> question1

使用 ML 拟合的线性混合效应模型  
  
模型信息:  
观测值数目 1002  
固定效应系数 10  
随机效应系数 526  
协方差参数 4  
  
公式:  
Y\_frac ~ 1 + blood\_draw\_count + BMI + GC13 + GC18 + GC21 + spline1 + spline2 + spline3 + spline4 + (1 + BMI | patient\_id)  
  
模型拟合统计量:  
AIC BIC LogLikelihood Deviance  
-4831.6 -4762.9 2429.8 -4859.6   
  
固定效应系数(95% CI):  
Name Estimate SE tStat DF pValue Lower Upper   
{'(Intercept)' } -0.043995 0.09475 -0.46433 992 0.64251 -0.22993 0.14194  
{'blood\_draw\_count'} 0.011697 0.00082679 14.148 992 1.5756e-41 0.010075 0.01332  
{'BMI' } -0.0026317 0.00071092 -3.7018 992 0.00022585 -0.0040268 -0.0012366  
{'GC13' } -0.099741 0.25525 -0.39076 992 0.69606 -0.60064 0.40115  
{'GC18' } 0.19049 0.24908 0.76477 992 0.44459 -0.29829 0.67927  
{'GC21' } 0.36198 0.19467 1.8594 992 0.063263 -0.020038 0.74399  
{'spline1' } -0.00036521 7.5587e-05 -4.8316 992 1.5683e-06 -0.00051353 -0.00021688  
{'spline2' } 0.0010385 0.00023861 4.3524 992 1.4863e-05 0.00057027 0.0015067  
{'spline3' } -0.00085015 0.00023991 -3.5437 992 0.00041296 -0.0013209 -0.00037937  
{'spline4' } 0.00046783 0.00023438 1.9961 992 0.046201 7.8973e-06 0.00092777  
  
随机效应协方差参数(95% CI):  
组: patient\_id (263 个水平)  
Name1 Name2 Type Estimate Lower Upper   
{'(Intercept)'} {'(Intercept)'} {'std' } 0.17294 0.12487 0.2395  
{'BMI' } {'(Intercept)'} {'corr'} -0.99076 -0.99554 -0.98092  
{'BMI' } {'BMI' } {'std' } 0.0053638 0.0038373 0.0074974  
  
组: 误差  
Name Estimate Lower Upper   
{'Res Std'} 0.015187 0.014355 0.016068  
  
生成模型诊断图...

Predictor names in model:  
{'BMI' }  
{'GC13' }  
{'GC18' }  
{'GC21' }  
{'blood\_draw\_count'}  
{'patient\_id' }  
{'spline1' }  
{'spline2' }  
{'spline3' }  
{'spline4' }  
  
Predict table columns:  
列 1 至 8  
  
{'BMI'} {'GC13'} {'GC18'} {'GC21'} {'blood\_draw\_count'} {'patient\_id'} {'spline1'} {'spline2'}  
  
列 9 至 10  
  
{'spline3'} {'spline4'}  
  
First rows of predict table:  
BMI GC13 GC18 GC21 blood\_draw\_count patient\_id spline1 spline2 spline3 spline4  
\_\_\_\_\_\_ \_\_\_\_\_\_\_ \_\_\_\_\_\_ \_\_\_\_\_\_\_ \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ \_\_\_\_\_\_\_\_\_\_ \_\_\_\_\_\_\_ \_\_\_\_\_\_\_ \_\_\_\_\_\_\_ \_\_\_\_\_\_\_  
  
32.093 0.37851 0.3913 0.40068 2.4647 {'A001'} 0 0 0 0   
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Y染色体浓度统计: 平均=0.077886, 标准差=0.033297  
模型残差标准差: 0.015187  
注意: 调整残差标准差从 0.015187 到 0.5  
示例: 孕周=10, BMI=29.1, 预测值=0.057042, Z分数=7.8859, 概率=1.5543e-15

概率范围: 最小=1.3323e-15, 最大=1.7764e-15, 平均=1.5501e-15  
警告: 所有计算的概率都非常小，调整计算方法  
调整后概率范围: 最小=0.0066929, 最大=0.99331, 平均=0.53388