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# Predicting Renal Failure in Patients with C3 Glomerulopathy

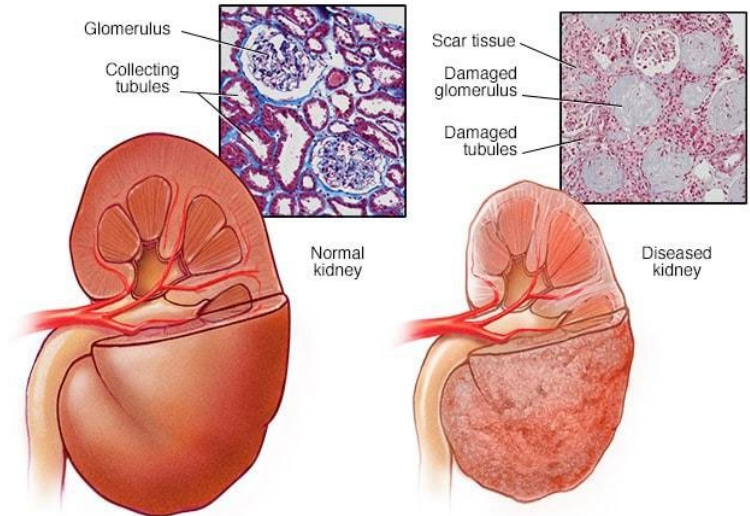
**ISIB 2022**

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# Kidney Disease

- Progressive disease in which the kidneys lose their ability to properly filter waste and excess fluids from the blood
- Glomerulus-filtering unit of the kidney
  - Glomerular filtration rate (GFR) is a measure of kidney function
- Current treatment option
  - Kidney Transplant



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<https://www.mayoclinic.org/diseases-conditions/chronic-kidney-disease/symptoms-causes/syc-20354521>.






# **C3 Glomerulopathy (C3G)**

- A form of kidney disease in which an abundance of the protein C3 is present in the glomerular capillaries
- 1 in 1,000,000 people have C3G
- Sub-types of C3G
  - Dense Deposit Disease (DDD)
  - C3 Glomerulonephritis (C3GN)

# Purpose

- About half of patients with C3G have end-stage renal disease (ESRD) within 10 years
- Improve predictions of future renal failure using various biomarkers
- GFR vs. eGFR
- Capping eGFR measurements

## 5 Stages Of Kidney Disease

| Stage 1   | Stage 2  | Stage 3A  | Stage 3B  | Stage 4   | Stage 5    |
|---|--|---|---|---|------------|
| $GFR \geq 90$   | $89 \geq GFR \geq 60$  | $59 \geq GFR \geq 40$   | $44 \geq GFR \geq 30$   | $29 \geq GFR \geq 15$   | $GFR < 15$ |
|  |  |  |  |  |            |
| Normal or high function   | Mildly decreased function  | Mild to moderately decreased function   | Severely decreased function   | Kidney failure  |            |

<http://www.renalcareconsult.com/renal-disease-education/stages-of-kidney-disease/>

# The Data - UI C3G Natural History Study

## Observations

- Initially 1935 observations from 208 individuals
- Predictions made from 467 observations from 109 individuals

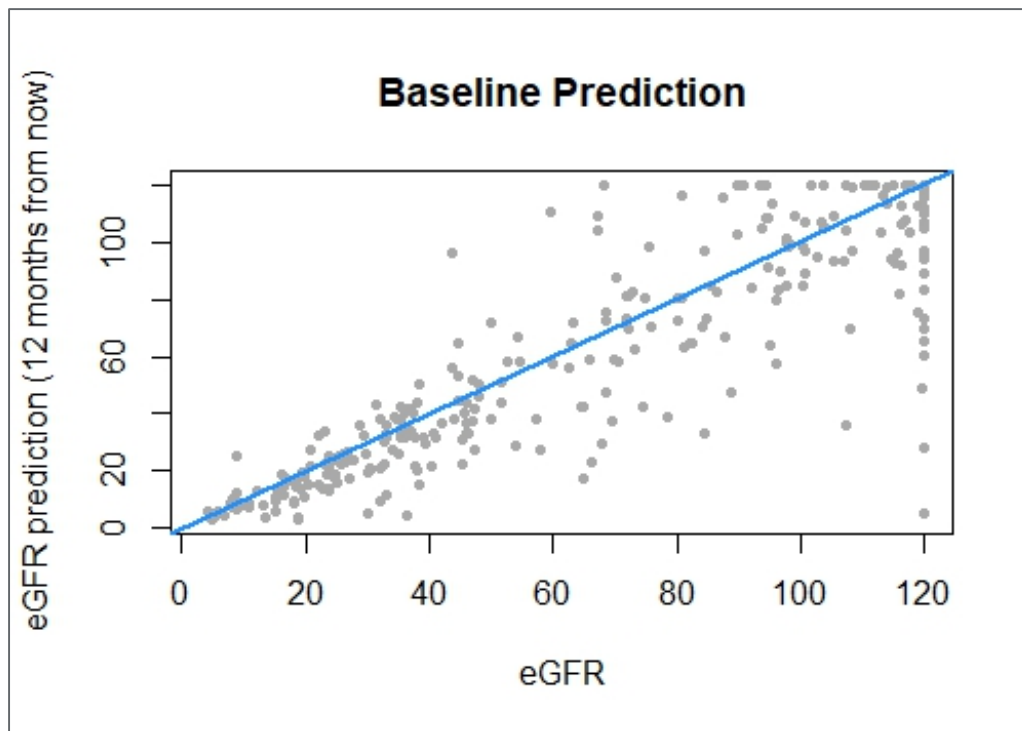
## Measurements

- eGFR
- C3
- UPCR
- UACR
- Soluble C5b-9 level
- Chronic Kidney Disease stage
- Sex
- Etiology
- Years with disease
- Age at Biopsy
- Race/Ethnicity
- Transplant Status

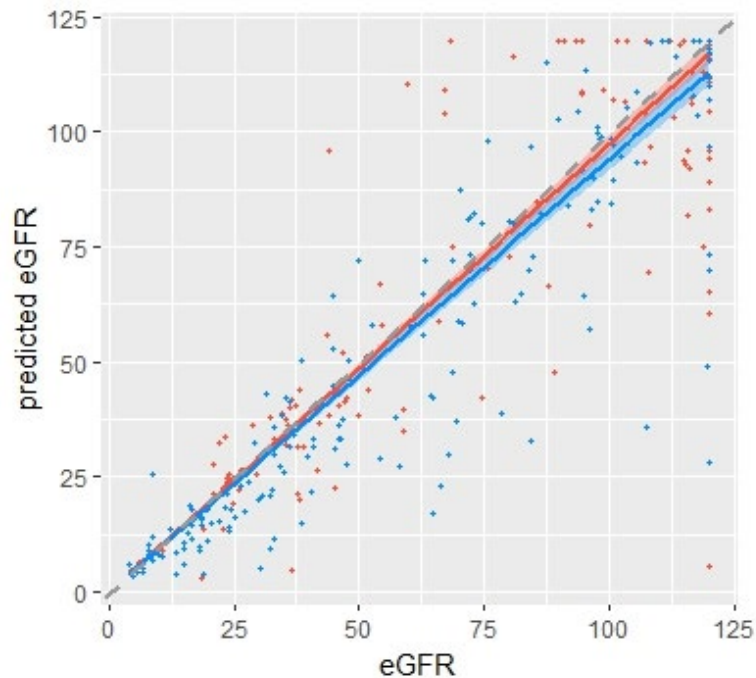
# Three Models

1. Baseline
2. Years with disease
3. Incorporating biomarkers

# 1. Baseline Prediction

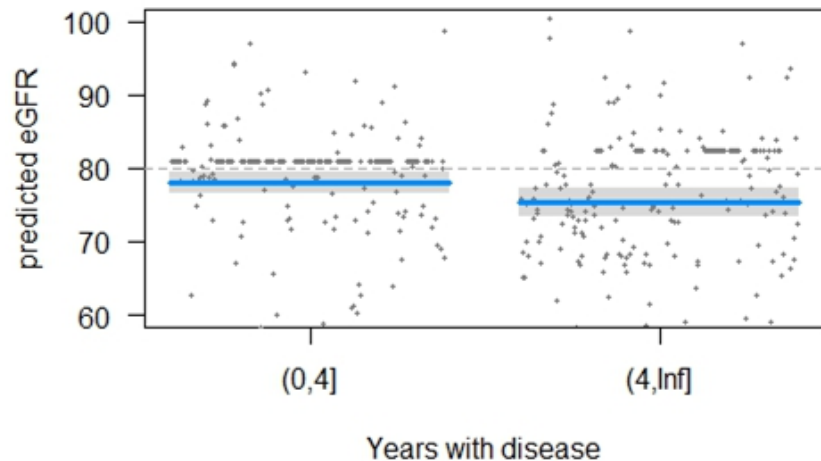


## 2. Years with Disease



<4 years: 3% decline  
>4 years: 6% decline

DiseaseTime  
— (0,4]  
— (4,Inf]



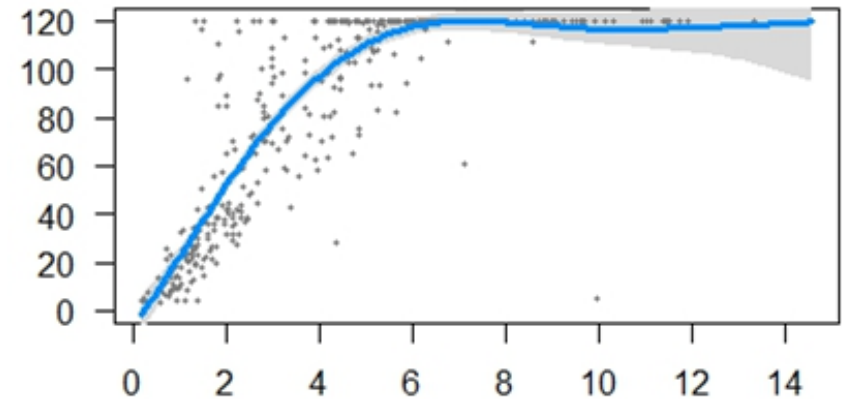
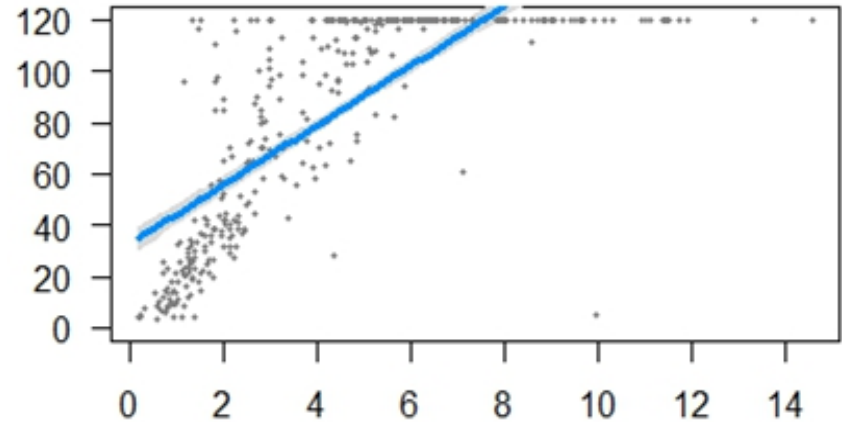


# 3. Biomarkers

- eGFR
- Years with disease
- Urine Protein-Creatinine Ratio (UPCR)
- Soluble C5b-9 level

# Methods

- Linear Models
- Generalised Additive Models (GAMs)
  - Goal: extend linear-regression models to be more flexible while avoiding overfitting the data



# Generalised Additive Models (GAMs)

- *GAM*: a sum of smooth functions

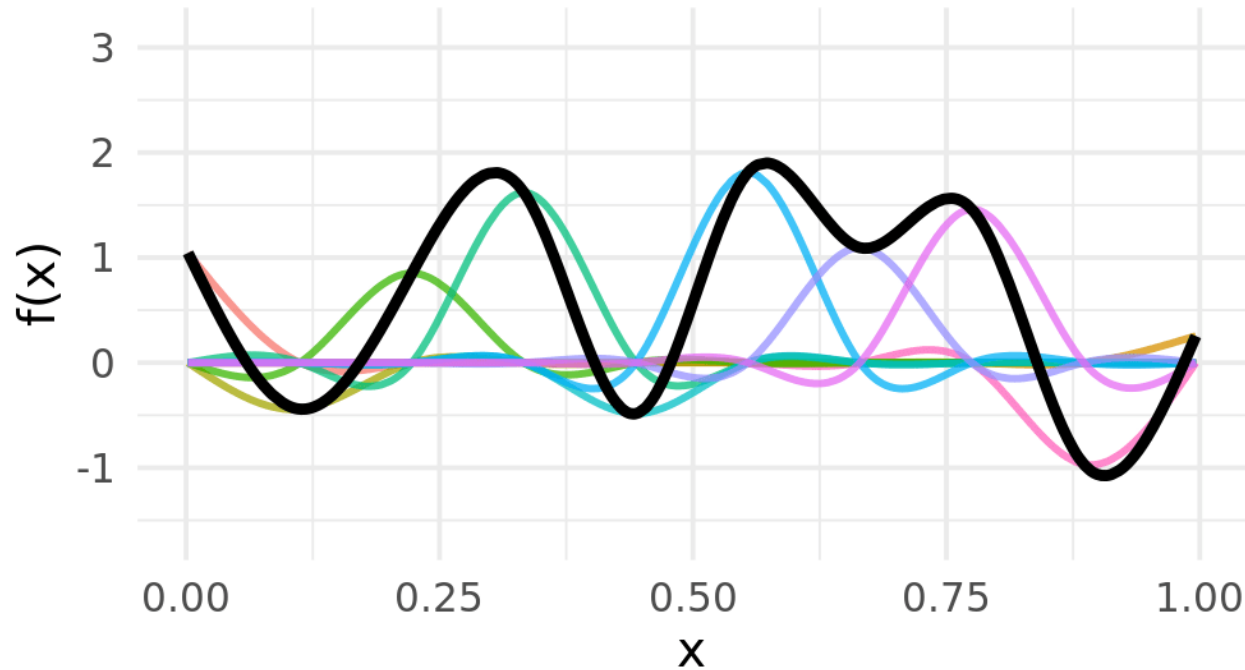
$$y_i = \beta_0 + \sum_j s_j(x_{ji}) + \epsilon_i$$

- *Splines*: functions made of simpler functions,  $b_k$ , each with weight  $\beta_k$

$$s(x) = \sum_{k=1}^K \beta_k b_k(x)$$

Equations from: Simpson, Gavin, 'Generalised Additive Models (GAMs)' for the 'Statistical Methods' webinar series hosted by the Ecological Forecasting Initiative and the ESA Statistical Ecology Section. Given on January 3, 2022. [bit.ly/gam-efi-22](https://bit.ly/gam-efi-22).

# GAMs



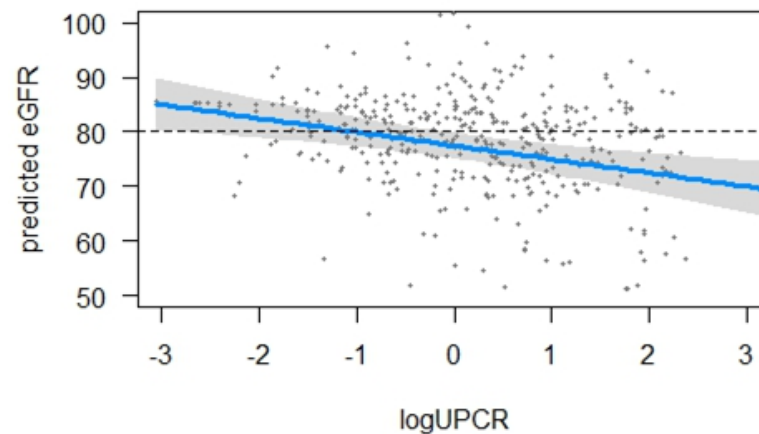
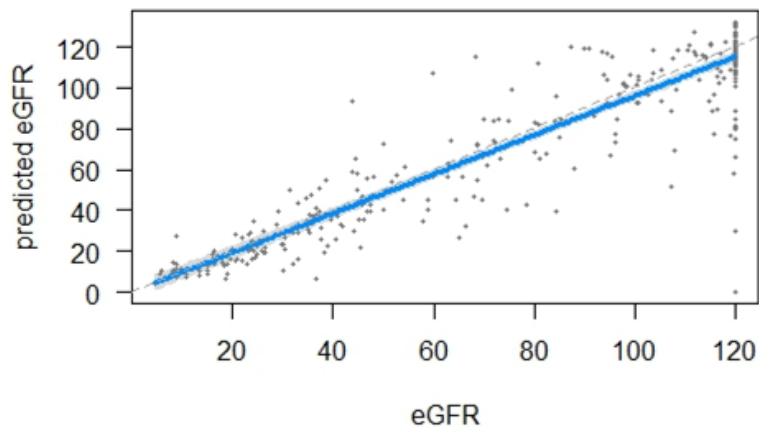
Animation from: Simpson, Gavin, 'Generalised Additive Models (GAMs)' for the 'Statistical Methods' webinar series hosted by the Ecological Forecasting Initiative and the ESA Statistical Ecology Section. Given on January 3, 2022. [bit.ly/gam-efi-22](https://bit.ly/gam-efi-22).

# Final Model

eGFR  
coefficient = 0.95971

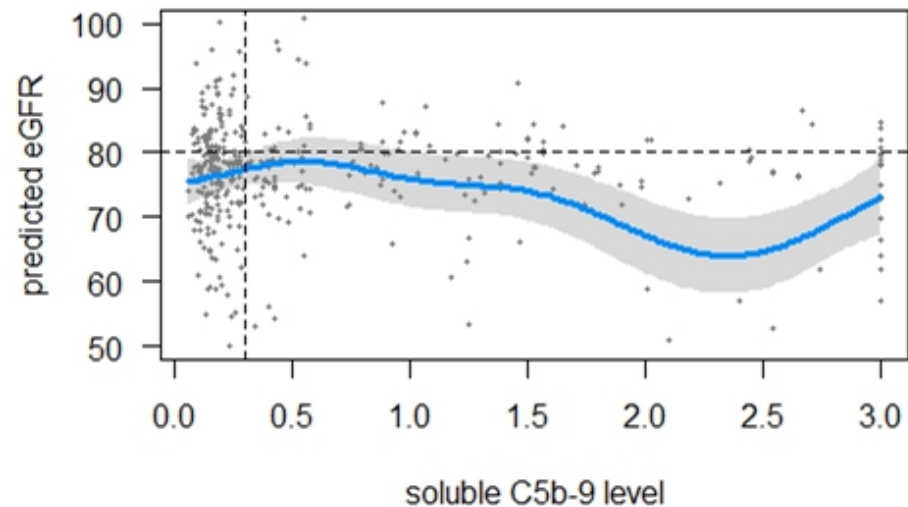
```
fit <- gam(eGFR2_cap ~ eGFR2_12m6w_cap +  
  logUPCR_12m6w +  
  s(soluble_level, sp=0.07) +  
  s(YrsDisease),  
  data=c3g)
```

log(UPCR)  
coefficient = -2.486

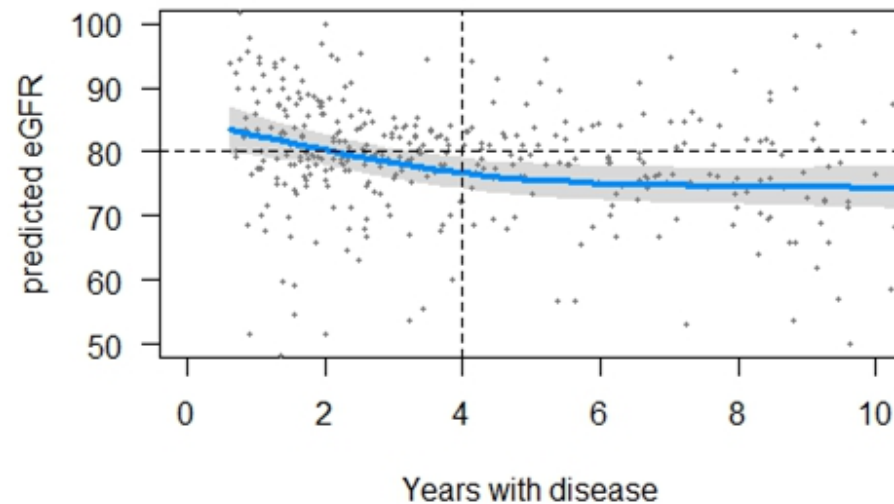


# Final Model

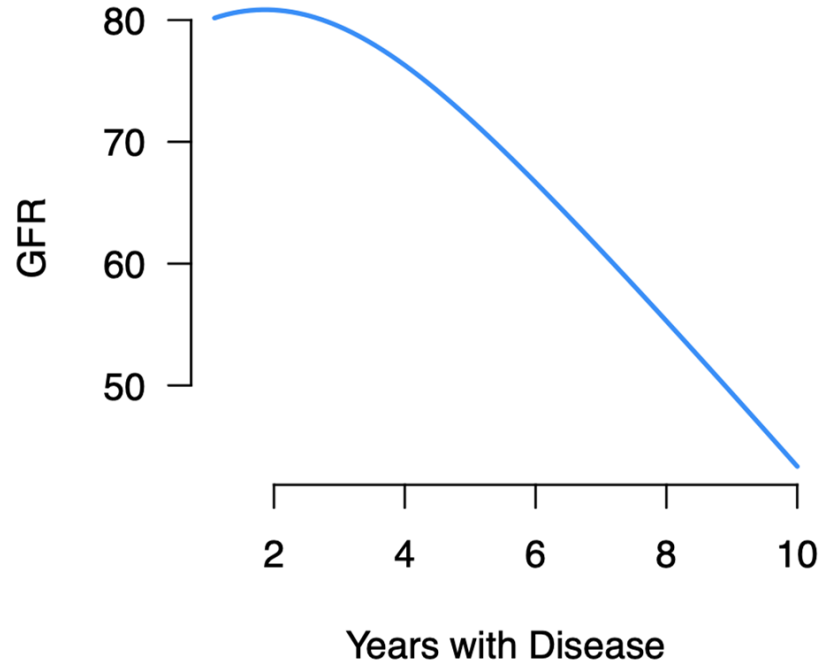
soluble level



years with disease



# Final Model - Patient Trajectory



# Model Accuracy

- Adjusted R-squared:
  - Adjusted R-squared for baseline prediction = 0.879
  - Adjusted R-squared for years prediction = 0.879
  - Adjusted R-squared for our model = 0.89
- Cross Validation:
  - Generalised Cross Validation
    - GCV for baseline prediction = 230.08
    - GCV for years prediction = 230
    - GCV for our model = 212.01
  - Training and testing splits



# Limitations

- Some observations come from the same individual multiple times
- Not taking into account dependence
- Have missing data

# Acknowledgements

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