

# Preoperative Atelectasis

## Part 6: Statistical Modelling of SpO2

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### Setup

#### Packages used

```
if (!require("pacman", quietly = TRUE)) {  
  install.packages("pacman")  
}  
  
pacman::p_load(  
  tidyverse, # Used for basic data handling and visualization.  
  RColorBrewer, #Color palettes for data visualization.  
  table1, #Used to add lables to variables.
```

```

gridExtra, #Used to arrange multiple ggplots in a grid.
grid, #Used to arrange multiple ggplots in a grid.
mgcv, #Used to model non-linear relationships with a general additive model.
gt, #Used to present a summary of the results of regression models.
gtsummary, #Used to create table to summarize regression models.
gratia #Used together with ggplot2 to create smooth partial effects plot
      # from gam models.
)

```

## Session and package dependencies

```

R version 4.3.2 (2023-10-31 ucrt)
Platform: x86_64-w64-mingw32/x64 (64-bit)
Running under: Windows 11 x64 (build 22621)

```

Matrix products: default

locale:

```

[1] LC_COLLATE=Spanish_Mexico.utf8  LC_CTYPE=Spanish_Mexico.utf8
[3] LC_MONETARY=Spanish_Mexico.utf8 LC_NUMERIC=C
[5] LC_TIME=Spanish_Mexico.utf8

```

time zone: Europe/Berlin

tzcode source: internal

attached base packages:

```

[1] grid      stats      graphics  grDevices utils      datasets  methods
[8] base

```

other attached packages:

```

[1] gratia_0.8.1      gtsummary_1.7.2   gt_0.10.0         mgcv_1.9-0
[5] nlme_3.1-164      gridExtra_2.3     table1_1.4.3      RColorBrewer_1.1-3
[9] lubridate_1.9.3   forcats_1.0.0     stringr_1.5.1     dplyr_1.1.4
[13] purrr_1.0.2       readr_2.1.4       tidyr_1.3.0       tibble_3.2.1
[17] ggplot2_3.4.4     tidyverse_2.0.0   pacman_0.5.1

```

## Model SpO2

The SpO2 variable does not have a normal distribution. Furthermore, the distance between 1% increases in SpO2 cannot be considered equidistant increases since values are determined from the S-shaped curve of hemoglobin saturation. This is the reason why the distribution of SpO2 is negatively skewed, with upper values reaching the saturation point of the hemoglobin curve.

Therefore, modelling SpO2 as a linear term could be potentially misleading. Nonetheless, a model assuming a gaussian distribution for SpO2 may potentially be easier to understand and communicate.

Thus, I first created model SpO2 assuming a gaussian distribution and then applied a fractional regression model which is more appropriate for the distribution of this variable. The rationale for this was that if conclusions were not different with both models, presenting a model assuming a gaussian distribution would have been easier to understand and communicate. However, since conclusions were indeed different, I will present the results for the more appropriate fractional regression model.

### Fractional regression model

Convert SpO2 to fractional values between 0 and 1 to model.

```
data <- data %>% mutate(spo2_fraction = spo2_VP0/100)
```

### Empty model

First, I will fit an empty model

```
Family: quasibinomial
Link function: logit
```

```
Formula:
spo2_fraction ~ 1
```

```
Parametric coefficients:
```

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  2.94355     0.03744   78.62  <2e-16 ***
```

```
---
```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
R-sq.(adj) =      0    Deviance explained = -3.04e-13%
GCV = 0.015586  Scale est. = 0.015728  n = 236
```

## Smooth BMI

Model with a smooth BMI term as the only explanatory variable.

Since we are now using a different family function (quasibinomial with logit link) and we are no longer assuming a Gaussian distribution, it is important to determine the  $k$  value that offers the best representation of the change in the outcome variable with this function. I checked this by varying the value of  $k$  in the following code and  $k=8^*$  offered the best visual representation with the largest increase in deviance explained and optimal  $k$ .value. This can be replicated by varying the value of  $k$  in the code:

```
Family: quasibinomial
Link function: logit
```

```
Formula:
spo2_fraction ~ s(BMI, k = 8)
```

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.98458	0.03212	92.92	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

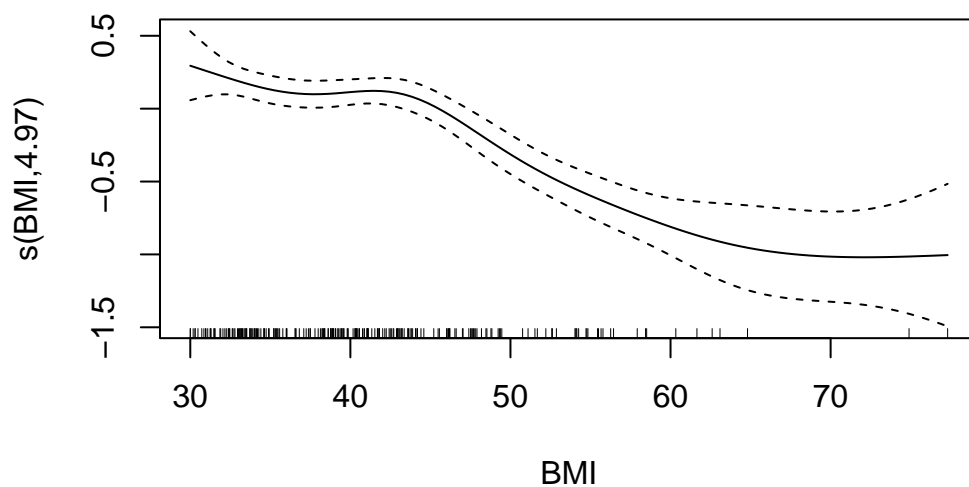
Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(BMI)	4.968	5.829	21.79	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

```
R-sq.(adj) =  0.386    Deviance explained = 34.1%
GCV = 0.010718  Scale est. = 0.010826  n = 236
```



### OSA only

Fit a model that only contains OSA:

Family: quasibinomial

Link function: logit

Formula:

spo2\_fraction ~ sleep\_apnea

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.00191	0.03833	78.326	< 2e-16 ***
sleep_apneaYes	-0.59672	0.10971	-5.439	1.34e-07 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.115 Deviance explained = 10.3%

GCV = 0.014099 Scale est. = 0.014441 n = 236

### Atelectasis percent

Fit a model that only contains atelectasis percent:

Family: quasibinomial

Link function: logit

Formula:

spo2\_fraction ~ atelectasis\_percent\_factor

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	3.31028	0.03416	96.903	< 2e-16	***
atelectasis_percent_factor2.5%	-0.54251	0.10713	-5.064	8.45e-07	***
atelectasis_percent_factor5%	-0.79798	0.08751	-9.118	< 2e-16	***
atelectasis_percent_factor7.5%	-0.87205	0.06127	-14.233	< 2e-16	***
atelectasis_percent_factor10%	-0.99665	0.11831	-8.424	4.10e-15	***
atelectasis_percent_factor12.5%	-0.86794	0.29467	-2.945	0.00356	**
atelectasis_percent_factor15%	-0.99665	0.14287	-6.976	3.26e-11	***
atelectasis_percent_factor17.5%	-1.21954	0.09601	-12.703	< 2e-16	***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

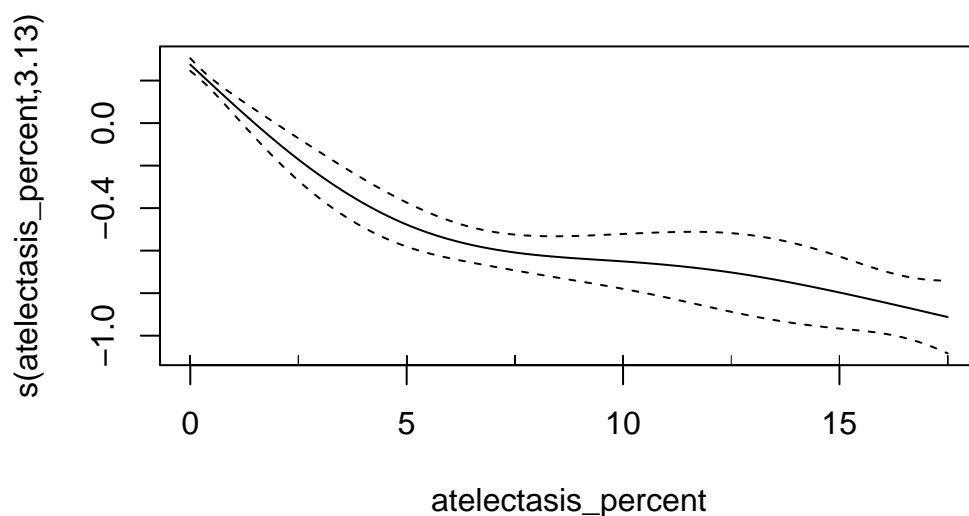
R-sq.(adj) = 0.676 Deviance explained = 62.6%

GCV = 0.006189 Scale est. = 0.0063048 n = 236

### Atelectasis percent smooth term

Fit a model that contains atelectasis percent under a smooth term.

Note that this is a different function than models created in Part 4 since a gaussian function is no longer used. Thus, I determined the optimal k value which is  $k=5$ . This is comparable to having atelectasis percentage as categorical as will be shown later. However, the smooth term will allow to have a visual representation of the partial effect of atelectasis percent on SpO2. Thus, I will keep the smooth term to model the effect of atelectasis.



Family: quasibinomial

Link function: logit

Formula:

spo2\_fraction ~ s(atelectasis\_percent, k = 5)

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.02654	0.02526	119.8	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(atelectasis_percent)	3.131	3.592	105.3	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.676 Deviance explained = 62.3%

GCV = 0.0060413 Scale est. = 0.0062171 n = 236

**s(BMI) + s(atelectasis percentage)**

Fit model sBMI plus atelectasis percentage:

Family: quasibinomial

Link function: logit

Formula:

spo2\_fraction ~ s(BMI, k = 8) + s(atelectasis\_percent, k = 5)

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.02704	0.02516	120.3	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(BMI)	3.461	4.248	1.12	0.314
s(atelectasis_percent)	3.059	3.524	54.23	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.688 Deviance explained = 63.3%

GCV = 0.0060456 Scale est. = 0.0061669 n = 236

## OSA + BMI

Model sleep apnea plus sBMI:

Family: quasibinomial

Link function: logit

Formula:

spo2\_fraction ~ s(BMI, k = 8) + sleep\_apnea

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.02564	0.03246	93.208	< 2e-16 ***
sleep_apneaYes	-0.45017	0.09492	-4.743	3.71e-06 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1



Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(BMI)	5.055	5.91	19.95	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.43 Deviance explained = 39.8%

GCV = 0.0098803 Scale est. = 0.0099659 n = 236

### **sBMI + OSA + atelectasis percent**

Model sBMI + sleep apnea + atelectasis percent:

Family: quasibinomial

Link function: logit

Formula:

spo2\_fraction ~ s(BMI, k = 8) + sleep\_apnea + s(atelectasis\_percent,  
k = 5)

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.03409	0.02603	116.576	<2e-16 ***
sleep_apneaYes	-0.09196	0.07673	-1.199	0.232

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(BMI)	1.083	1.160	1.794	0.192
s(atelectasis_percent)	3.091	3.554	49.259	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.681 Deviance explained = 62.8%

GCV = 0.0060627 Scale est. = 0.0062147 n = 236

### **Adjusted model BMI**

Fit model for BMI adjusted for confounders:

Family: quasibinomial  
Link function: logit

Formula:

spo2\_fraction ~ s(BMI, k = 8) + sex + age + sleep\_apnea + hb +  
altitude\_cat

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.528269	0.428386	8.236	1.50e-14 ***
sexWoman	-0.117513	0.112300	-1.046	0.296
age	-0.001045	0.003139	-0.333	0.740
sleep_apneaYes	-0.474332	0.102125	-4.645	5.82e-06 ***
hb	-0.024104	0.026525	-0.909	0.364
altitude_catModerate altitude	-0.028400	0.088623	-0.320	0.749

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(BMI)	5.032	5.886	19.54	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.424 Deviance explained = 40.5%  
GCV = 0.010074 Scale est. = 0.0099703 n = 234

### Adjusted model Atelectasis Percent

Fit model for atelectasis percent adjusted for confounders:

Family: quasibinomial  
Link function: logit

Formula:

spo2\_fraction ~ s(atelectasis\_percent, k = 5) + sex + age + sleep\_apnea +  
hb + altitude\_cat

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	2.9670765	0.3292438	9.012	<2e-16 ***
sexWoman	-0.0317677	0.0875122	-0.363	0.717

age	-0.0003715	0.0024969	-0.149	0.882
sleep_apneaYes	-0.0973732	0.0836521	-1.164	0.246
hb	0.0079574	0.0203634	0.391	0.696
altitude_catModerate altitude	-0.0525988	0.0688772	-0.764	0.446

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(atelectasis_percent)	3.099	3.563	89.51	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.678 Deviance explained = 63.2%

GCV = 0.0061173 Scale est. = 0.0061931 n = 234

### Fully adjusted model

Fit fully adjusted model including both BMI and atelectasis percentage:

Family: quasibinomial

Link function: logit

Formula:

spo2\_fraction ~ s(BMI, k = 8) + s(atelectasis\_percent, k = 5) +  
sex + age + sleep\_apnea + hb + altitude\_cat

Parametric coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	3.0862682	0.3351823	9.208	<2e-16 ***
sexWoman	-0.0680870	0.0900036	-0.756	0.450
age	-0.0008286	0.0025147	-0.329	0.742
sleep_apneaYes	-0.1097329	0.0844916	-1.299	0.195
hb	0.0032139	0.0205653	0.156	0.876
altitude_catModerate altitude	-0.0350273	0.0699253	-0.501	0.617

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Approximate significance of smooth terms:

	edf	Ref.df	F	p-value
s(BMI)	3.244	4.015	1.063	0.366
s(atelectasis_percent)	2.998	3.469	45.713	<2e-16 ***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

R-sq.(adj) = 0.687 Deviance explained = 64.2%

GCV = 0.0061332 Scale est. = 0.0061365 n = 234

Build a dataframe to compare models:

Sort by deviance

	Model	aR2	dev
1	Fully_adjusted	68.7	64.2
2	sBMI_atel	68.8	63.3
3	adjusted_atelectasis	67.8	63.2
4	sBMI_atel_OSA	68.1	62.8
5	atel_only	67.6	62.6
6	atel_smooth	67.6	62.3
7	adjusted_BMI	42.4	40.5
8	sBMI_OSA	43.0	39.8
9	sBMI	38.6	34.1
10	OSA_only	11.5	10.3
11	empty	0.0	0.0

Sort by R2

	Model	aR2	dev
1	sBMI_atel	68.8	63.3
2	Fully_adjusted	68.7	64.2
3	sBMI_atel_OSA	68.1	62.8
4	adjusted_atelectasis	67.8	63.2
5	atel_only	67.6	62.6
6	atel_smooth	67.6	62.3
7	sBMI_OSA	43.0	39.8
8	adjusted_BMI	42.4	40.5
9	sBMI	38.6	34.1
10	OSA_only	11.5	10.3
11	empty	0.0	0.0

**Table S2**

Create table for models:

Group	Characteristic	OR	95% CI	p-value
BMI only	s(BMI)			<0.001
OSA only	Obstructive sleep apnea			
	No	—	—	
	Yes	0.55	0.44, 0.68	<0.001
Atelectasis percent only	s(atelectasis_percent)			<0.001
BMI + OSA	Obstructive sleep apnea			
	No	—	—	
	Yes	0.64	0.53, 0.77	<0.001
BMI + Atelectasis percent	s(BMI)			<0.001
	s(BMI)			0.3
	s(atelectasis_percent)			<0.001
BMI + OSA + Atelectasis percent	Obstructive sleep apnea			
	No	—	—	
	Yes	0.91	0.78, 1.06	0.2
	s(BMI)			0.2
	s(atelectasis_percent)			<0.001
BMI + OSA + age + sex + hb + altitude	Sex			
	Man	—	—	
	Woman	0.89	0.71, 1.11	0.3
	Age	1.00	0.99, 1.01	0.7
	Obstructive sleep apnea			
	No	—	—	
	Yes	0.62	0.51, 0.76	<0.001
	Hemoglobin	0.98	0.93, 1.03	0.4
	altitude_cat			

Group	Characteristic	OR	95% CI	p-value
Atelectasis percent + OSA + age + sex + hb + altitude	Low altitude	—	—	0.7
	Moderate altitude	0.97	0.82, 1.16	
	s(BMI)			<0.001
	Sex			
	Man	—	—	0.7
	Woman	0.97	0.82, 1.15	
	Age	1.00	1.0, 1.00	0.9
	Obstructive sleep apnea			
	No	—	—	0.2
	Yes	0.91	0.77, 1.07	
	Hemoglobin	1.01	0.97, 1.05	0.7
	altitude_cat			
	Low altitude	—	—	0.4
	Moderate altitude	0.95	0.83, 1.09	
Fully adjusted model	s(atelectasis_percent)			<0.001
	Sex			
	Man	—	—	0.5
	Woman	0.93	0.78, 1.11	
	Age	1.00	0.99, 1.00	0.7
	Obstructive sleep apnea			
	No	—	—	0.2
	Yes	0.90	0.76, 1.06	
	Hemoglobin	1.00	0.96, 1.04	0.9
	altitude_cat			
	Low altitude	—	—	0.6
	Moderate altitude	0.97	0.84, 1.11	
	s(BMI)			0.4

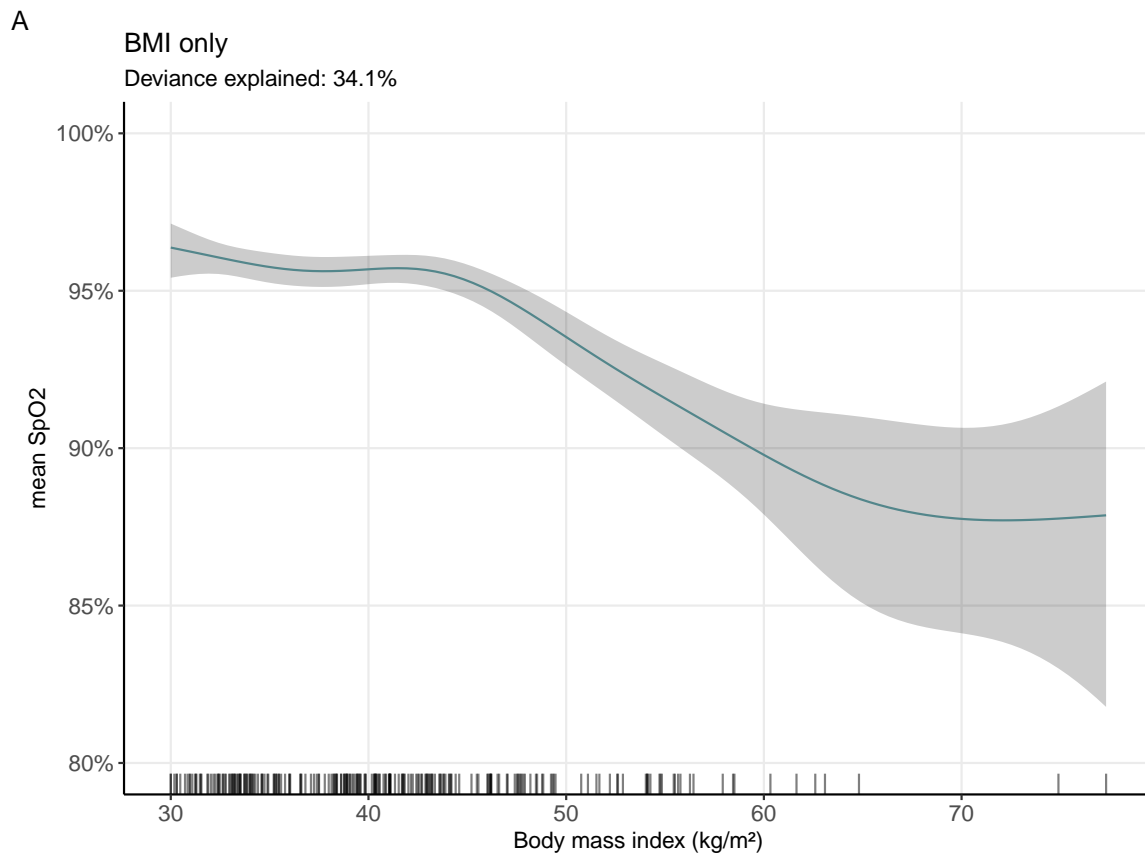
Save Table S2

### Figure SpO2:

#### Figure 3a: sBMI

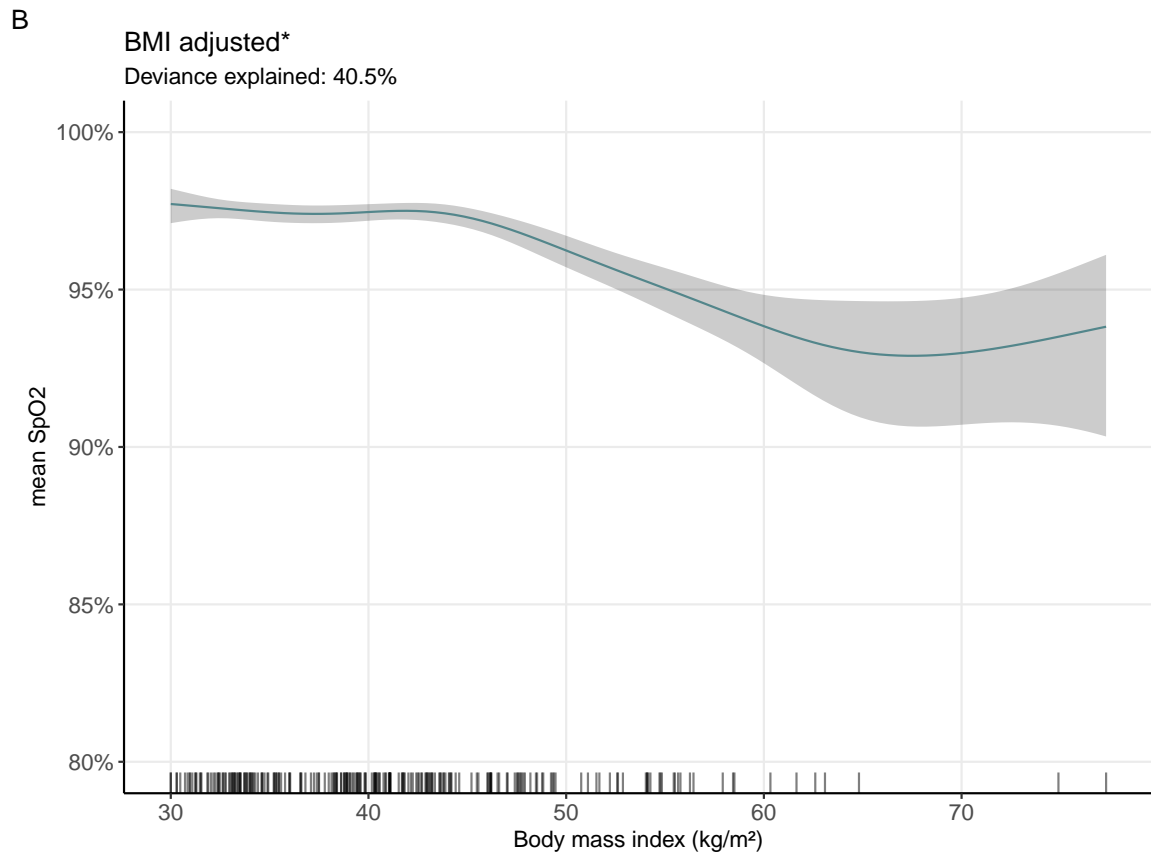
Now, take the inverse logit function to assess partial effect on mean SpO2.

Partial effect on mean SpO2:



#### Figure 3b: sBMI\_adjusted

Partial effect on mean SpO2:

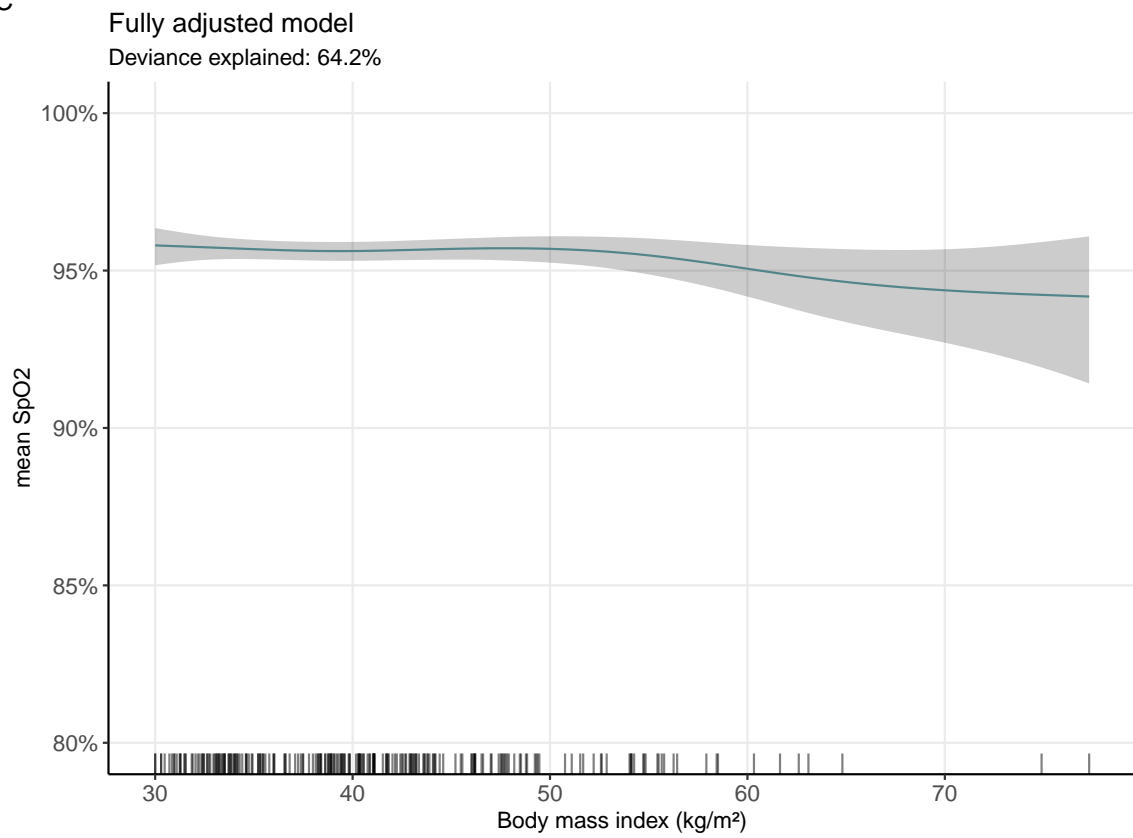


**Figure 3c: Fully adjusted BMI**

Partial effect on mean SpO2:



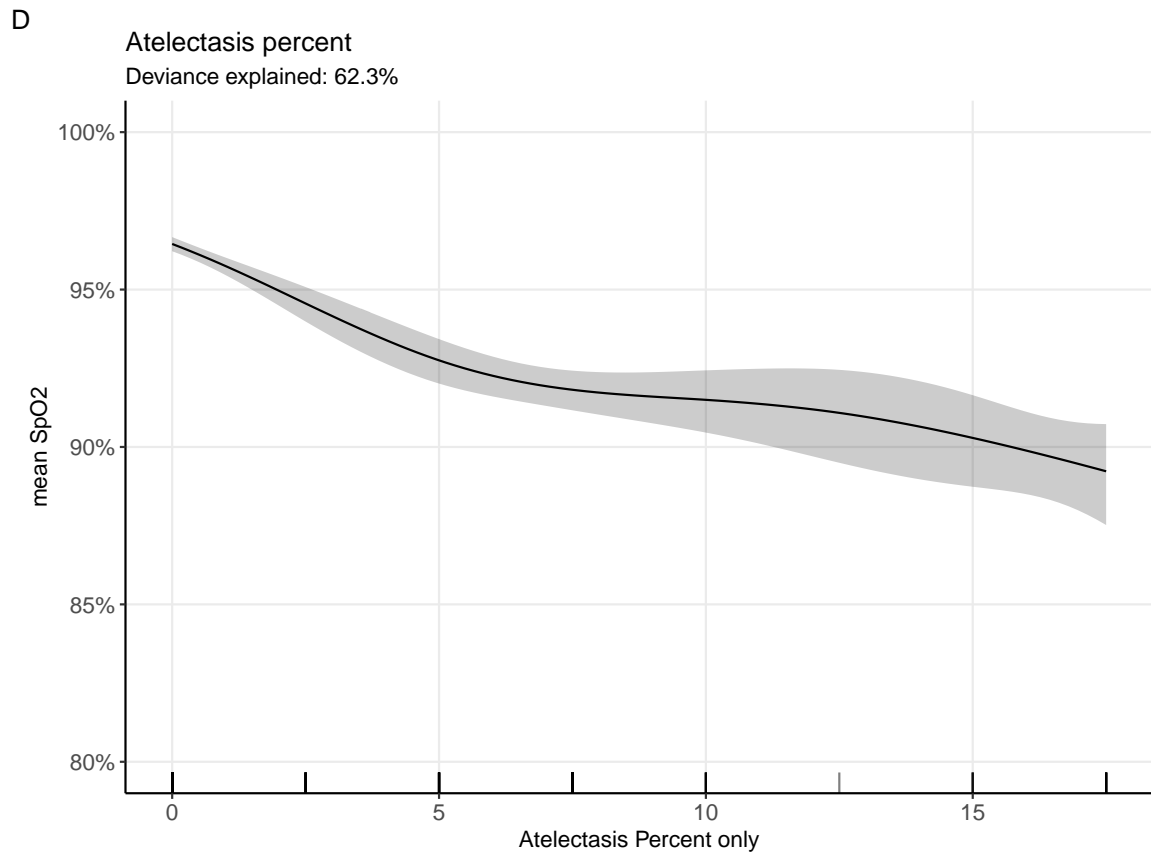
C



**Figure 3d: sAtelectasis percent**

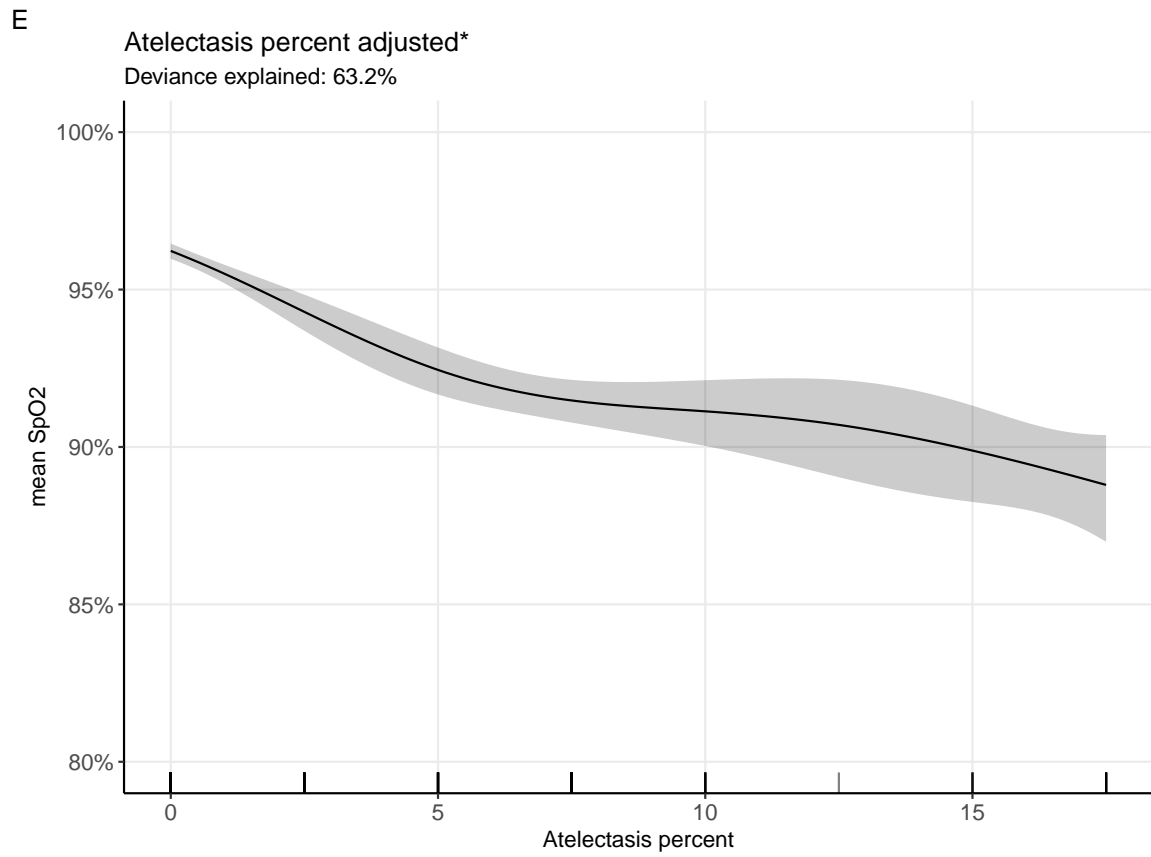
Check residuals:

Draw a personalized plot:



**Figure 3e: Atelectasis percent adjusted**

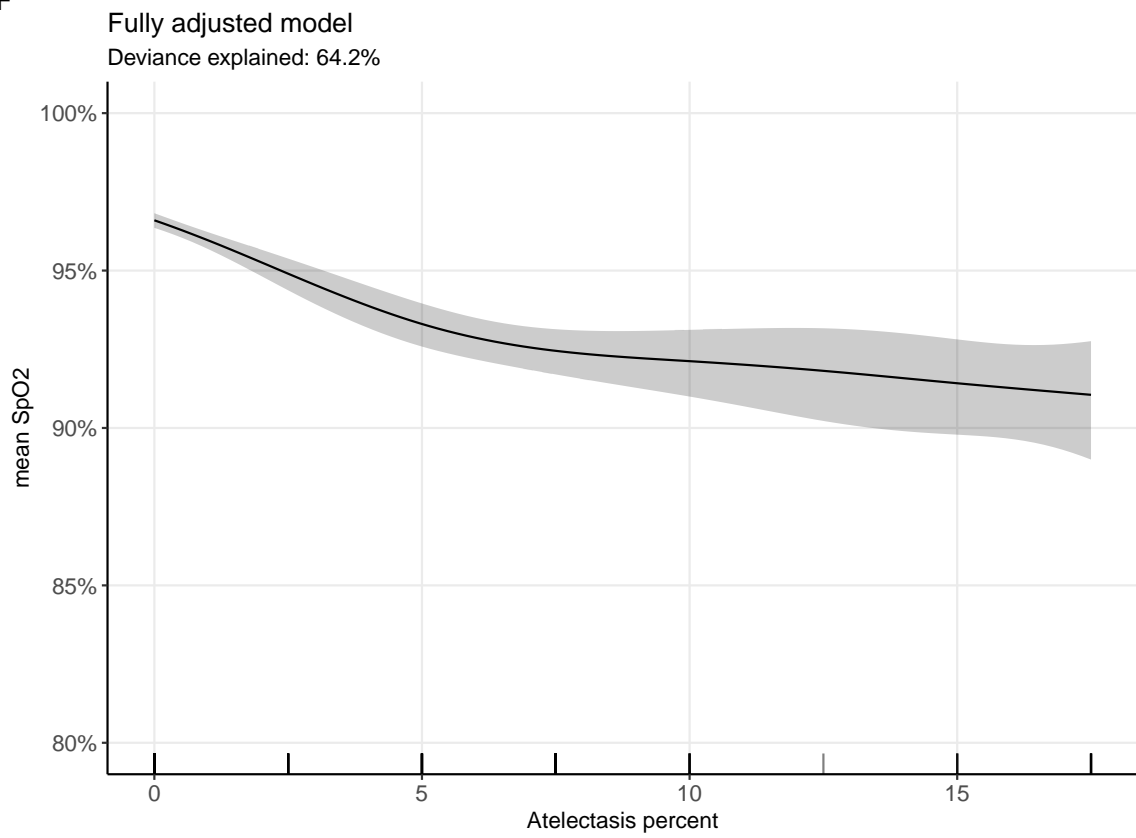
Partial effect on mean SpO2:



**Figure 3f: Fully adjusted Atelectasis Percent**

Partial effect on mean SpO2:

F



**Figure 3**

