Data Application

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11/14/2021

Descriptives

This dataset includes 88' patients treated with radiotherapy for locally advanced non-small cell lung cancer. These data are all from patients' initial timepoint, without SBRT, and with radiation to the ipsilateral lung (but either left or right lung). 76 of the patients received concurrent chemotherapy, although I don't have data on which patients.

Lung toxicities were graded between 0 and 5, and then made into a binary variable with toxicities ≥ 2 classified as being a toxicity (and grades 0 and 1 being no toxicity).

Several dosimetrics were considered, but we will focus here on low VQ 20. As I understand it, V is one imaging dosimetric measured after patients inhale something, while Q is another imaging dosimetric measured after patients are injected with something. VQ refers to voxels on both images that were in agreement about whether the voxel of lung tissue received radiation exposure. Low VQ 20 refers to the percentage of voxels that received ≥ 20 Gy of radiation.

The paper that Phil shared with me also found that a non-imaging dosimetric called ADL is independently predictive of toxicity in addition to low VQ 20.

First, some descriptive statistics:

```
## [1] "Distribution of VQ 20:"

##          0%        25%        50%        75%       100%
## 0.00000000 0.01948441 0.05544634 0.12283149 0.42268380

## [1] "Distribution of ADL:"

##      0%     25%     50%     75%    100%
##  0.0000  0.9975  1.9350 12.3375 55.3600

## [1] "Which lung irradiated:"

##
##  LEFT_LUNG-GTV RIGHT_LUNG-GTV
##             37             51

## [1] "Lung Toxicity Distribution (grades 0-5):"

##
##  0  1  2  3  5
## 49 24 11  2  2

## [1] "Lung Toxicity Distribution (binary):"

##
##  0  1
## 73 15
```
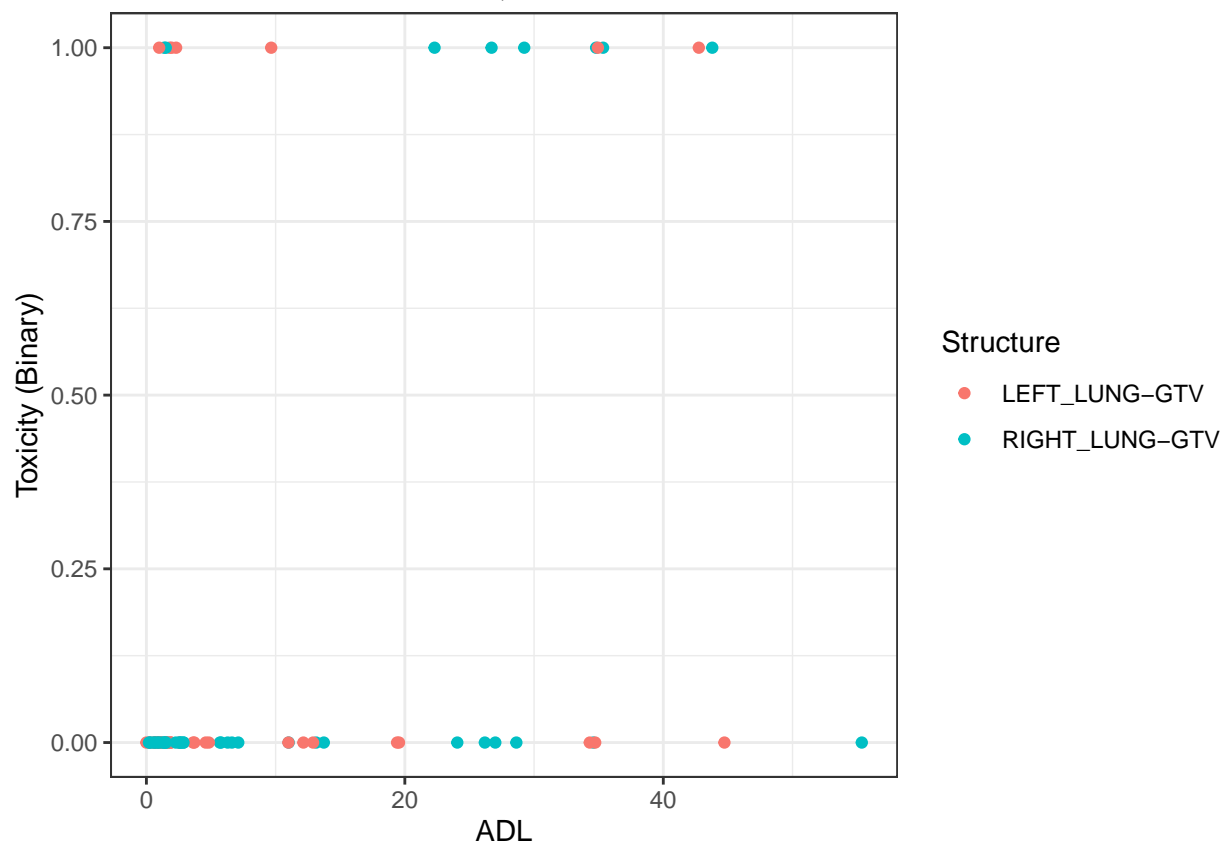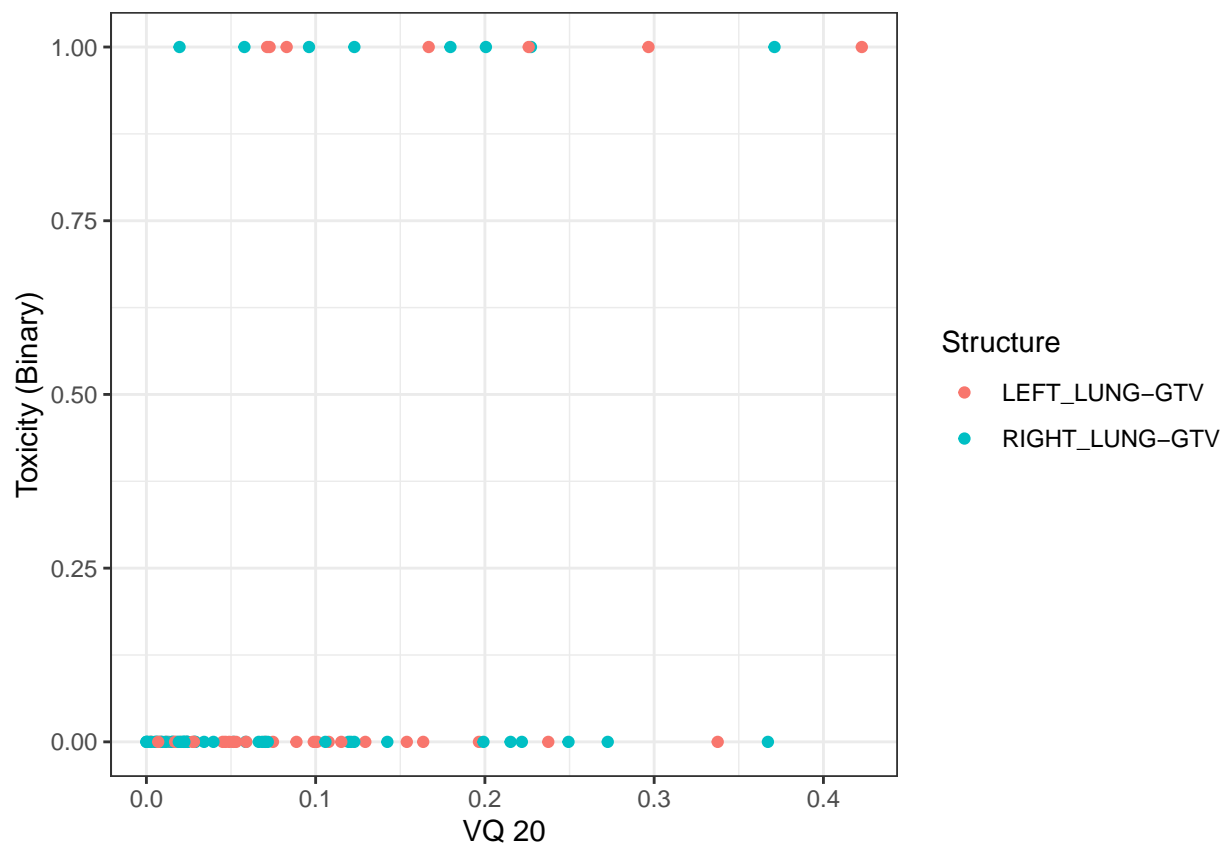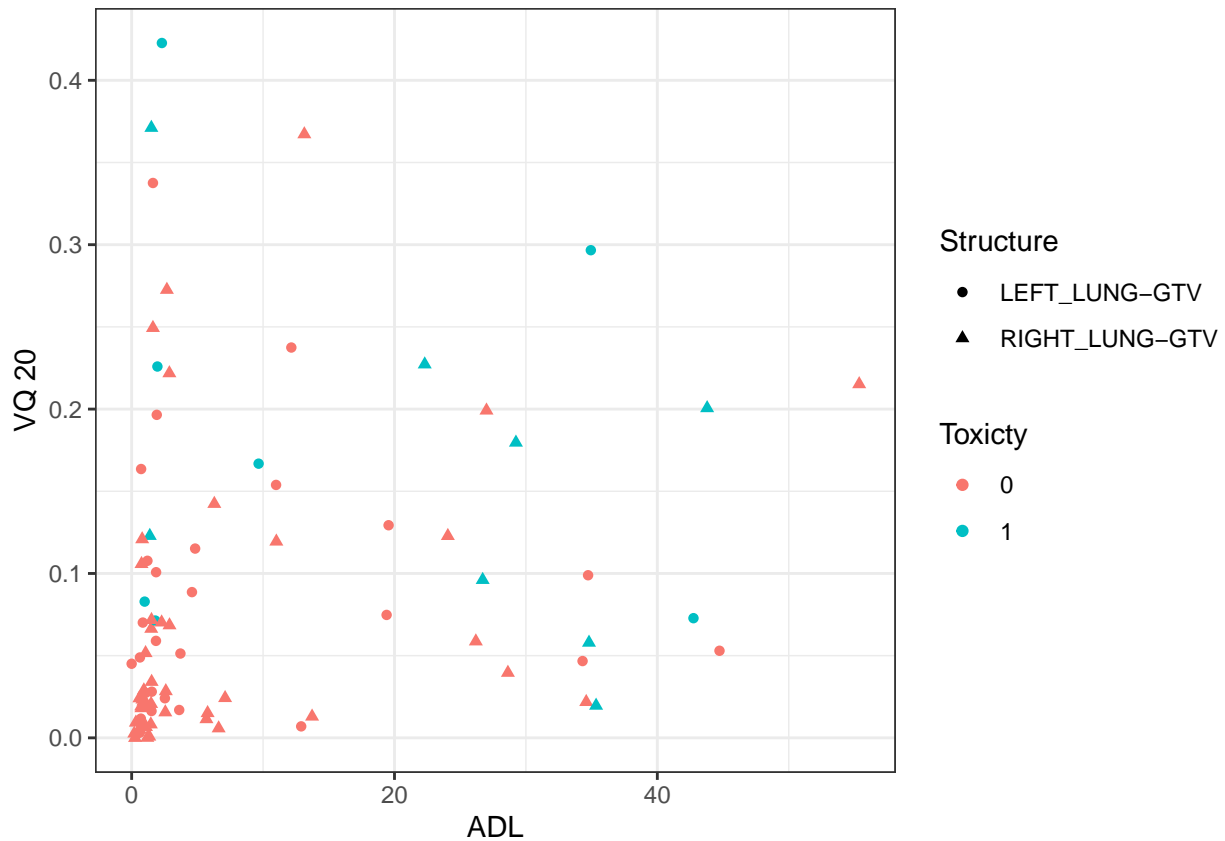
Model Results

At present, I'm fitting two models: one with only VQ20 as an HPR predictor, and another model with VQ20 as the HPR predictor, and with ADL and which lung as linear predictors. Results:

```
## Running MCMC with 4 sequential chains...
##
## Chain 1 finished in 14.0 seconds.
## Chain 2 finished in 13.2 seconds.
## Chain 3 finished in 19.2 seconds.
## Chain 4 finished in 12.7 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 14.7 seconds.
## Total execution time: 59.4 seconds.

##
## Warning: 34 of 8000 (0.0%) transitions ended with a divergence.
## This may indicate insufficient exploration of the posterior distribution.
## Possible remedies include:
##    * Increasing adapt_delta closer to 1 (default is 0.8)
##    * Reparameterizing the model (e.g. using a non-centered parameterization)
##    * Using informative or weakly informative prior distributions

## Warning: Dropping 'draws_df' class as required metadata was removed.

## Running MCMC with 4 sequential chains...
##
```

```
## Chain 1 finished in 14.6 seconds.
## Chain 2 finished in 9.6 seconds.
## Chain 3 finished in 9.3 seconds.
## Chain 4 finished in 12.4 seconds.
##
## All 4 chains finished successfully.
## Mean chain execution time: 11.5 seconds.
## Total execution time: 46.2 seconds.

##
## Warning: 61 of 8000 (1.0%) transitions ended with a divergence.
## This may indicate insufficient exploration of the posterior distribution.
## Possible remedies include:
##    * Increasing adapt_delta closer to 1 (default is 0.8)
##    * Reparameterizing the model (e.g. using a non-centered parameterization)
##    * Using informative or weakly informative prior distributions

## Warning: Dropping 'draws_df' class as required metadata was removed.

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```
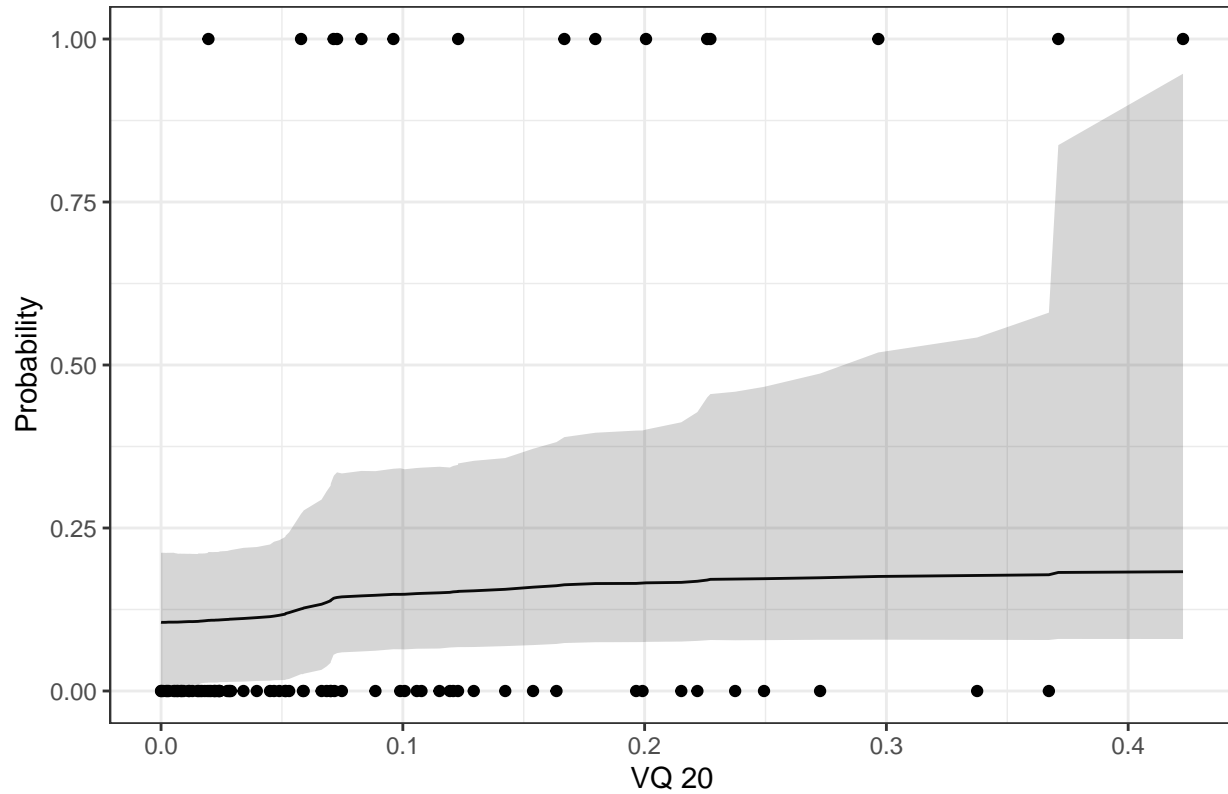
No Linear Predictors
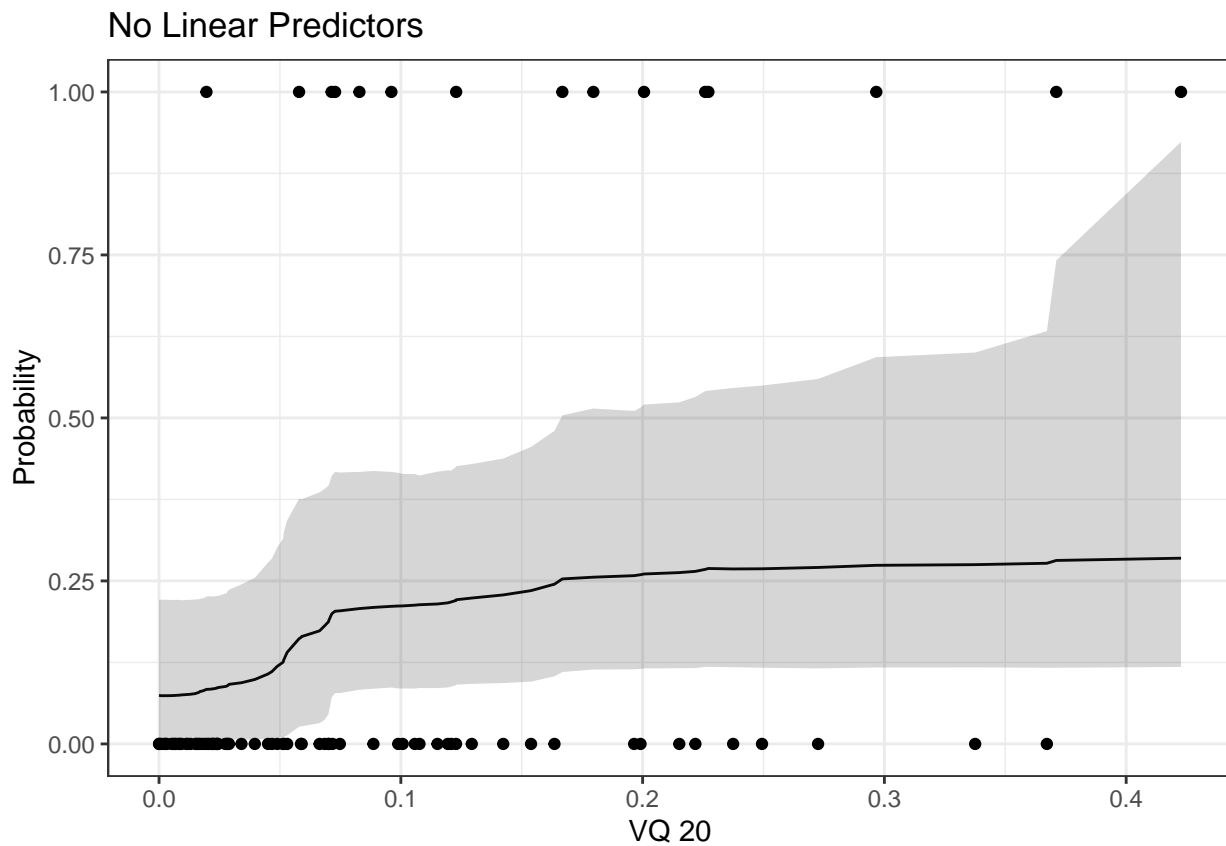
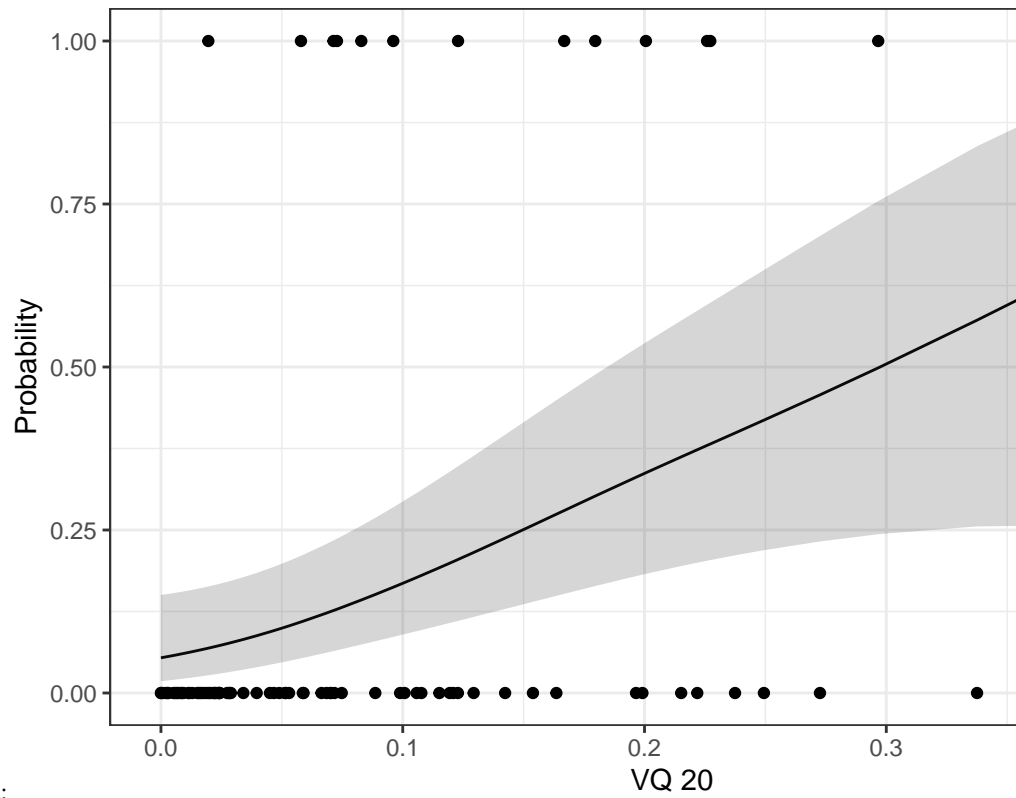## Lung Location and ADL as Linear Predictors

| Variable	Median OR	Mean OR	Lower	Upper
ADL	1.06	1.06	1.02	1.11
RightLung	0.75	0.76	0.21	2.87

Things I could change:

- I could also constrain this to be monotonic, but I haven't done that yet and the fit doesn't seem to suffer that much for it.

- I could try modeling ADL as a second HPR term.

No Linear Predictors

For comparison, the results from GPR:

Lung Location and ADL as Linear Predictors
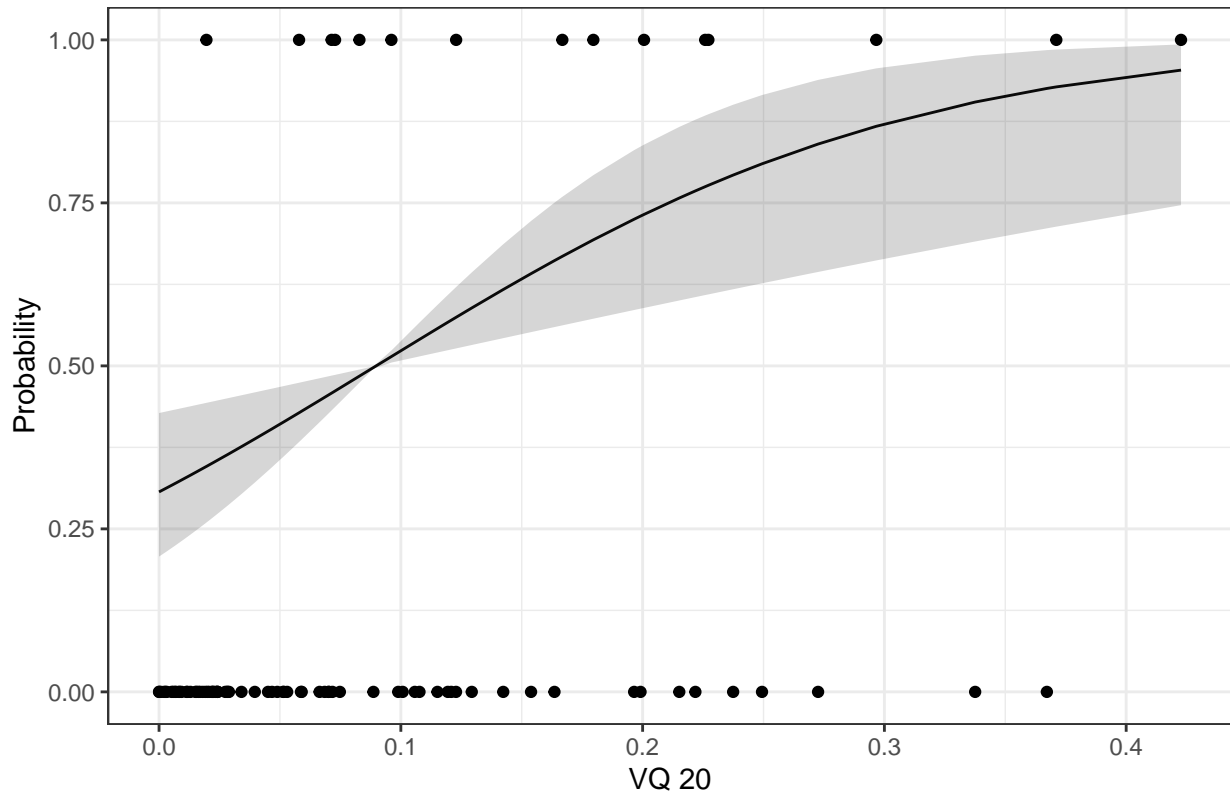
Variable	OR	Lower	Upper
RightLung	0.76	0.21	2.75
ADL	1.06	1.01	1.10