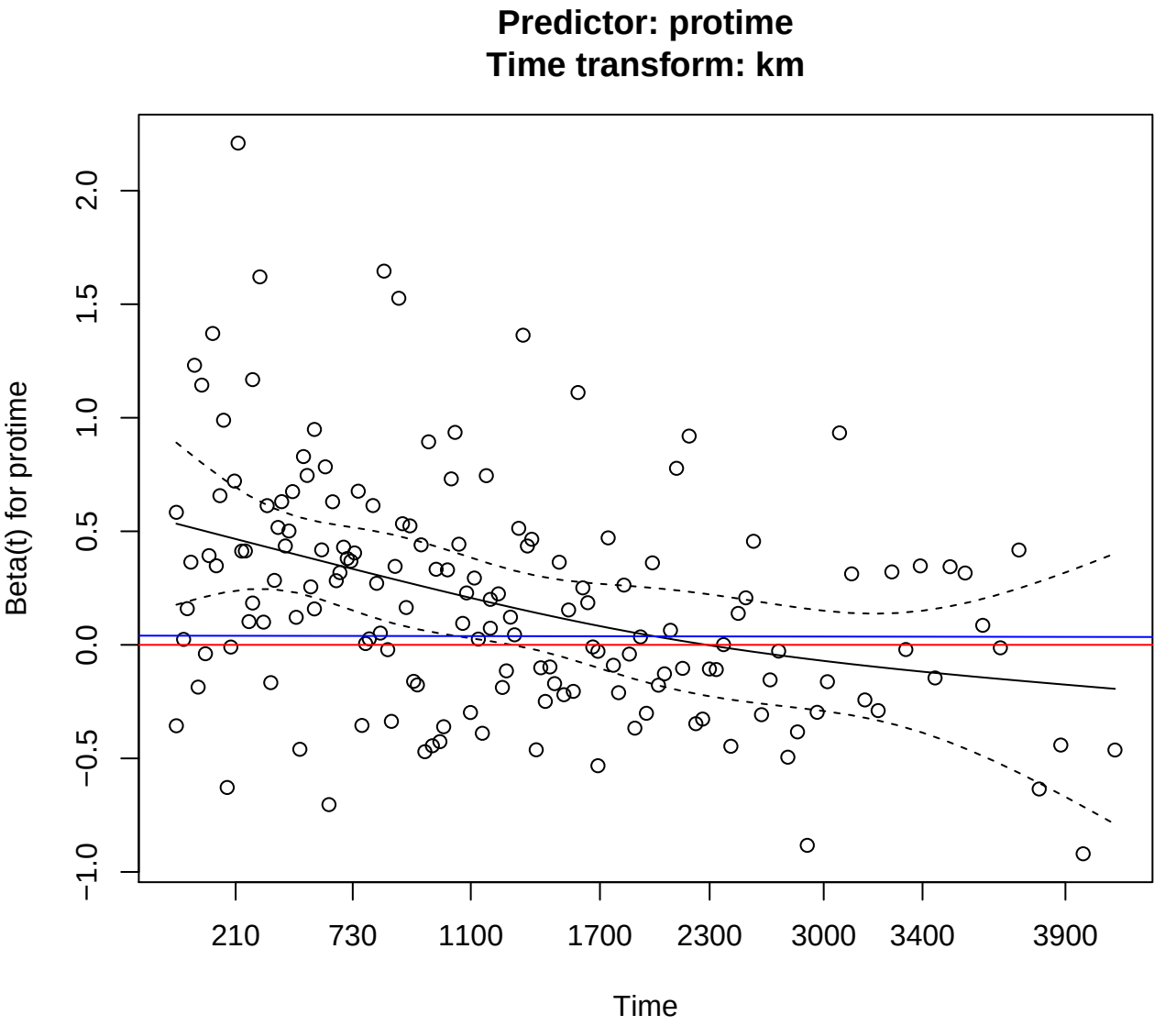


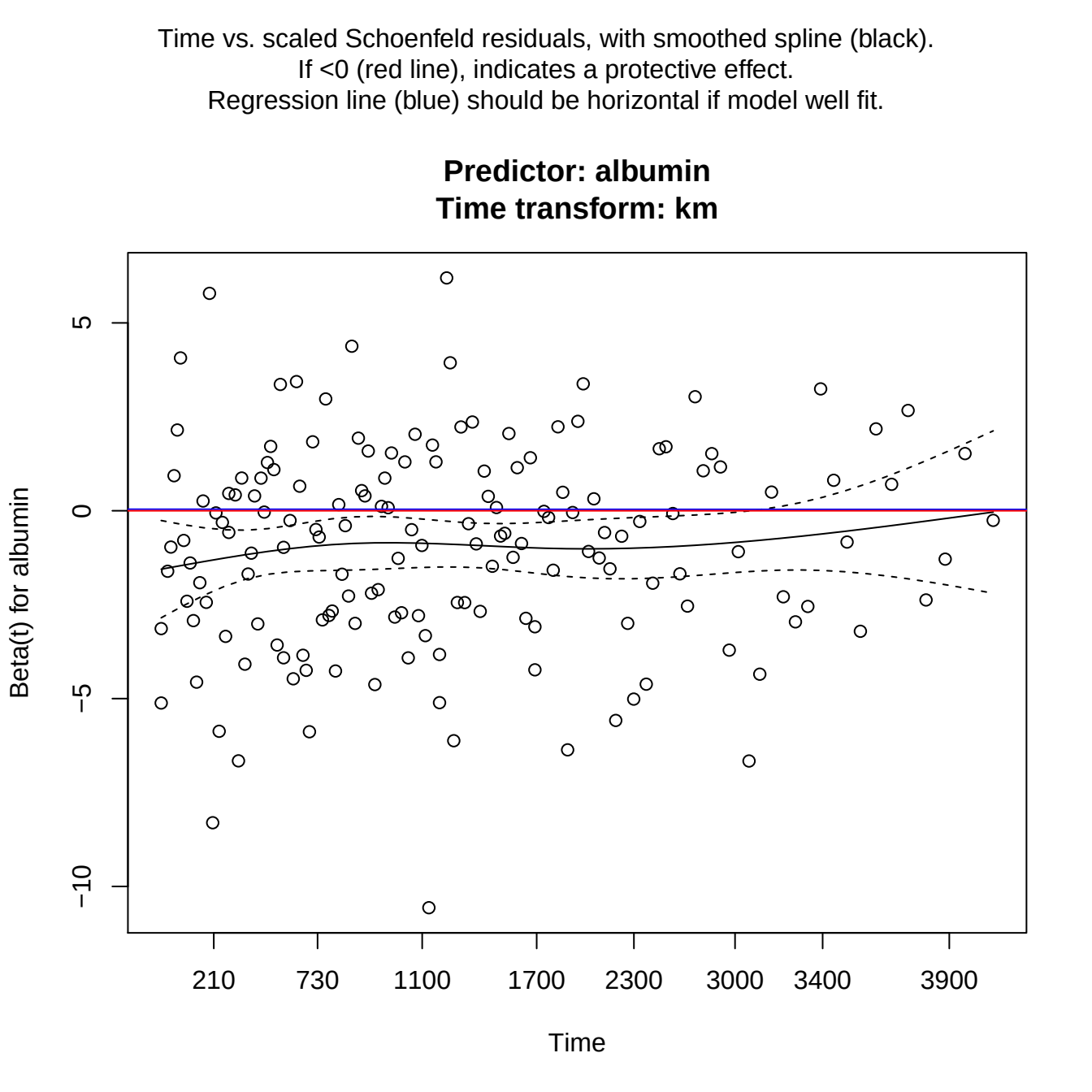

Time vs. scaled Schoenfeld residuals, with smoothed spline (black).
If <0 (red line), indicates a protective effect.
Regression line (blue) should be horizontal if model well fit.
Predictor: edema
Time transform: km
Beta(t) for edema
10
5
0
−5
210
730
1100
1700
2300
3000
3400
3900
Time

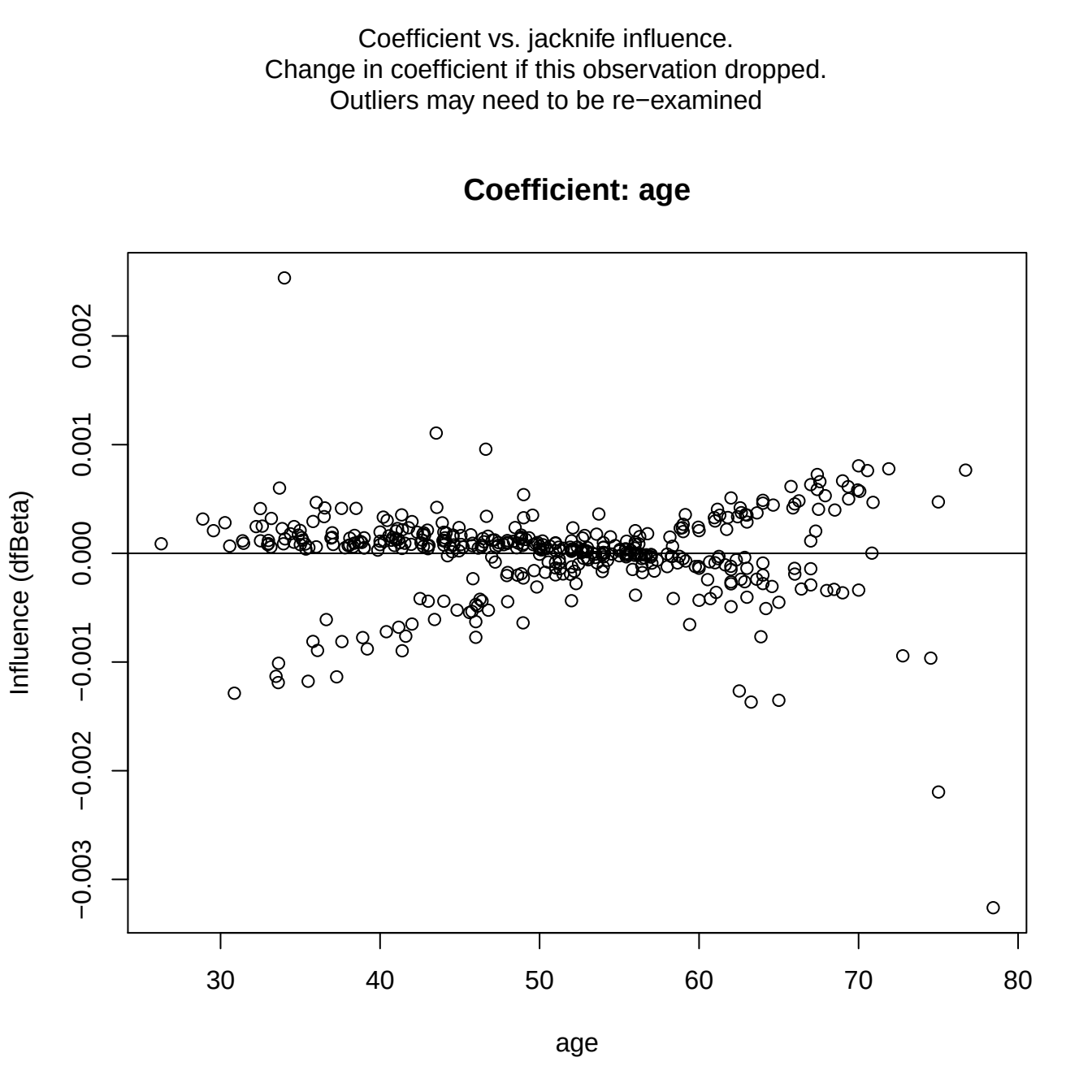
Time vs. scaled Schoenfeld residuals, with smoothed spline (black).
If <0 (red line), indicates a protective effect.
Regression line (blue) should be horizontal if model well fit.

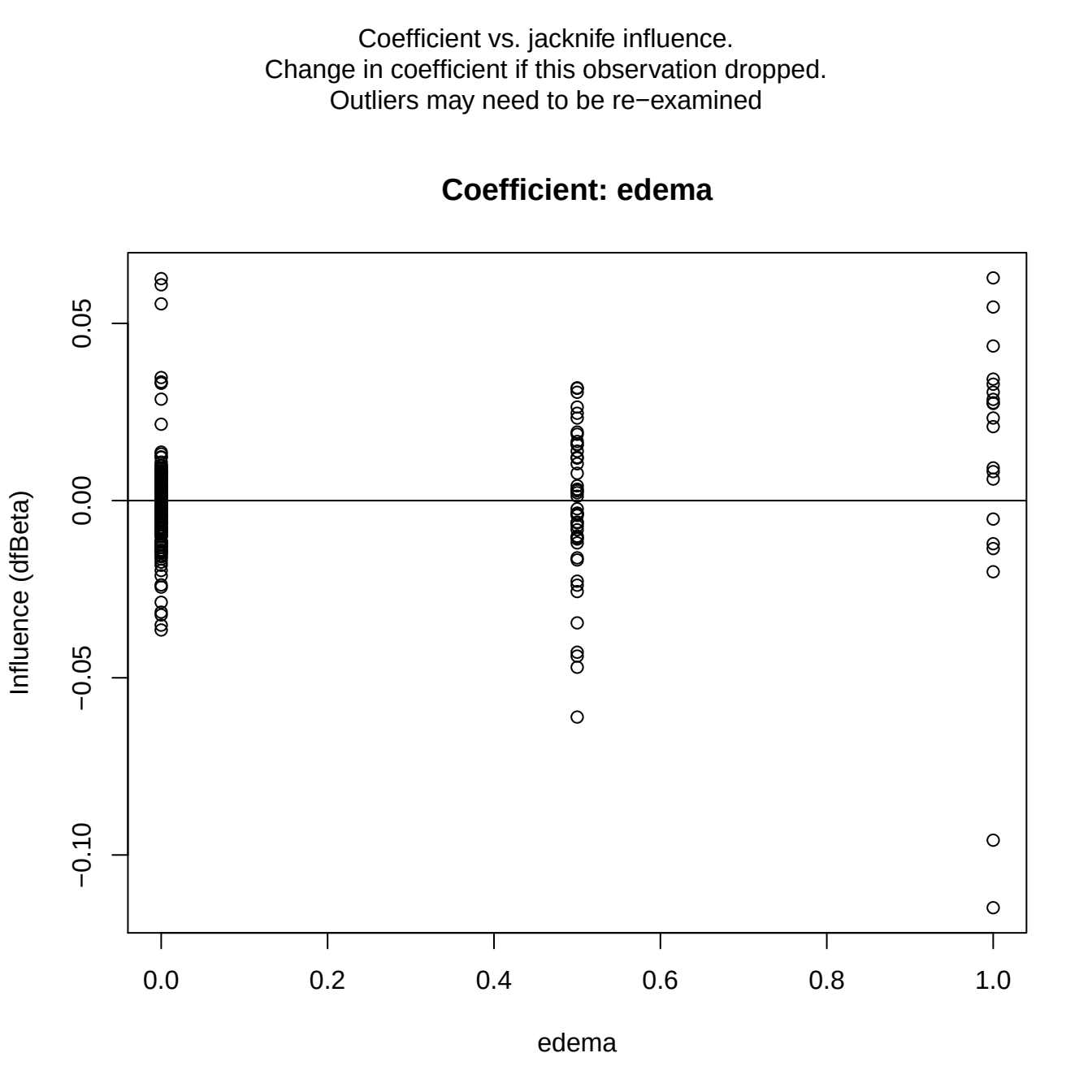


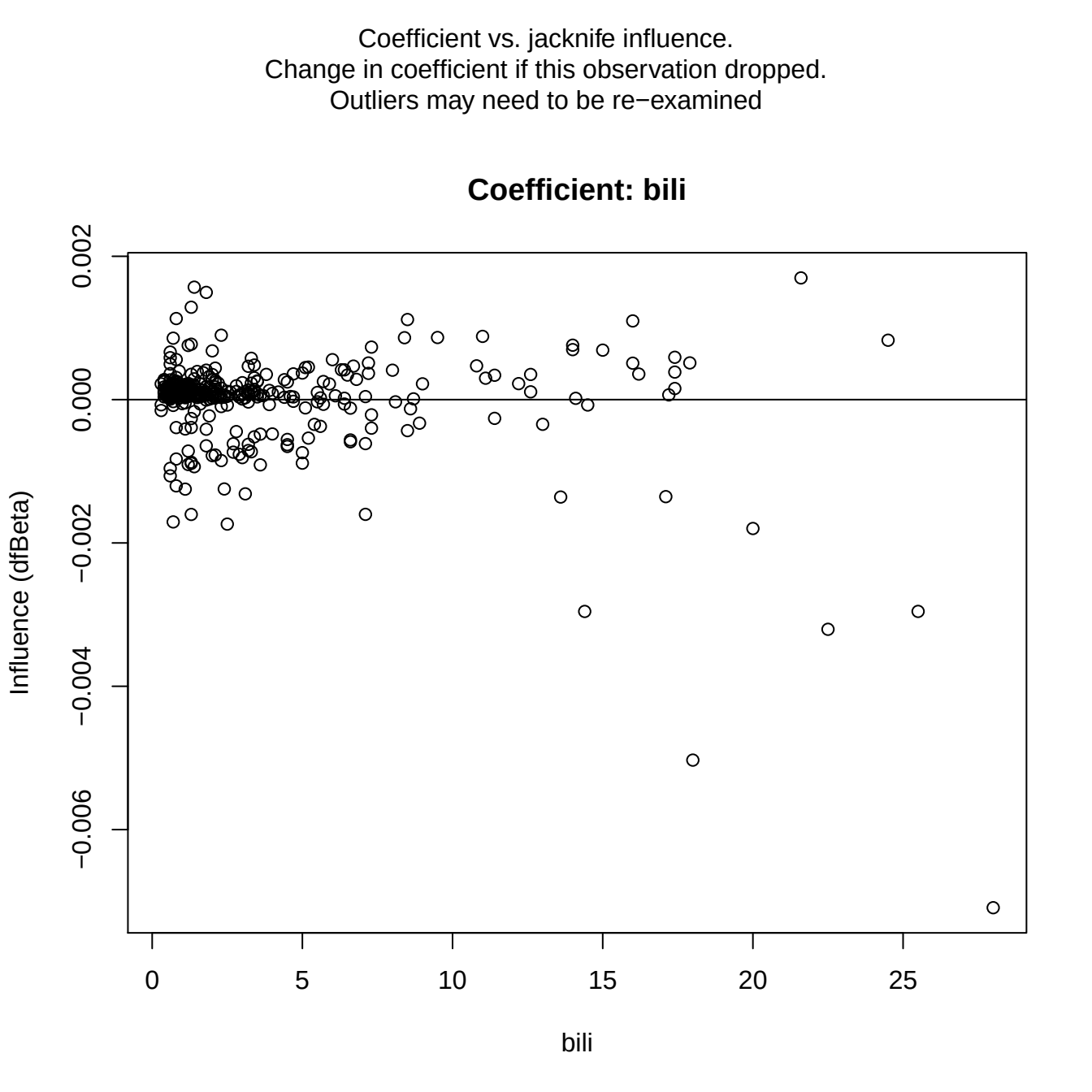
Time vs. scaled Schoenfeld residuals, with smoothed spline (black).
If <0 (red line), indicates a protective effect.
Regression line (blue) should be horizontal if model well fit.

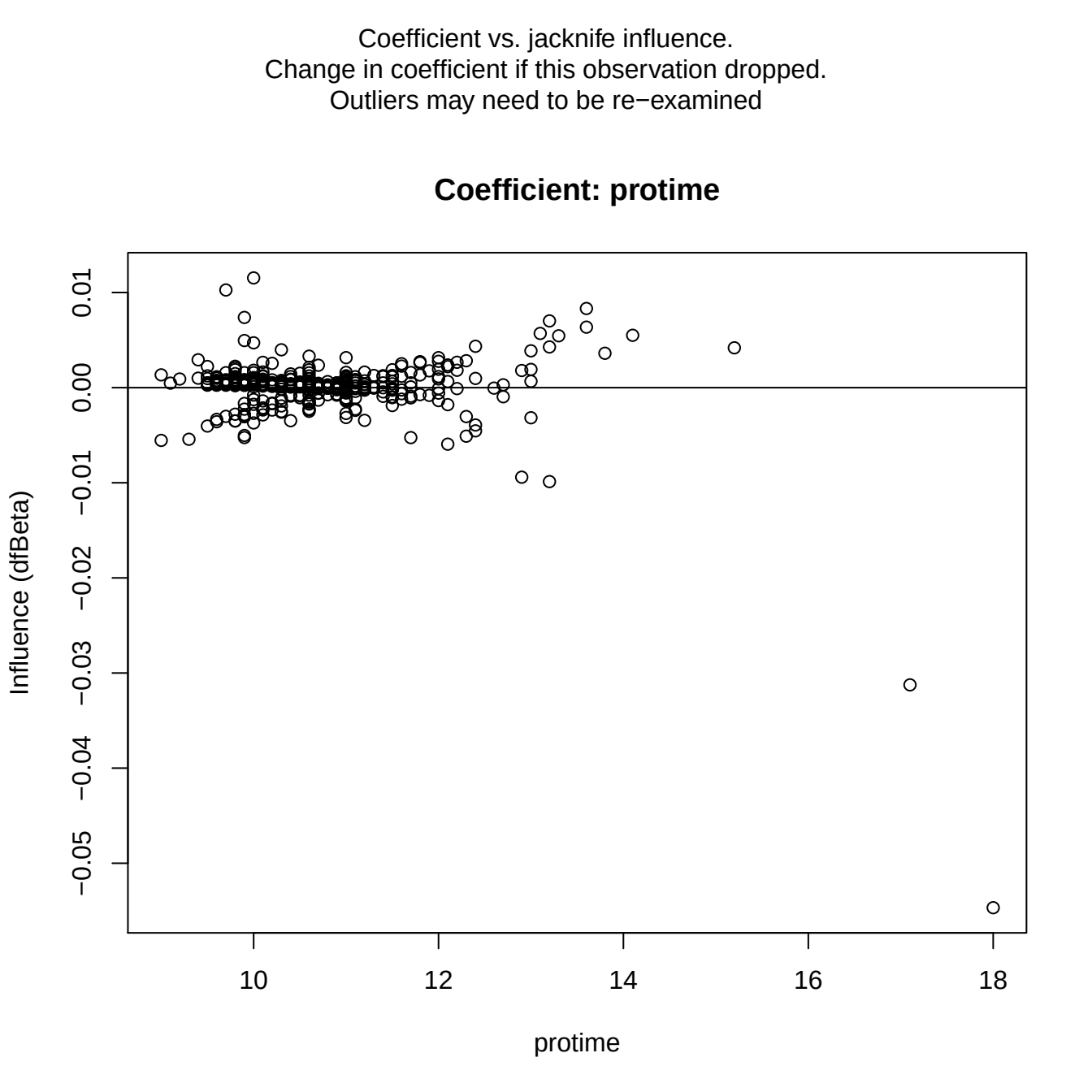


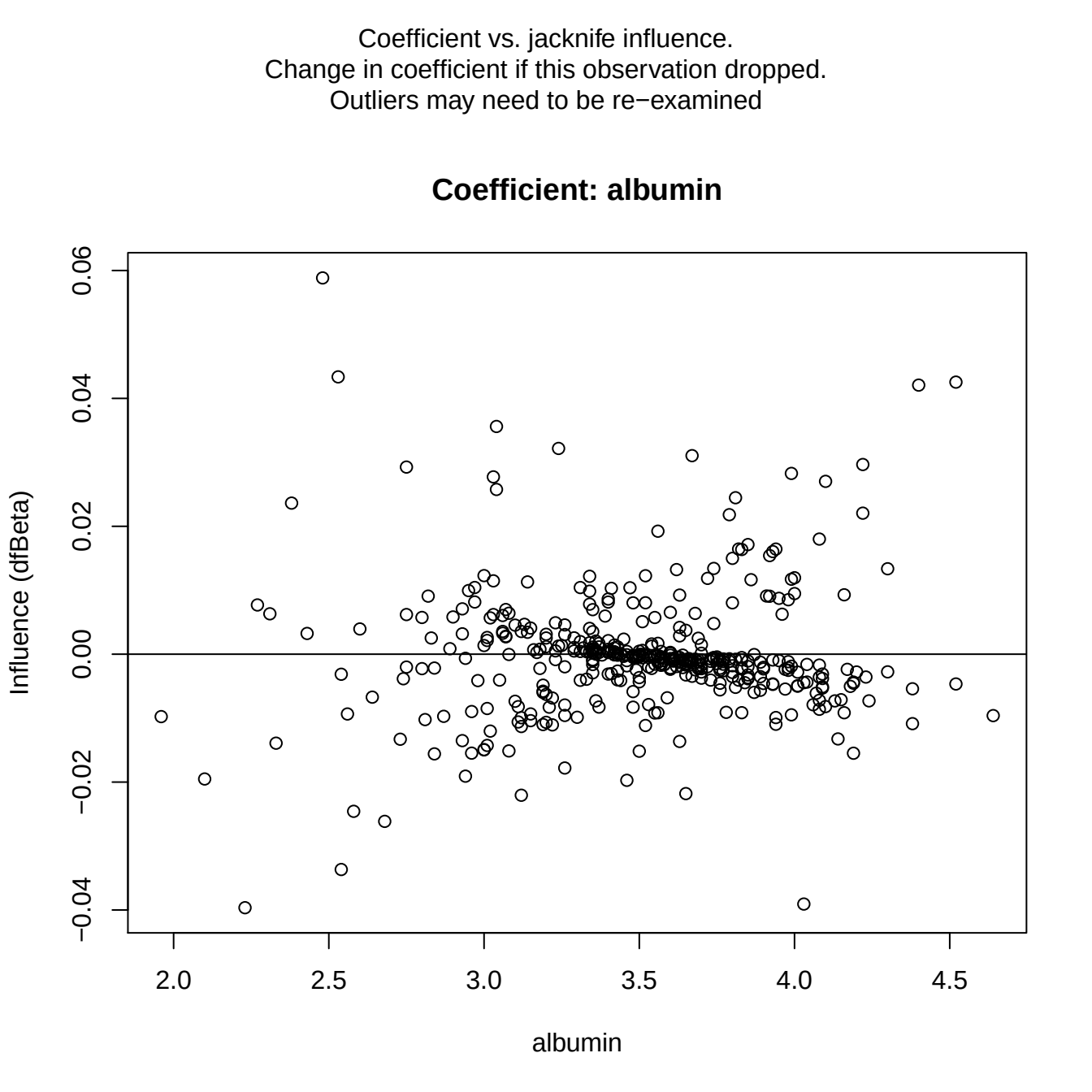

Time vs. scaled Schoenfeld residuals, with smoothed spline (black).
If <0 (red line), indicates a protective effect.
Regression line (blue) should be horizontal if model well fit.
Predictor: albumin
Time transform: km
Beta(t) for albumin
5
0
−5
−10
210
730
1100
1700
2300
3000
3400
3900
Time

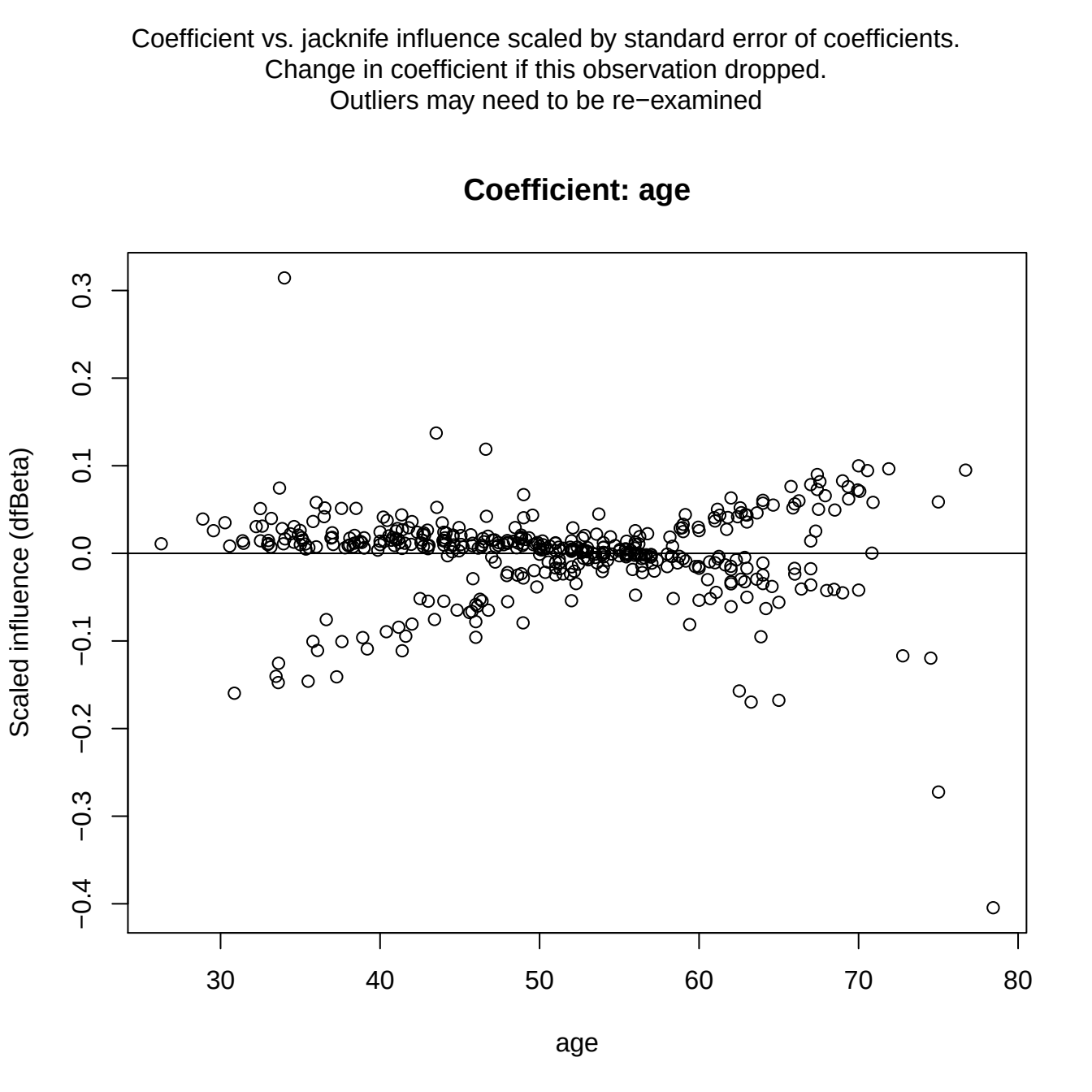

Coefficient vs. jacknife influence.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: age
Influence (dfBeta)
0.002
0.001
0.000
−0.001
−0.002
−0.003
30
40
50
60
70
80
age

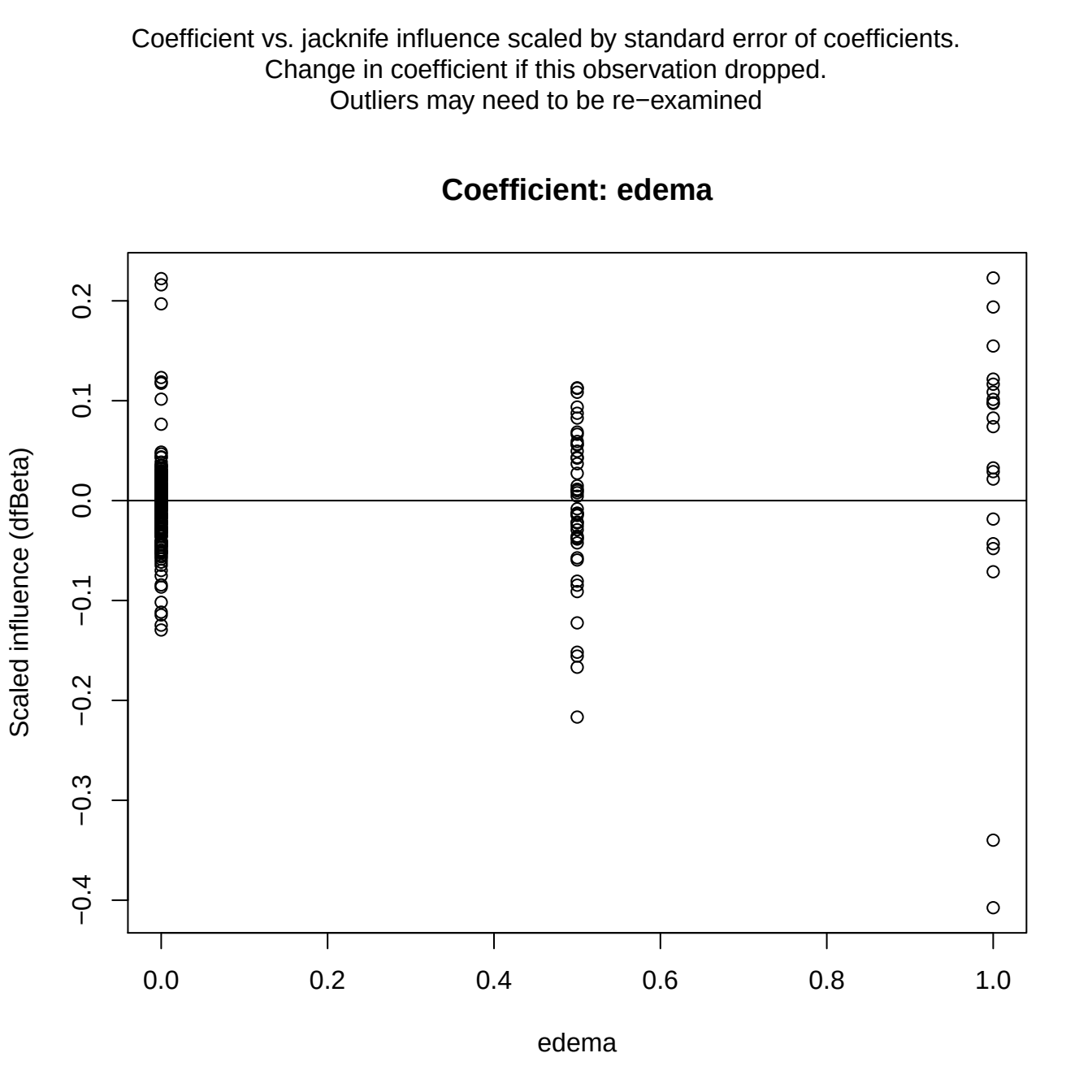

Coefficient vs. jacknife influence.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: edema
Influence (dfBeta)
0.05
0.00
−0.05
−0.10
0.0
0.2
0.4
0.6
0.8
1.0
edema

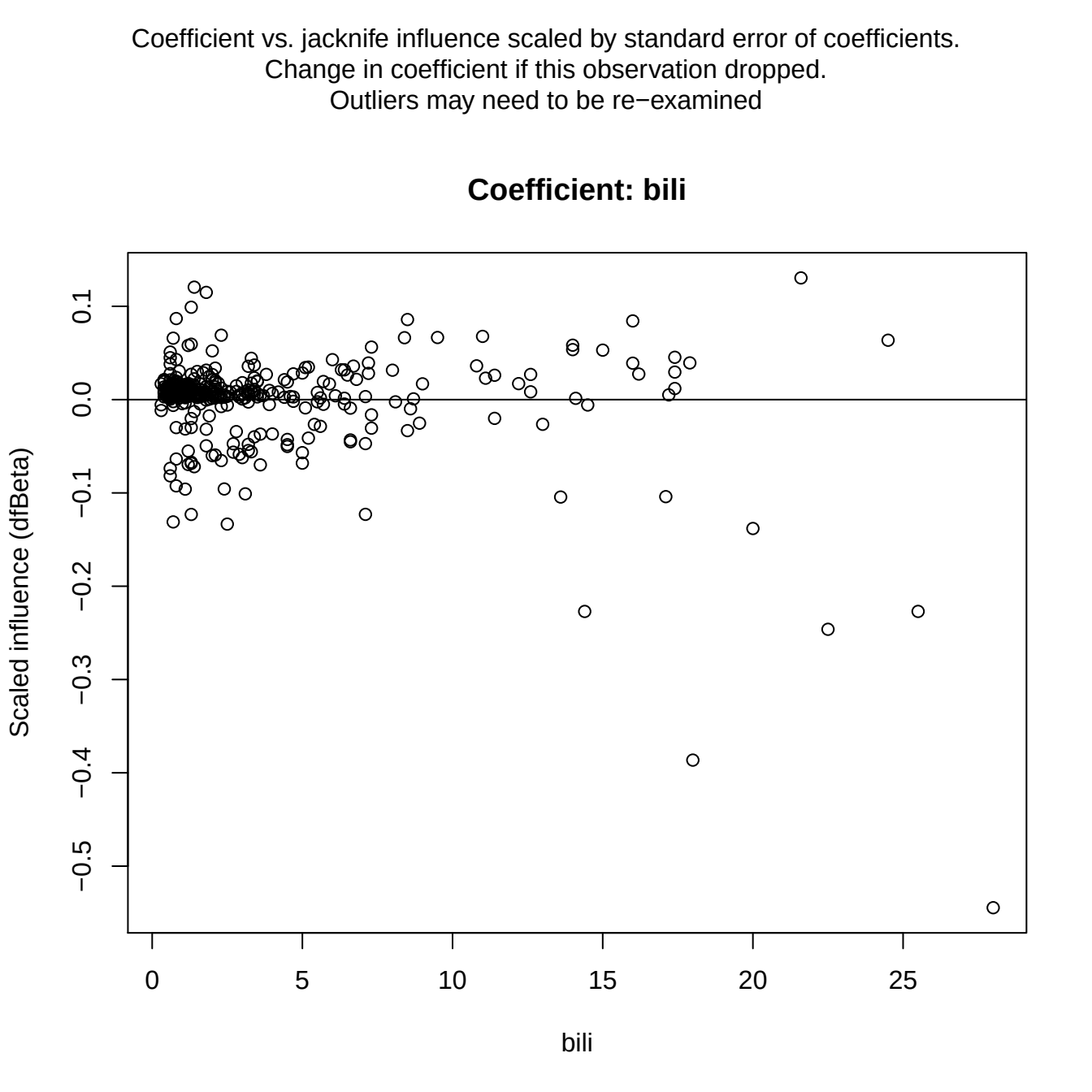

Coefficient vs. jacknife influence.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: bili
Influence (dfBeta)
0.002
0.000
−0.002
−0.004
−0.006
0
5
10
15
20
25
bili

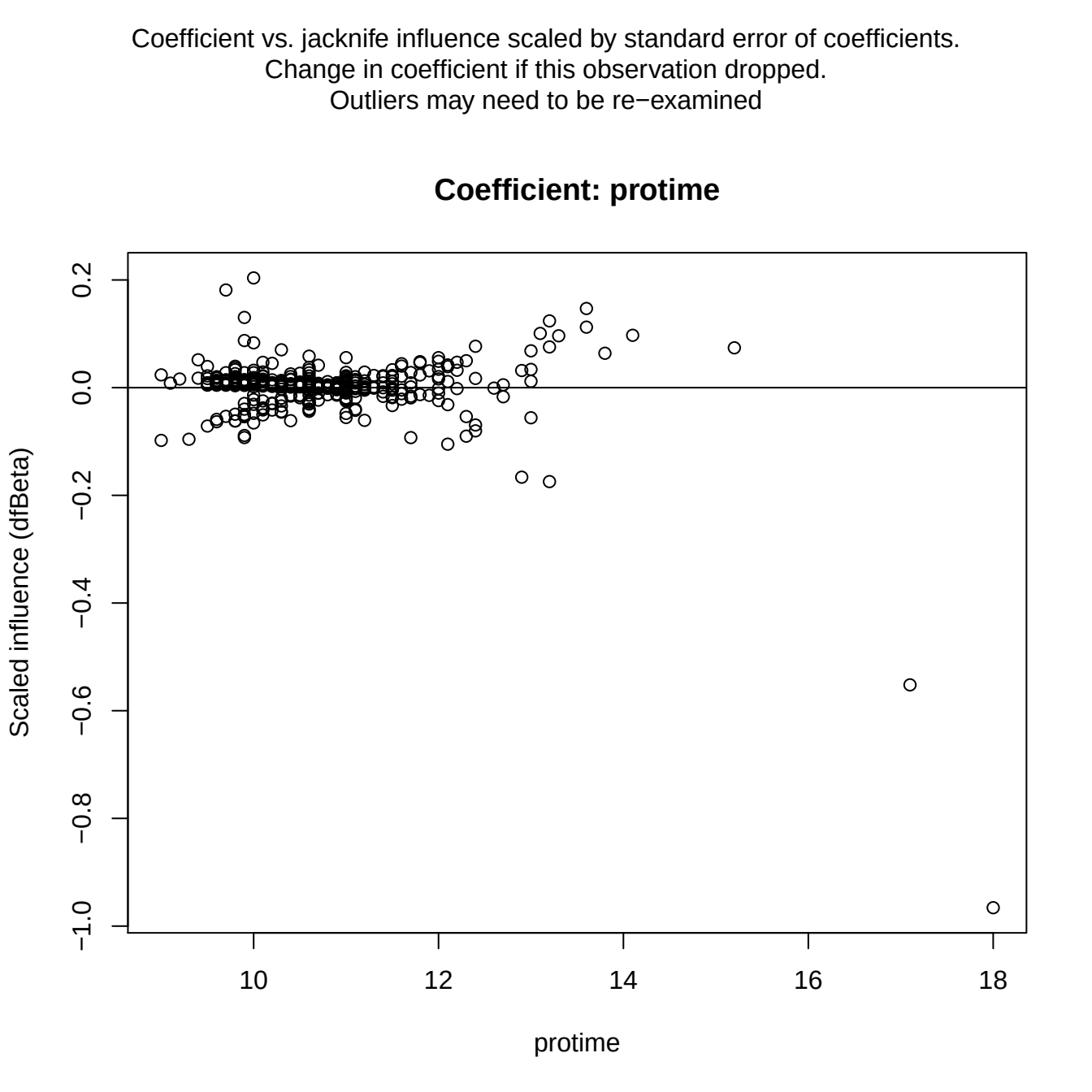

Coefficient vs. jacknife influence.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: protime
Influence (dfBeta)
0.01
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
10
12
14
16
18
protime

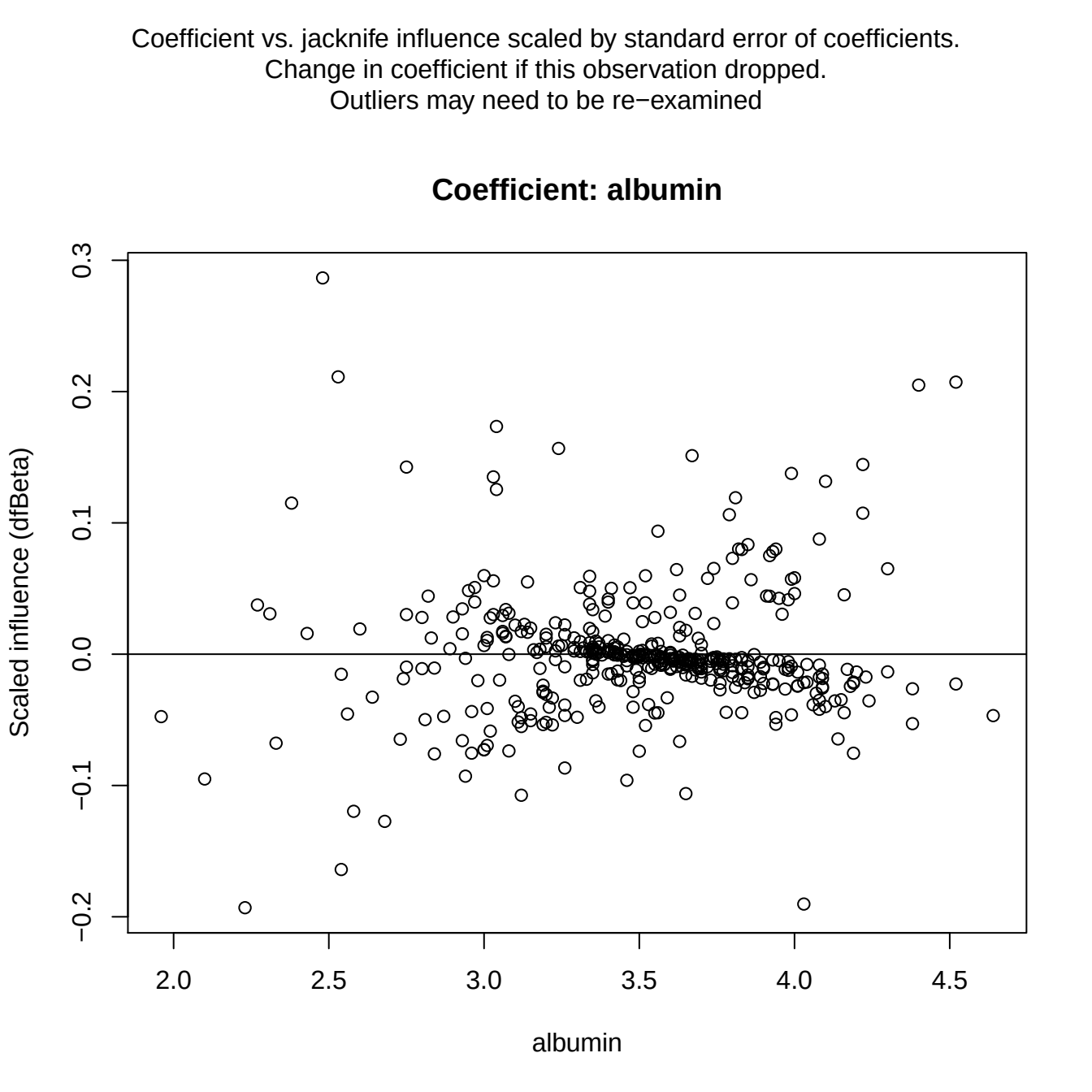

Coefficient vs. jacknife influence.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: albumin
Influence (dfBeta)
0.06
0.04
0.02
0.00
−0.02
−0.04
2.0
2.5
3.0
3.5
4.0
4.5
albumin

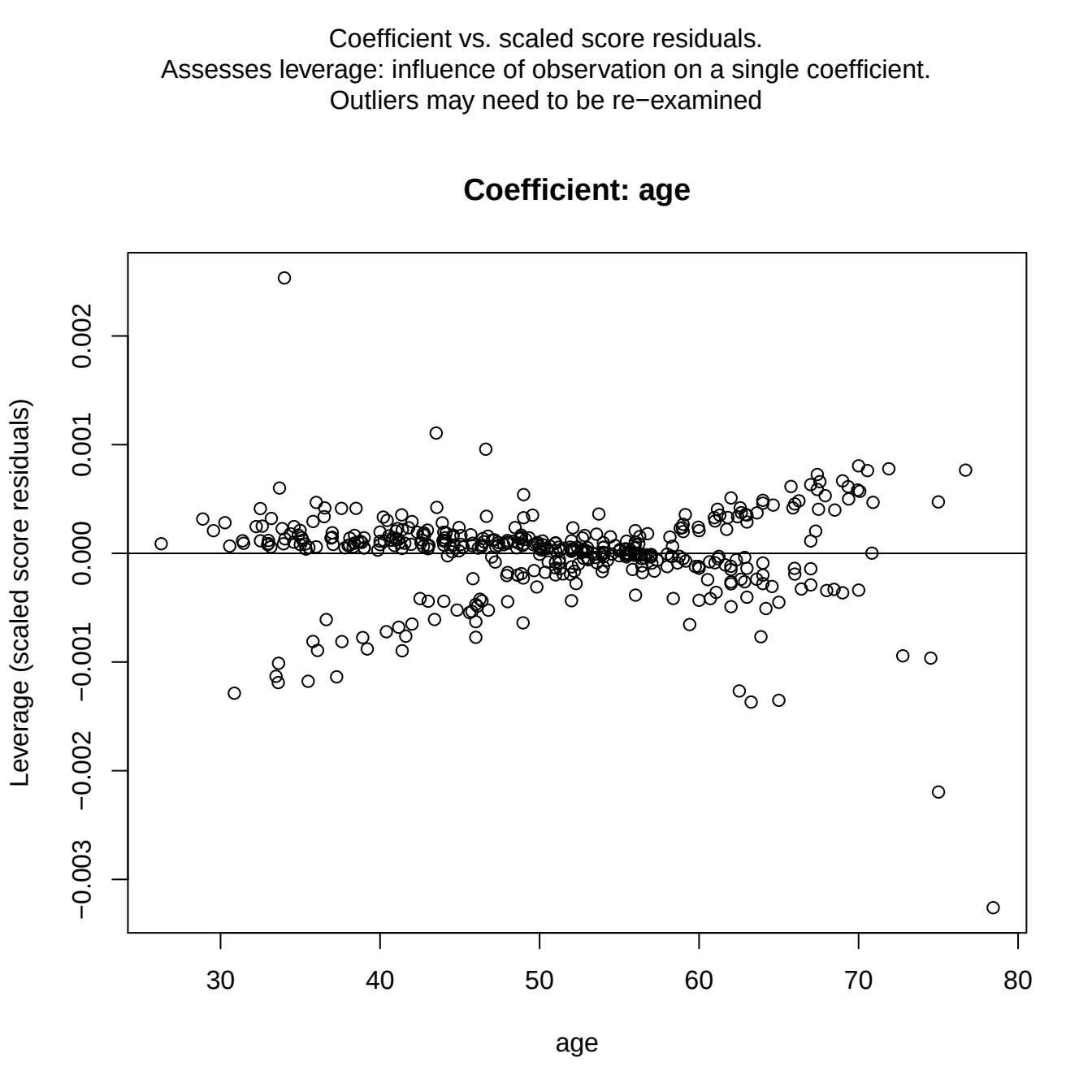

Coefficient vs. jacknife influence scaled by standard error of coefficients.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: age
Scaled influence (dfBeta)
0.3
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.4
30
40
50
60
70
80
age

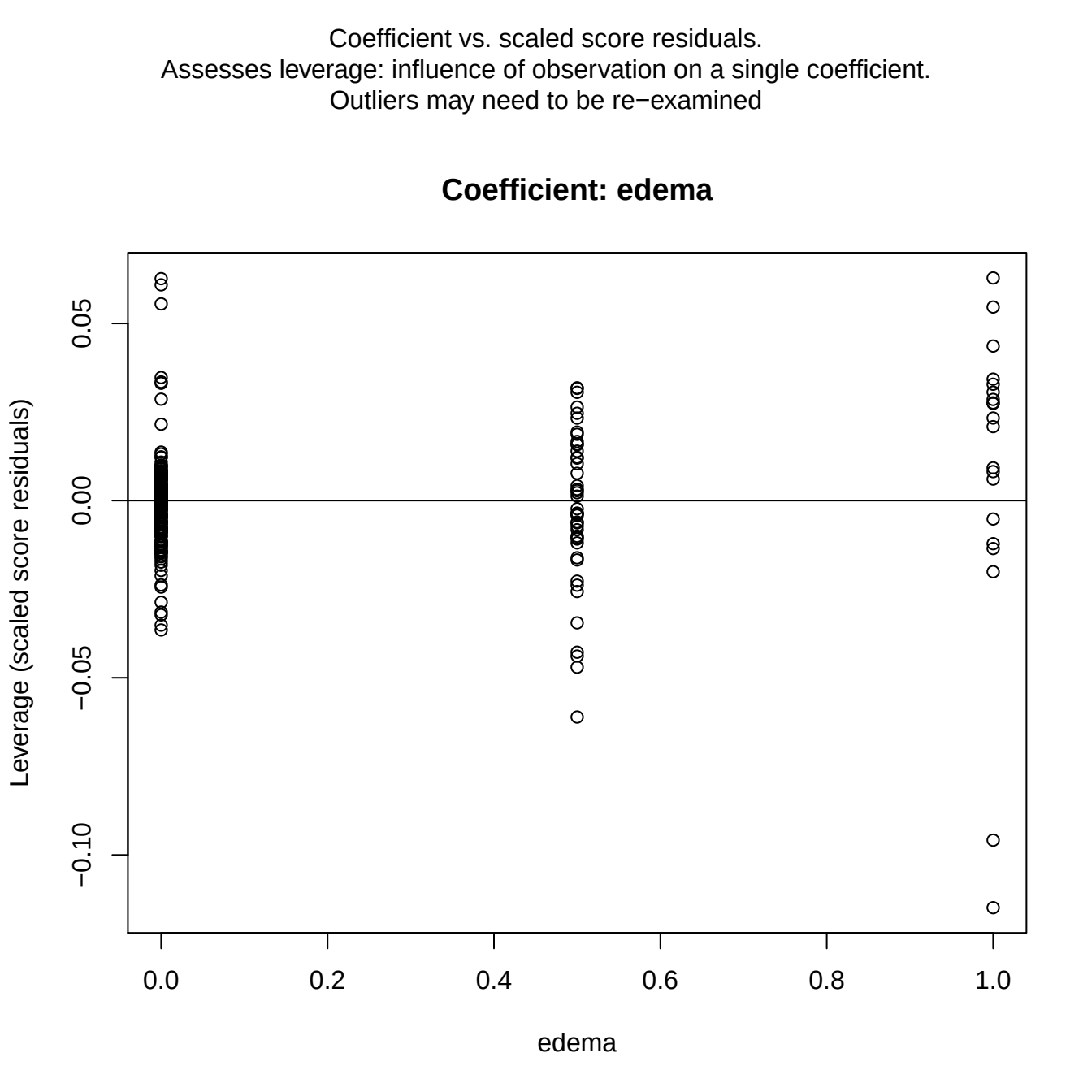

Coefficient vs. jacknife influence scaled by standard error of coefficients.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: edema
Scaled influence (dfBeta)
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.4
0.0
0.2
0.4
0.6
0.8
1.0
edema

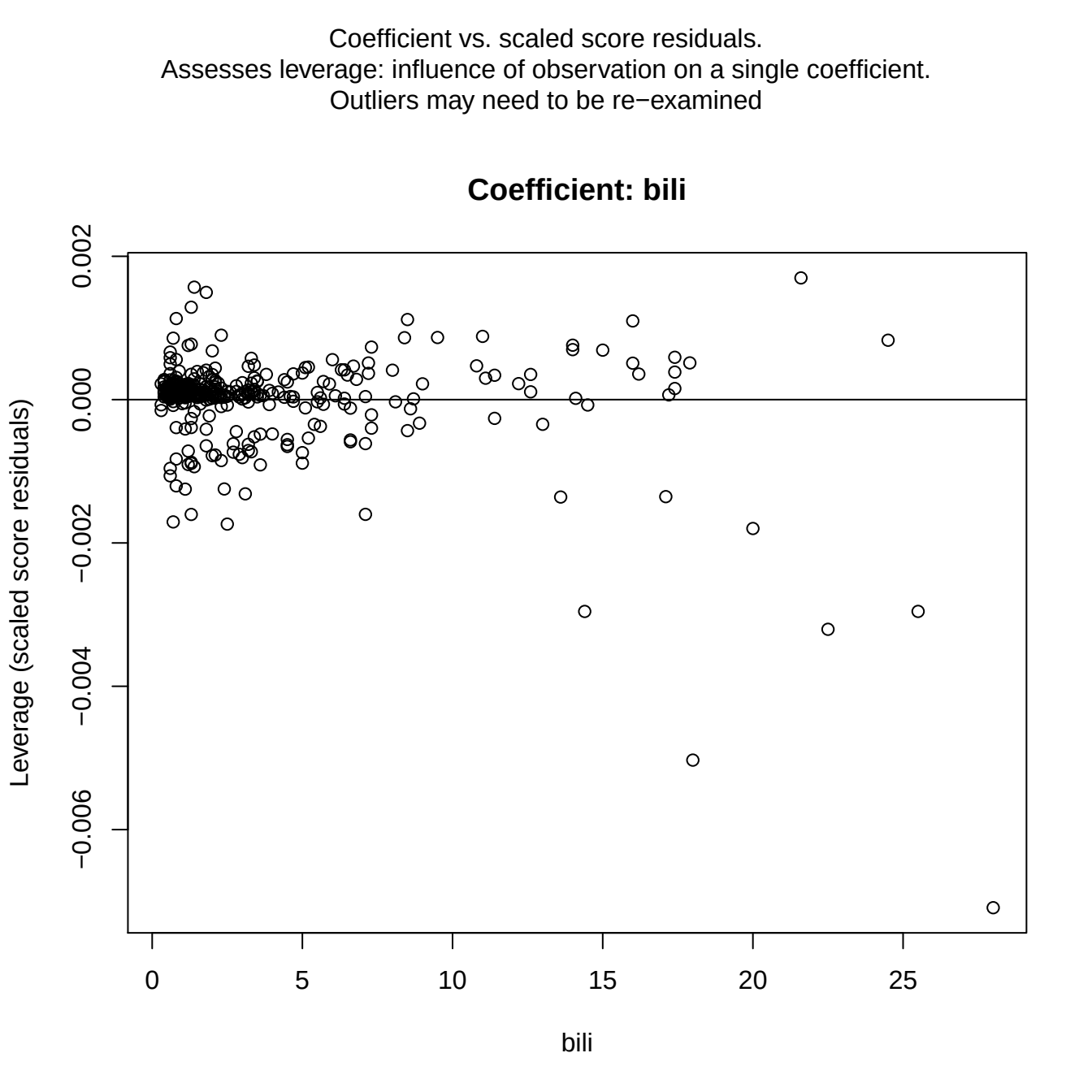

Coefficient vs. jacknife influence scaled by standard error of coefficients.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: bili
Scaled influence (dfBeta)
0.1
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
0
5
10
15
20
25
bili

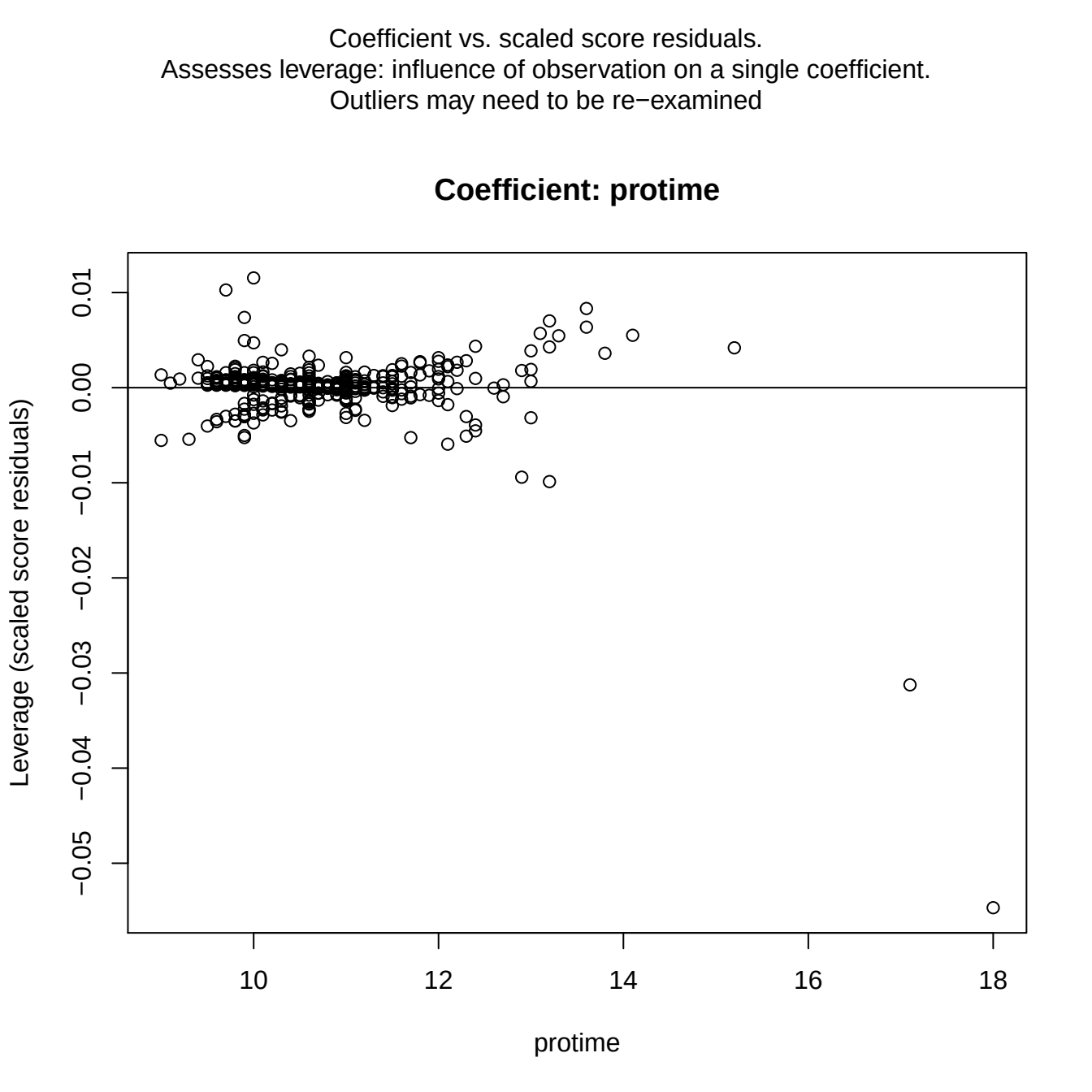

Coefficient vs. jacknife influence scaled by standard error of coefficients.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: protime
Scaled influence (dfBeta)
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
10
12
14
16
18
protime


Coefficient vs. jacknife influence scaled by standard error of coefficients.
Change in coefficient if this observation dropped.
Outliers may need to be re−examined
Coefficient: albumin
Scaled influence (dfBeta)
0.3
0.2
0.1
0.0
−0.1
−0.2
2.0
2.5
3.0
3.5
4.0
4.5
albumin

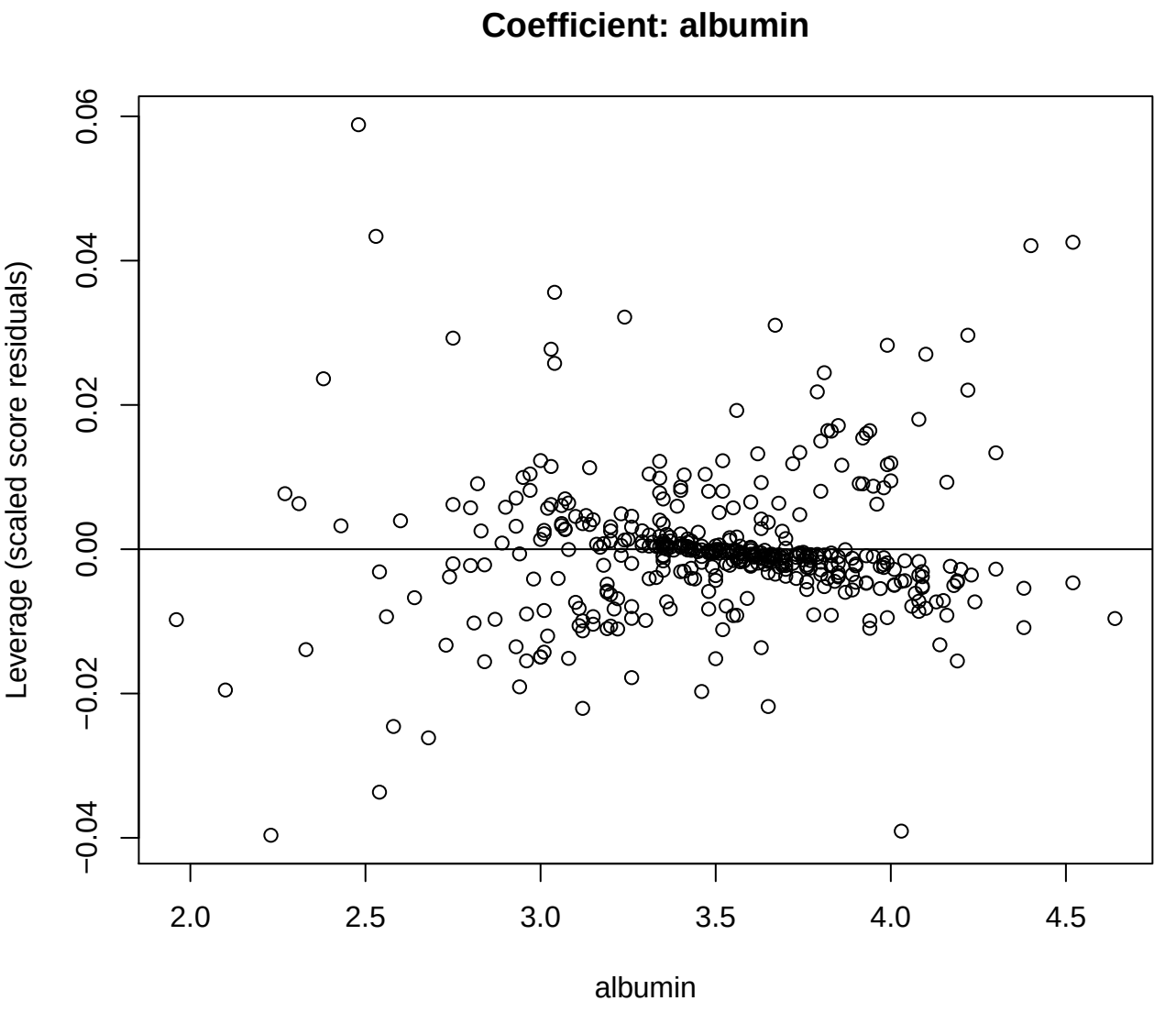

Coefficient vs. scaled score residuals.
Assesses leverage: influence of observation on a single coefficient.
Outliers may need to be re−examined
Coefficient: age
Leverage (scaled score residuals)
0.002
0.001
0.000
−0.001
−0.002
−0.003
30
40
50
60
70
80
age

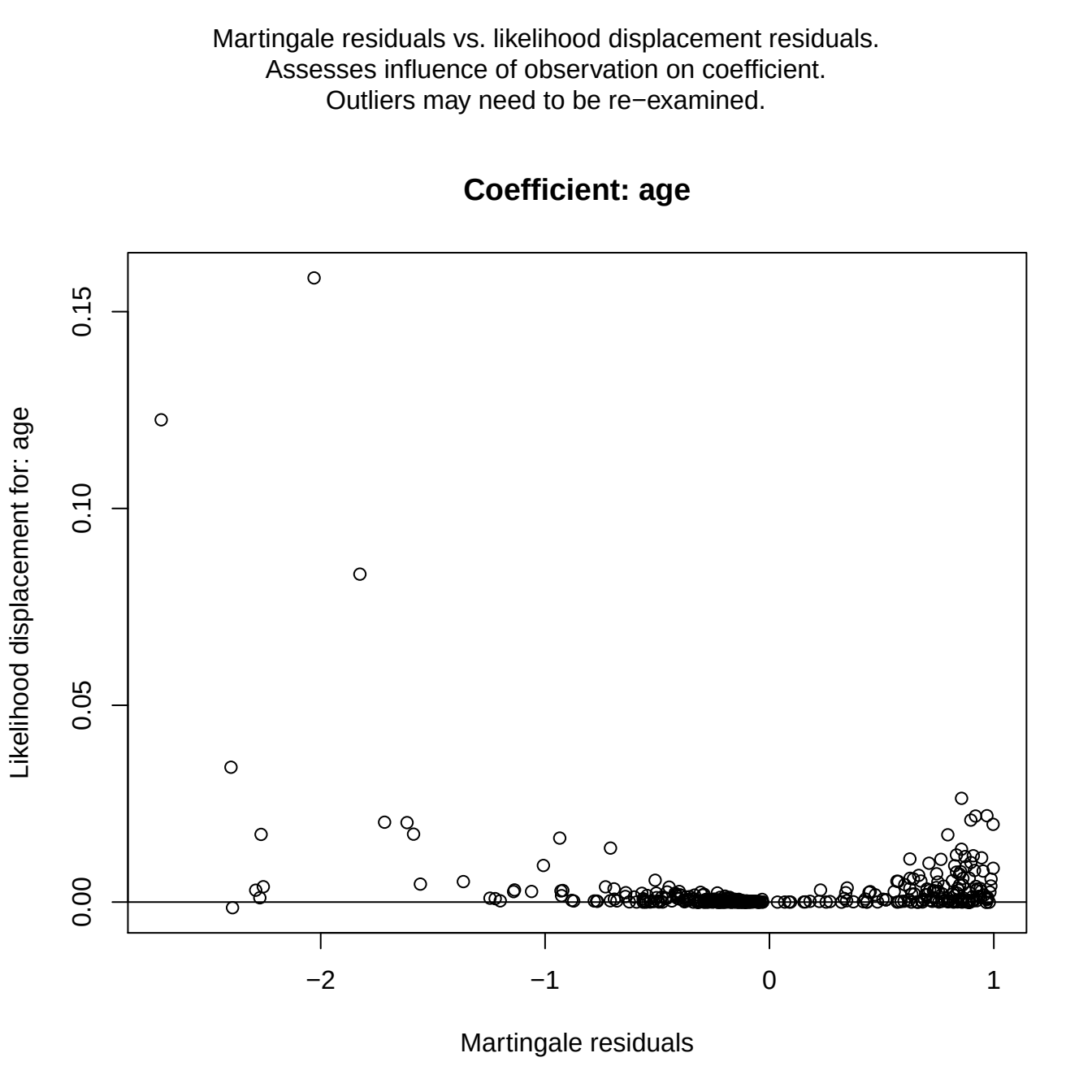

Coefficient vs. scaled score residuals.
Assesses leverage: influence of observation on a single coefficient.
Outliers may need to be re−examined
Coefficient: edema
Leverage (scaled score residuals)
0.05
0.00
−0.05
−0.10
0.0
0.2
0.4
0.6
0.8
1.0
edema

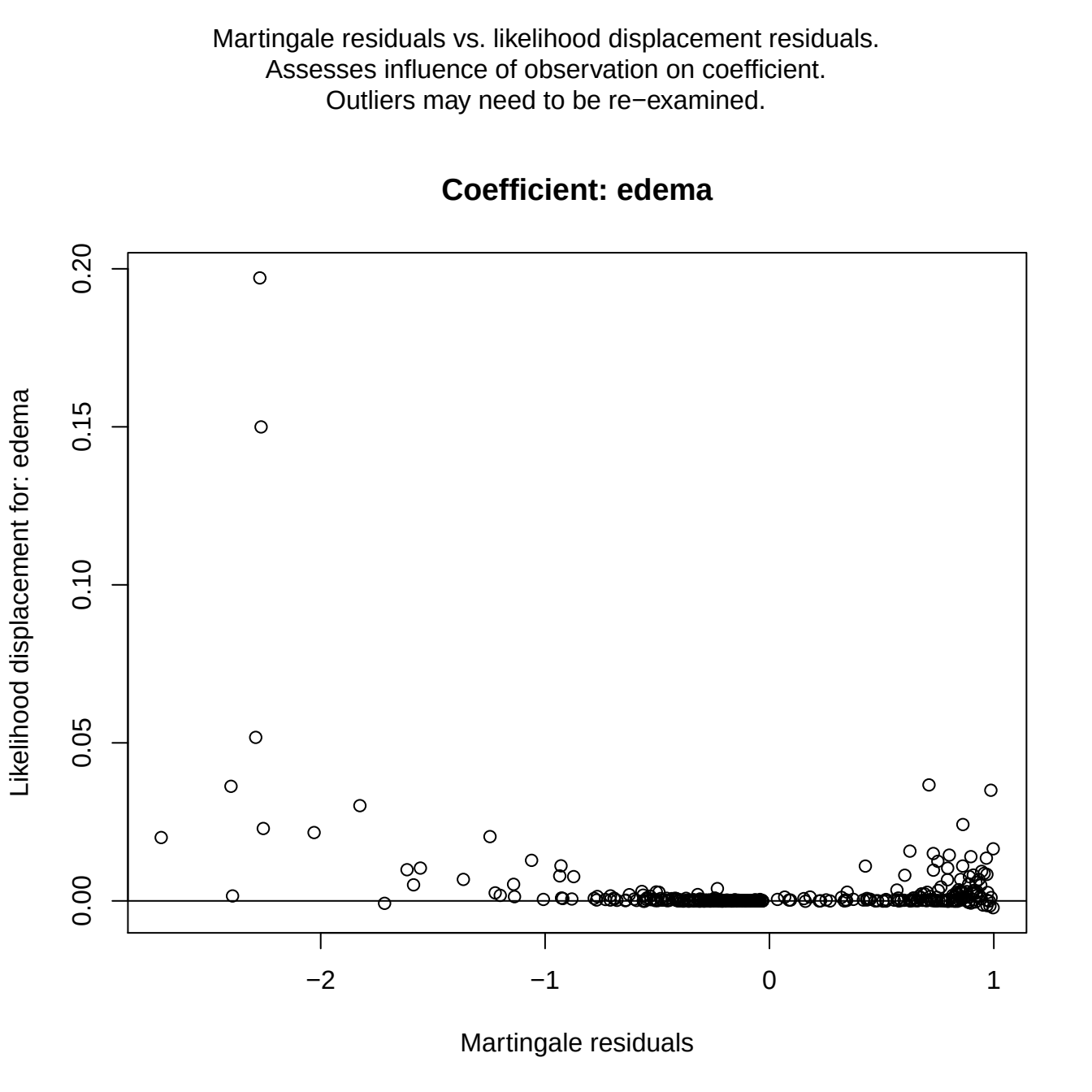

Coefficient vs. scaled score residuals.
Assesses leverage: influence of observation on a single coefficient.
Outliers may need to be re−examined
Coefficient: bili
Leverage (scaled score residuals)
0.002
0.000
−0.002
−0.004
−0.006
0
5
10
15
20
25
bili

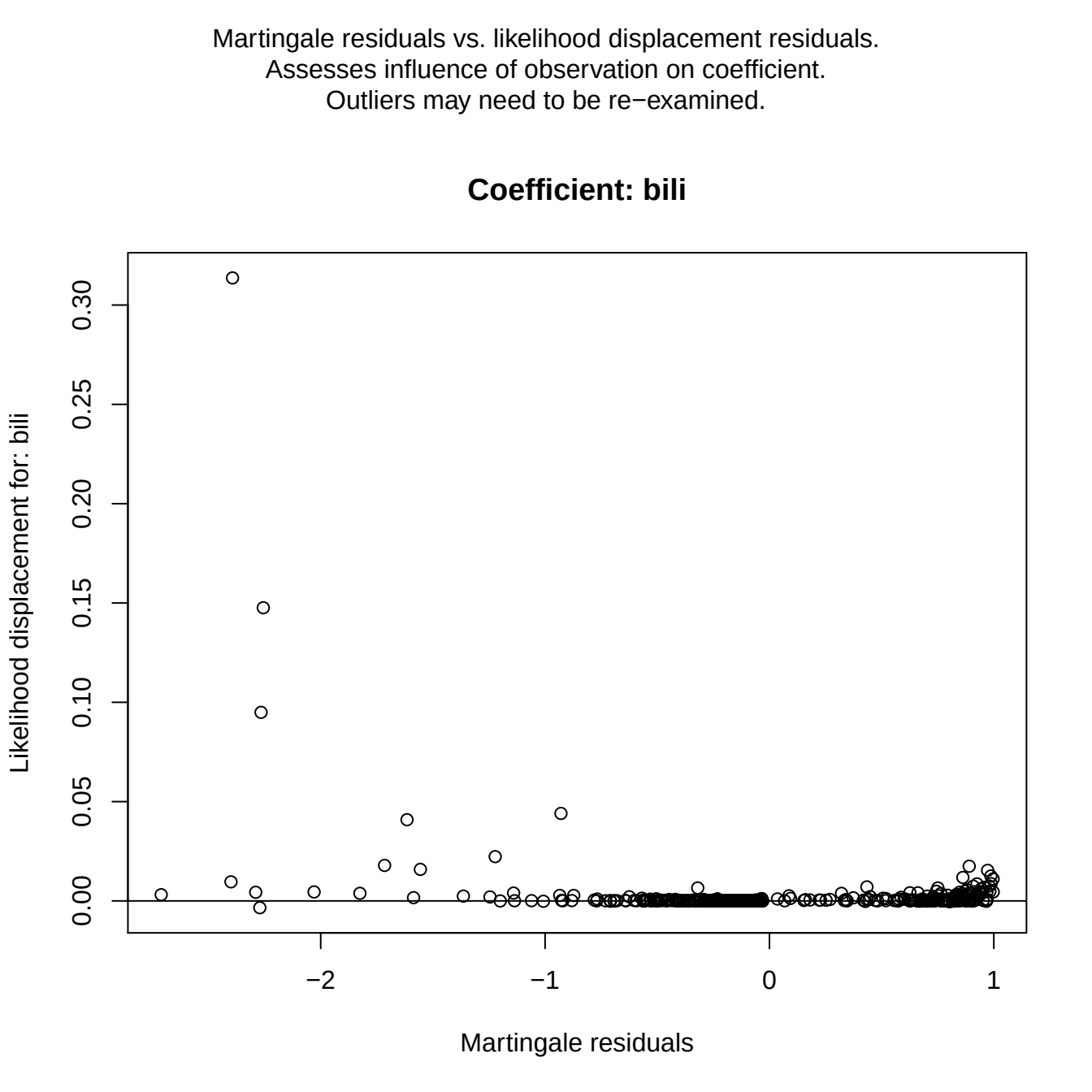

Coefficient vs. scaled score residuals.
Assesses leverage: influence of observation on a single coefficient.
Outliers may need to be re−examined
Coefficient: protime
Leverage (scaled score residuals)
0.01
0.00
−0.01
−0.02
−0.03
−0.04
−0.05
10
12
14
16
18
protime

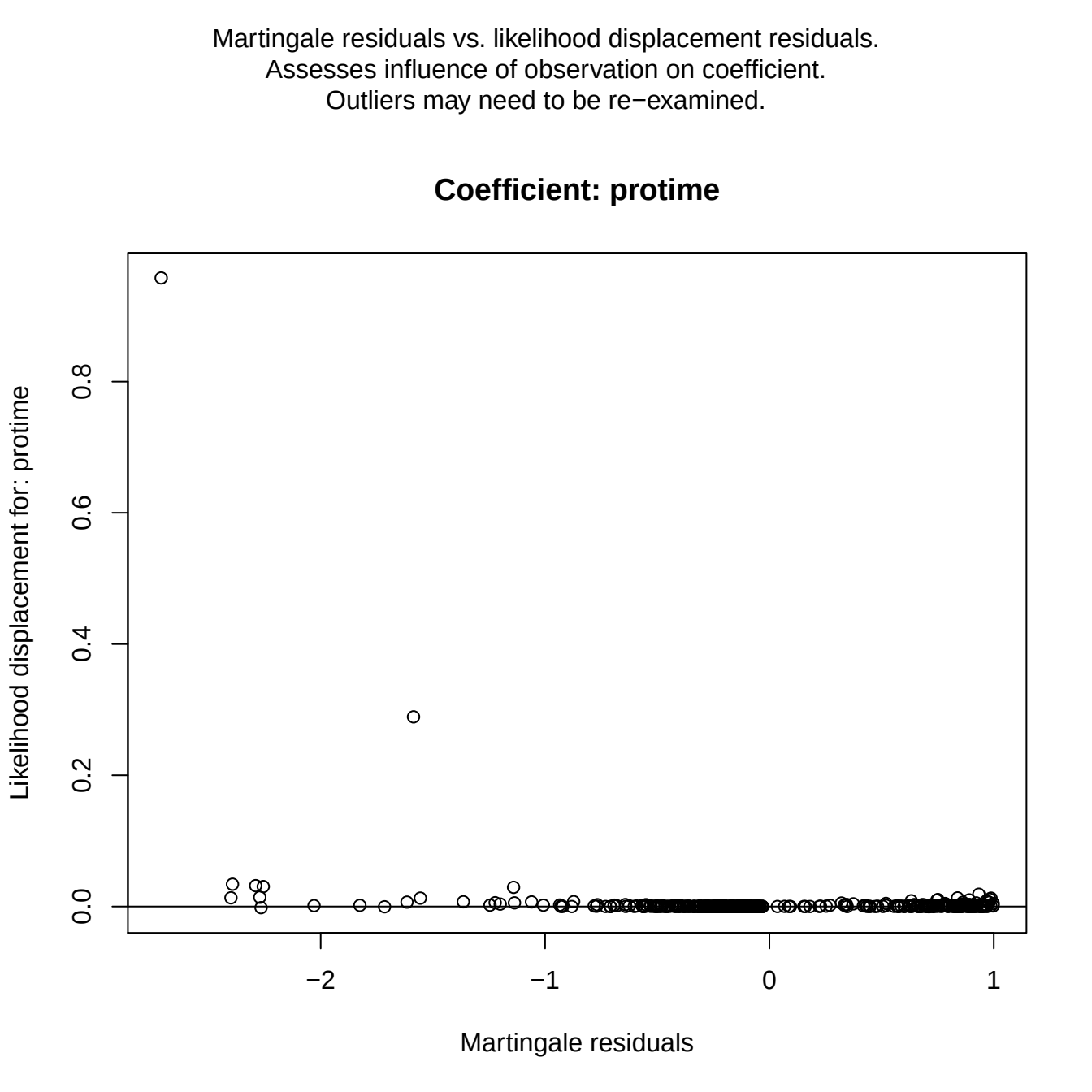
Coefficient vs. scaled score residuals.
Assesses leverage: influence of observation on a single coefficient.
Outliers may need to be re−examined

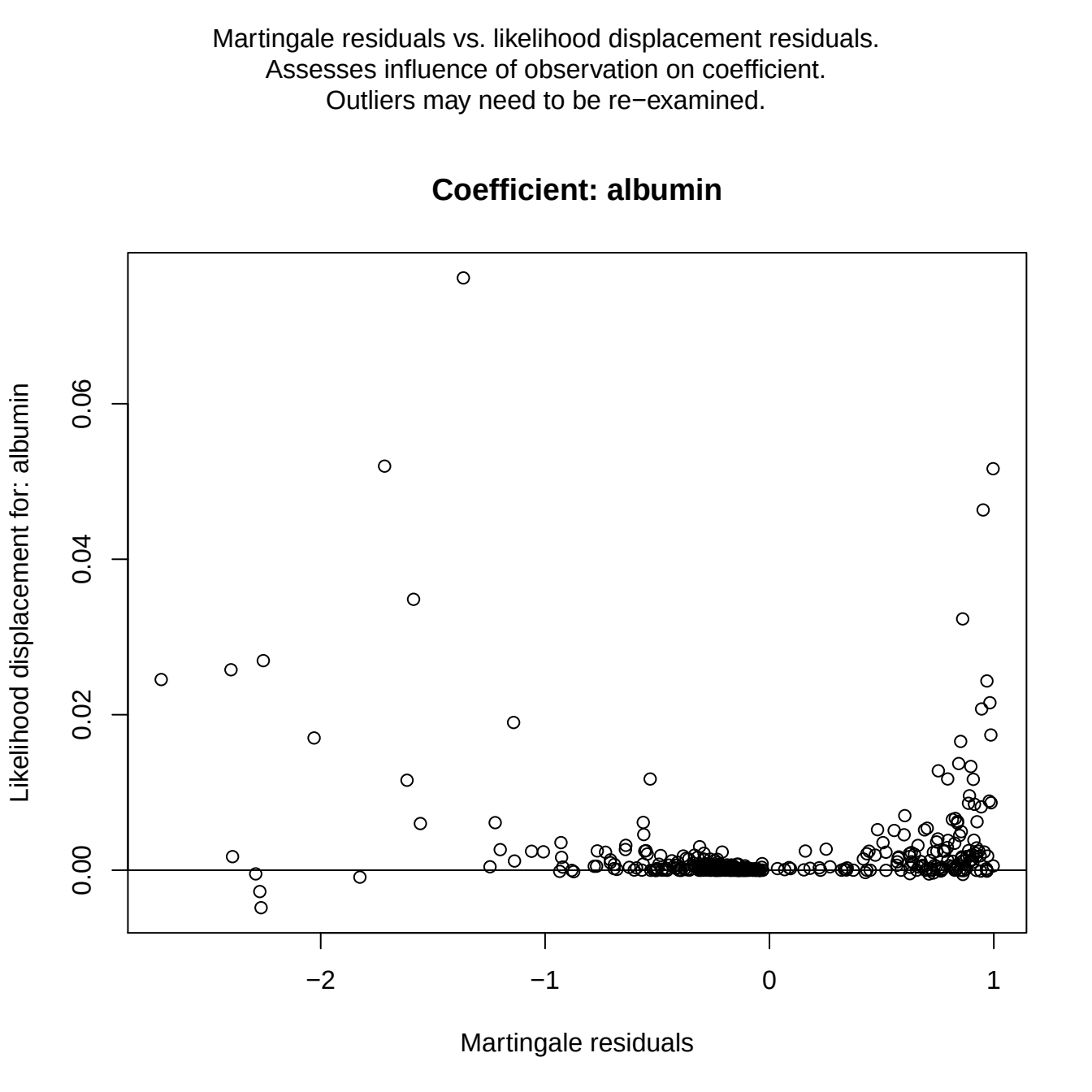



Martingale residuals vs. likelihood displacement residuals.
Assesses influence of observation on coefficient.
Outliers may need to be re−examined.
Coefficient: age
Likelihood displacement for: age
0.00
0.05
0.10
0.15
−2
−1
0
1
Martingale residuals


Martingale residuals vs. likelihood displacement residuals.
Assesses influence of observation on coefficient.
Outliers may need to be re−examined.
Coefficient: edema
Likelihood displacement for: edema
0.00
0.05
0.10
0.15
0.20
−2
−1
0
1
Martingale residuals


Martingale residuals vs. likelihood displacement residuals.
Assesses influence of observation on coefficient.
Outliers may need to be re−examined.
Coefficient: bili
Likelihood displacement for: bili
0.00
0.05
0.10
0.15
0.20
0.25
0.30
−2
−1
0
1
Martingale residuals


Martingale residuals vs. likelihood displacement residuals.
Assesses influence of observation on coefficient.
Outliers may need to be re−examined.
Coefficient: protime
Likelihood displacement for: protime
0.0
0.2
0.4
0.6
0.8
−2
−1
0
1
Martingale residuals


Martingale residuals vs. likelihood displacement residuals.
Assesses influence of observation on coefficient.
Outliers may need to be re−examined.
Coefficient: albumin
Likelihood displacement for: albumin
0.00
0.02
0.04
0.06
−2
−1
0
1
Martingale residuals