Final project quarto

library(gtsummary)

#StandWithUkraine

load(here::here("data","diabetes.rda"))

library(gtsummary)  
library(dplyr)

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':  
  
 filter, lag

The following objects are masked from 'package:base':  
  
 intersect, setdiff, setequal, union

library(haven)  
  
  
  
diabetes <- diabetes %>%  
 rename\_all(~ gsub("-", "\_", .))  
  
# Generate the summary table  
summary\_table <- tbl\_summary(  
 diabetes,  
 label = list(  
 pregnancy\_num = "num of Pregnancies",  
 glucose\_mg\_dl = "Glucose concentration (mg/dl)",  
 dbp\_mm\_hg = "dose of theophylline (mm/hg)",  
 triceps\_mm = "tricep thickness (mm)",  
 insulin\_microiu\_ml = "serum insulin levels (mL)",  
 bmi = "BMI",  
 pedigree = "Pedigree score",  
 age = "Age (yrs)")  
)  
  
# Customize summary table statistics  
statistic <- list(  
 all\_continuous() ~ "{mean} ({sd})",  
 all\_categorical() ~ "{n} / {N} ({p}%)",  
 age ~ "{mean}"  
)  
  
# Generate tidy parameters  
tidy\_fun <- broom.helpers::tidy\_parameters  
  
# Print the summary table  
summary\_table

Table printed with `knitr::kable()`, not {gt}. Learn why at  
https://www.danieldsjoberg.com/gtsummary/articles/rmarkdown.html  
To suppress this message, include `message = FALSE` in the code chunk header.

| **Characteristic** | **N = 768** |
| --- | --- |
| num of Pregnancies | 3.0 (1.0, 6.0) |
| Glucose concentration (mg/dl) | 117 (99, 141) |
| Unknown | 5 |
| dose of theophylline (mm/hg) | 72 (64, 80) |
| Unknown | 35 |
| tricep thickness (mm) | 29 (22, 36) |
| Unknown | 227 |
| serum insulin levels (mL) | 125 (76, 190) |
| Unknown | 374 |
| BMI | 32 (28, 37) |
| Unknown | 11 |
| Pedigree score | 0.37 (0.24, 0.63) |
| Age (yrs) | 29 (24, 41) |
| diabetes\_5y |  |
| neg | 500 (65%) |
| pos | 268 (35%) |

library(gtsummary)  
library(haven)  
  
   
diabetes

pregnancy\_num glucose\_mg\_dl dbp\_mm\_hg triceps\_mm insulin\_microiu\_ml bmi  
1 6 148 72 35 NA 33.6  
2 1 85 66 29 NA 26.6  
3 8 183 64 NA NA 23.3  
4 1 89 66 23 94 28.1  
5 0 137 40 35 168 43.1  
6 5 116 74 NA NA 25.6  
7 3 78 50 32 88 31.0  
8 10 115 NA NA NA 35.3  
9 2 197 70 45 543 30.5  
10 8 125 96 NA NA NA  
11 4 110 92 NA NA 37.6  
12 10 168 74 NA NA 38.0  
13 10 139 80 NA NA 27.1  
14 1 189 60 23 846 30.1  
15 5 166 72 19 175 25.8  
16 7 100 NA NA NA 30.0  
17 0 118 84 47 230 45.8  
18 7 107 74 NA NA 29.6  
19 1 103 30 38 83 43.3  
20 1 115 70 30 96 34.6  
21 3 126 88 41 235 39.3  
22 8 99 84 NA NA 35.4  
23 7 196 90 NA NA 39.8  
24 9 119 80 35 NA 29.0  
25 11 143 94 33 146 36.6  
26 10 125 70 26 115 31.1  
27 7 147 76 NA NA 39.4  
28 1 97 66 15 140 23.2  
29 13 145 82 19 110 22.2  
30 5 117 92 NA NA 34.1  
31 5 109 75 26 NA 36.0  
32 3 158 76 36 245 31.6  
33 3 88 58 11 54 24.8  
34 6 92 92 NA NA 19.9  
35 10 122 78 31 NA 27.6  
36 4 103 60 33 192 24.0  
37 11 138 76 NA NA 33.2  
38 9 102 76 37 NA 32.9  
39 2 90 68 42 NA 38.2  
40 4 111 72 47 207 37.1  
41 3 180 64 25 70 34.0  
42 7 133 84 NA NA 40.2  
43 7 106 92 18 NA 22.7  
44 9 171 110 24 240 45.4  
45 7 159 64 NA NA 27.4  
46 0 180 66 39 NA 42.0  
47 1 146 56 NA NA 29.7  
48 2 71 70 27 NA 28.0  
49 7 103 66 32 NA 39.1  
50 7 105 NA NA NA NA  
51 1 103 80 11 82 19.4  
52 1 101 50 15 36 24.2  
53 5 88 66 21 23 24.4  
54 8 176 90 34 300 33.7  
55 7 150 66 42 342 34.7  
56 1 73 50 10 NA 23.0  
57 7 187 68 39 304 37.7  
58 0 100 88 60 110 46.8  
59 0 146 82 NA NA 40.5  
60 0 105 64 41 142 41.5  
61 2 84 NA NA NA NA  
62 8 133 72 NA NA 32.9  
63 5 44 62 NA NA 25.0  
64 2 141 58 34 128 25.4  
65 7 114 66 NA NA 32.8  
66 5 99 74 27 NA 29.0  
67 0 109 88 30 NA 32.5  
68 2 109 92 NA NA 42.7  
69 1 95 66 13 38 19.6  
70 4 146 85 27 100 28.9  
71 2 100 66 20 90 32.9  
72 5 139 64 35 140 28.6  
73 13 126 90 NA NA 43.4  
74 4 129 86 20 270 35.1  
75 1 79 75 30 NA 32.0  
76 1 NA 48 20 NA 24.7  
77 7 62 78 NA NA 32.6  
78 5 95 72 33 NA 37.7  
79 0 131 NA NA NA 43.2  
80 2 112 66 22 NA 25.0  
81 3 113 44 13 NA 22.4  
82 2 74 NA NA NA NA  
83 7 83 78 26 71 29.3  
84 0 101 65 28 NA 24.6  
85 5 137 108 NA NA 48.8  
86 2 110 74 29 125 32.4  
87 13 106 72 54 NA 36.6  
88 2 100 68 25 71 38.5  
89 15 136 70 32 110 37.1  
90 1 107 68 19 NA 26.5  
91 1 80 55 NA NA 19.1  
92 4 123 80 15 176 32.0  
93 7 81 78 40 48 46.7  
94 4 134 72 NA NA 23.8  
95 2 142 82 18 64 24.7  
96 6 144 72 27 228 33.9  
97 2 92 62 28 NA 31.6  
98 1 71 48 18 76 20.4  
99 6 93 50 30 64 28.7  
100 1 122 90 51 220 49.7  
101 1 163 72 NA NA 39.0  
102 1 151 60 NA NA 26.1  
103 0 125 96 NA NA 22.5  
104 1 81 72 18 40 26.6  
105 2 85 65 NA NA 39.6  
106 1 126 56 29 152 28.7  
107 1 96 122 NA NA 22.4  
108 4 144 58 28 140 29.5  
109 3 83 58 31 18 34.3  
110 0 95 85 25 36 37.4  
111 3 171 72 33 135 33.3  
112 8 155 62 26 495 34.0  
113 1 89 76 34 37 31.2  
114 4 76 62 NA NA 34.0  
115 7 160 54 32 175 30.5  
116 4 146 92 NA NA 31.2  
117 5 124 74 NA NA 34.0  
118 5 78 48 NA NA 33.7  
119 4 97 60 23 NA 28.2  
120 4 99 76 15 51 23.2  
121 0 162 76 56 100 53.2  
122 6 111 64 39 NA 34.2  
123 2 107 74 30 100 33.6  
124 5 132 80 NA NA 26.8  
125 0 113 76 NA NA 33.3  
126 1 88 30 42 99 55.0  
127 3 120 70 30 135 42.9  
128 1 118 58 36 94 33.3  
129 1 117 88 24 145 34.5  
130 0 105 84 NA NA 27.9  
131 4 173 70 14 168 29.7  
132 9 122 56 NA NA 33.3  
133 3 170 64 37 225 34.5  
134 8 84 74 31 NA 38.3  
135 2 96 68 13 49 21.1  
136 2 125 60 20 140 33.8  
137 0 100 70 26 50 30.8  
138 0 93 60 25 92 28.7  
139 0 129 80 NA NA 31.2  
140 5 105 72 29 325 36.9  
141 3 128 78 NA NA 21.1  
142 5 106 82 30 NA 39.5  
143 2 108 52 26 63 32.5  
144 10 108 66 NA NA 32.4  
145 4 154 62 31 284 32.8  
146 0 102 75 23 NA NA  
147 9 57 80 37 NA 32.8  
148 2 106 64 35 119 30.5  
149 5 147 78 NA NA 33.7  
150 2 90 70 17 NA 27.3  
151 1 136 74 50 204 37.4  
152 4 114 65 NA NA 21.9  
153 9 156 86 28 155 34.3  
154 1 153 82 42 485 40.6  
155 8 188 78 NA NA 47.9  
156 7 152 88 44 NA 50.0  
157 2 99 52 15 94 24.6  
158 1 109 56 21 135 25.2  
159 2 88 74 19 53 29.0  
160 17 163 72 41 114 40.9  
161 4 151 90 38 NA 29.7  
162 7 102 74 40 105 37.2  
163 0 114 80 34 285 44.2  
164 2 100 64 23 NA 29.7  
165 0 131 88 NA NA 31.6  
166 6 104 74 18 156 29.9  
167 3 148 66 25 NA 32.5  
168 4 120 68 NA NA 29.6  
169 4 110 66 NA NA 31.9  
170 3 111 90 12 78 28.4  
171 6 102 82 NA NA 30.8  
172 6 134 70 23 130 35.4  
173 2 87 NA 23 NA 28.9  
174 1 79 60 42 48 43.5  
175 2 75 64 24 55 29.7  
176 8 179 72 42 130 32.7  
177 6 85 78 NA NA 31.2  
178 0 129 110 46 130 67.1  
179 5 143 78 NA NA 45.0  
180 5 130 82 NA NA 39.1  
181 6 87 80 NA NA 23.2  
182 0 119 64 18 92 34.9  
183 1 NA 74 20 23 27.7  
184 5 73 60 NA NA 26.8  
185 4 141 74 NA NA 27.6  
186 7 194 68 28 NA 35.9  
187 8 181 68 36 495 30.1  
188 1 128 98 41 58 32.0  
189 8 109 76 39 114 27.9  
190 5 139 80 35 160 31.6  
191 3 111 62 NA NA 22.6  
192 9 123 70 44 94 33.1  
193 7 159 66 NA NA 30.4  
194 11 135 NA NA NA 52.3  
195 8 85 55 20 NA 24.4  
196 5 158 84 41 210 39.4  
197 1 105 58 NA NA 24.3  
198 3 107 62 13 48 22.9  
199 4 109 64 44 99 34.8  
200 4 148 60 27 318 30.9  
201 0 113 80 16 NA 31.0  
202 1 138 82 NA NA 40.1  
203 0 108 68 20 NA 27.3  
204 2 99 70 16 44 20.4  
205 6 103 72 32 190 37.7  
206 5 111 72 28 NA 23.9  
207 8 196 76 29 280 37.5  
208 5 162 104 NA NA 37.7  
209 1 96 64 27 87 33.2  
210 7 184 84 33 NA 35.5  
211 2 81 60 22 NA 27.7  
212 0 147 85 54 NA 42.8  
213 7 179 95 31 NA 34.2  
214 0 140 65 26 130 42.6  
215 9 112 82 32 175 34.2  
216 12 151 70 40 271 41.8  
217 5 109 62 41 129 35.8  
218 6 125 68 30 120 30.0  
219 5 85 74 22 NA 29.0  
220 5 112 66 NA NA 37.8  
221 0 177 60 29 478 34.6  
222 2 158 90 NA NA 31.6  
223 7 119 NA NA NA 25.2  
224 7 142 60 33 190 28.8  
225 1 100 66 15 56 23.6  
226 1 87 78 27 32 34.6  
227 0 101 76 NA NA 35.7  
228 3 162 52 38 NA 37.2  
229 4 197 70 39 744 36.7  
230 0 117 80 31 53 45.2  
231 4 142 86 NA NA 44.0  
232 6 134 80 37 370 46.2  
233 1 79 80 25 37 25.4  
234 4 122 68 NA NA 35.0  
235 3 74 68 28 45 29.7  
236 4 171 72 NA NA 43.6  
237 7 181 84 21 192 35.9  
238 0 179 90 27 NA 44.1  
239 9 164 84 21 NA 30.8  
240 0 104 76 NA NA 18.4  
241 1 91 64 24 NA 29.2  
242 4 91 70 32 88 33.1  
243 3 139 54 NA NA 25.6  
244 6 119 50 22 176 27.1  
245 2 146 76 35 194 38.2  
246 9 184 85 15 NA 30.0  
247 10 122 68 NA NA 31.2  
248 0 165 90 33 680 52.3  
249 9 124 70 33 402 35.4  
250 1 111 86 19 NA 30.1  
251 9 106 52 NA NA 31.2  
252 2 129 84 NA NA 28.0  
253 2 90 80 14 55 24.4  
254 0 86 68 32 NA 35.8  
255 12 92 62 7 258 27.6  
256 1 113 64 35 NA 33.6  
257 3 111 56 39 NA 30.1  
258 2 114 68 22 NA 28.7  
259 1 193 50 16 375 25.9  
260 11 155 76 28 150 33.3  
261 3 191 68 15 130 30.9  
262 3 141 NA NA NA 30.0  
263 4 95 70 32 NA 32.1  
264 3 142 80 15 NA 32.4  
265 4 123 62 NA NA 32.0  
266 5 96 74 18 67 33.6  
267 0 138 NA NA NA 36.3  
268 2 128 64 42 NA 40.0  
269 0 102 52 NA NA 25.1  
270 2 146 NA NA NA 27.5  
271 10 101 86 37 NA 45.6  
272 2 108 62 32 56 25.2  
273 3 122 78 NA NA 23.0  
274 1 71 78 50 45 33.2  
275 13 106 70 NA NA 34.2  
276 2 100 70 52 57 40.5  
277 7 106 60 24 NA 26.5  
278 0 104 64 23 116 27.8  
279 5 114 74 NA NA 24.9  
280 2 108 62 10 278 25.3  
281 0 146 70 NA NA 37.9  
282 10 129 76 28 122 35.9  
283 7 133 88 15 155 32.4  
284 7 161 86 NA NA 30.4  
285 2 108 80 NA NA 27.0  
286 7 136 74 26 135 26.0  
287 5 155 84 44 545 38.7  
288 1 119 86 39 220 45.6  
289 4 96 56 17 49 20.8  
290 5 108 72 43 75 36.1  
291 0 78 88 29 40 36.9  
292 0 107 62 30 74 36.6  
293 2 128 78 37 182 43.3  
294 1 128 48 45 194 40.5  
295 0 161 50 NA NA 21.9  
296 6 151 62 31 120 35.5  
297 2 146 70 38 360 28.0  
298 0 126 84 29 215 30.7  
299 14 100 78 25 184 36.6  
300 8 112 72 NA NA 23.6  
301 0 167 NA NA NA 32.3  
302 2 144 58 33 135 31.6  
303 5 77 82 41 42 35.8  
304 5 115 98 NA NA 52.9  
305 3 150 76 NA NA 21.0  
306 2 120 76 37 105 39.7  
307 10 161 68 23 132 25.5  
308 0 137 68 14 148 24.8  
309 0 128 68 19 180 30.5  
310 2 124 68 28 205 32.9  
311 6 80 66 30 NA 26.2  
312 0 106 70 37 148 39.4  
313 2 155 74 17 96 26.6  
314 3 113 50 10 85 29.5  
315 7 109 80 31 NA 35.9  
316 2 112 68 22 94 34.1  
317 3 99 80 11 64 19.3  
318 3 182 74 NA NA 30.5  
319 3 115 66 39 140 38.1  
320 6 194 78 NA NA 23.5  
321 4 129 60 12 231 27.5  
322 3 112 74 30 NA 31.6  
323 0 124 70 20 NA 27.4  
324 13 152 90 33 29 26.8  
325 2 112 75 32 NA 35.7  
326 1 157 72 21 168 25.6  
327 1 122 64 32 156 35.1  
328 10 179 70 NA NA 35.1  
329 2 102 86 36 120 45.5  
330 6 105 70 32 68 30.8  
331 8 118 72 19 NA 23.1  
332 2 87 58 16 52 32.7  
333 1 180 NA NA NA 43.3  
334 12 106 80 NA NA 23.6  
335 1 95 60 18 58 23.9  
336 0 165 76 43 255 47.9  
337 0 117 NA NA NA 33.8  
338 5 115 76 NA NA 31.2  
339 9 152 78 34 171 34.2  
340 7 178 84 NA NA 39.9  
341 1 130 70 13 105 25.9  
342 1 95 74 21 73 25.9  
343 1 NA 68 35 NA 32.0  
344 5 122 86 NA NA 34.7  
345 8 95 72 NA NA 36.8  
346 8 126 88 36 108 38.5  
347 1 139 46 19 83 28.7  
348 3 116 NA NA NA 23.5  
349 3 99 62 19 74 21.8  
350 5 NA 80 32 NA 41.0  
351 4 92 80 NA NA 42.2  
352 4 137 84 NA NA 31.2  
353 3 61 82 28 NA 34.4  
354 1 90 62 12 43 27.2  
355 3 90 78 NA NA 42.7  
356 9 165 88 NA NA 30.4  
357 1 125 50 40 167 33.3  
358 13 129 NA 30 NA 39.9  
359 12 88 74 40 54 35.3  
360 1 196 76 36 249 36.5  
361 5 189 64 33 325 31.2  
362 5 158 70 NA NA 29.8  
363 5 103 108 37 NA 39.2  
364 4 146 78 NA NA 38.5  
365 4 147 74 25 293 34.9  
366 5 99 54 28 83 34.0  
367 6 124 72 NA NA 27.6  
368 0 101 64 17 NA 21.0  
369 3 81 86 16 66 27.5  
370 1 133 102 28 140 32.8  
371 3 173 82 48 465 38.4  
372 0 118 64 23 89 NA  
373 0 84 64 22 66 35.8  
374 2 105 58 40 94 34.9  
375 2 122 52 43 158 36.2  
376 12 140 82 43 325 39.2  
377 0 98 82 15 84 25.2  
378 1 87 60 37 75 37.2  
379 4 156 75 NA NA 48.3  
380 0 93 100 39 72 43.4  
381 1 107 72 30 82 30.8  
382 0 105 68 22 NA 20.0  
383 1 109 60 8 182 25.4  
384 1 90 62 18 59 25.1  
385 1 125 70 24 110 24.3  
386 1 119 54 13 50 22.3  
387 5 116 74 29 NA 32.3  
388 8 105 100 36 NA 43.3  
389 5 144 82 26 285 32.0  
390 3 100 68 23 81 31.6  
391 1 100 66 29 196 32.0  
392 5 166 76 NA NA 45.7  
393 1 131 64 14 415 23.7  
394 4 116 72 12 87 22.1  
395 4 158 78 NA NA 32.9  
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400 3 193 70 31 NA 34.9  
401 4 95 64 NA NA 32.0  
402 6 137 61 NA NA 24.2  
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404 9 72 78 25 NA 31.6  
405 5 168 64 NA NA 32.9  
406 2 123 48 32 165 42.1  
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408 0 101 62 NA NA 21.9  
409 8 197 74 NA NA 25.9  
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411 6 102 90 39 NA 35.7  
412 1 112 72 30 176 34.4  
413 1 143 84 23 310 42.4  
414 1 143 74 22 61 26.2  
415 0 138 60 35 167 34.6  
416 3 173 84 33 474 35.7  
417 1 97 68 21 NA 27.2  
418 4 144 82 32 NA 38.5  
419 1 83 68 NA NA 18.2  
420 3 129 64 29 115 26.4  
421 1 119 88 41 170 45.3  
422 2 94 68 18 76 26.0  
423 0 102 64 46 78 40.6  
424 2 115 64 22 NA 30.8  
425 8 151 78 32 210 42.9  
426 4 184 78 39 277 37.0  
427 0 94 NA NA NA NA  
428 1 181 64 30 180 34.1  
429 0 135 94 46 145 40.6  
430 1 95 82 25 180 35.0  
431 2 99 NA NA NA 22.2  
432 3 89 74 16 85 30.4  
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434 2 139 75 NA NA 25.6  
435 1 90 68 8 NA 24.5  
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438 5 147 75 NA NA 29.9  
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444 8 108 70 NA NA 30.5  
445 4 117 62 12 NA 29.7  
446 0 180 78 63 14 59.4  
447 1 100 72 12 70 25.3  
448 0 95 80 45 92 36.5  
449 0 104 64 37 64 33.6  
450 0 120 74 18 63 30.5  
451 1 82 64 13 95 21.2  
452 2 134 70 NA NA 28.9  
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454 2 119 NA NA NA 19.6  
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456 14 175 62 30 NA 33.6  
457 1 135 54 NA NA 26.7  
458 5 86 68 28 71 30.2  
459 10 148 84 48 237 37.6  
460 9 134 74 33 60 25.9  
461 9 120 72 22 56 20.8  
462 1 71 62 NA NA 21.8  
463 8 74 70 40 49 35.3  
464 5 88 78 30 NA 27.6  
465 10 115 98 NA NA 24.0  
466 0 124 56 13 105 21.8  
467 0 74 52 10 36 27.8  
468 0 97 64 36 100 36.8  
469 8 120 NA NA NA 30.0  
470 6 154 78 41 140 46.1  
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473 0 119 66 27 NA 38.8  
474 7 136 90 NA NA 29.9  
475 4 114 64 NA NA 28.9  
476 0 137 84 27 NA 27.3  
477 2 105 80 45 191 33.7  
478 7 114 76 17 110 23.8  
479 8 126 74 38 75 25.9  
480 4 132 86 31 NA 28.0  
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484 0 84 82 31 125 38.2  
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487 1 139 62 41 480 40.7  
488 0 173 78 32 265 46.5  
489 4 99 72 17 NA 25.6  
490 8 194 80 NA NA 26.1  
491 2 83 65 28 66 36.8  
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493 4 99 68 38 NA 32.8  
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499 7 195 70 33 145 25.1  
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517 9 145 88 34 165 30.3  
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542 3 128 72 25 190 32.4  
543 10 90 85 32 NA 34.9  
544 4 84 90 23 56 39.5  
545 1 88 78 29 76 32.0  
546 8 186 90 35 225 34.5  
547 5 187 76 27 207 43.6  
548 4 131 68 21 166 33.1  
549 1 164 82 43 67 32.8  
550 4 189 110 31 NA 28.5  
551 1 116 70 28 NA 27.4  
552 3 84 68 30 106 31.9  
553 6 114 88 NA NA 27.8  
554 1 88 62 24 44 29.9  
555 1 84 64 23 115 36.9  
556 7 124 70 33 215 25.5  
557 1 97 70 40 NA 38.1  
558 8 110 76 NA NA 27.8  
559 11 103 68 40 NA 46.2  
560 11 85 74 NA NA 30.1  
561 6 125 76 NA NA 33.8  
562 0 198 66 32 274 41.3  
563 1 87 68 34 77 37.6  
564 6 99 60 19 54 26.9  
565 0 91 80 NA NA 32.4  
566 2 95 54 14 88 26.1  
567 1 99 72 30 18 38.6  
568 6 92 62 32 126 32.0  
569 4 154 72 29 126 31.3  
570 0 121 66 30 165 34.3  
571 3 78 70 NA NA 32.5  
572 2 130 96 NA NA 22.6  
573 3 111 58 31 44 29.5  
574 2 98 60 17 120 34.7  
575 1 143 86 30 330 30.1  
576 1 119 44 47 63 35.5  
577 6 108 44 20 130 24.0  
578 2 118 80 NA NA 42.9  
579 10 133 68 NA NA 27.0  
580 2 197 70 99 NA 34.7  
581 0 151 90 46 NA 42.1  
582 6 109 60 27 NA 25.0  
583 12 121 78 17 NA 26.5  
584 8 100 76 NA NA 38.7  
585 8 124 76 24 600 28.7  
586 1 93 56 11 NA 22.5  
587 8 143 66 NA NA 34.9  
588 6 103 66 NA NA 24.3  
589 3 176 86 27 156 33.3  
590 0 73 NA NA NA 21.1  
591 11 111 84 40 NA 46.8  
592 2 112 78 50 140 39.4  
593 3 132 80 NA NA 34.4  
594 2 82 52 22 115 28.5  
595 6 123 72 45 230 33.6  
596 0 188 82 14 185 32.0  
597 0 67 76 NA NA 45.3  
598 1 89 24 19 25 27.8  
599 1 173 74 NA NA 36.8  
600 1 109 38 18 120 23.1  
601 1 108 88 19 NA 27.1  
602 6 96 NA NA NA 23.7  
603 1 124 74 36 NA 27.8  
604 7 150 78 29 126 35.2  
605 4 183 NA NA NA 28.4  
606 1 124 60 32 NA 35.8  
607 1 181 78 42 293 40.0  
608 1 92 62 25 41 19.5  
609 0 152 82 39 272 41.5  
610 1 111 62 13 182 24.0  
611 3 106 54 21 158 30.9  
612 3 174 58 22 194 32.9  
613 7 168 88 42 321 38.2  
614 6 105 80 28 NA 32.5  
615 11 138 74 26 144 36.1  
616 3 106 72 NA NA 25.8  
617 6 117 96 NA NA 28.7  
618 2 68 62 13 15 20.1  
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696 0.128 43 pos  
697 0.268 31 pos  
698 0.253 22 neg  
699 0.598 28 neg  
700 0.904 26 neg  
701 0.483 26 neg  
702 0.565 49 pos  
703 0.905 52 pos  
704 0.304 41 neg  
705 0.118 27 neg  
706 0.177 28 neg  
707 0.261 30 pos  
708 0.176 22 neg  
709 0.148 45 pos  
710 0.674 23 pos  
711 0.295 24 neg  
712 0.439 40 neg  
713 0.441 38 pos  
714 0.352 21 neg  
715 0.121 32 neg  
716 0.826 34 pos  
717 0.970 31 pos  
718 0.595 56 neg  
719 0.415 24 neg  
720 0.378 52 pos  
721 0.317 34 neg  
722 0.289 21 neg  
723 0.349 42 pos  
724 0.251 42 neg  
725 0.265 45 neg  
726 0.236 38 neg  
727 0.496 25 neg  
728 0.433 22 neg  
729 0.326 22 neg  
730 0.141 22 neg  
731 0.323 34 pos  
732 0.259 22 pos  
733 0.646 24 pos  
734 0.426 22 neg  
735 0.560 53 neg  
736 0.284 28 neg  
737 0.515 21 neg  
738 0.600 42 neg  
739 0.453 21 neg  
740 0.293 42 pos  
741 0.785 48 pos  
742 0.400 26 neg  
743 0.219 22 neg  
744 0.734 45 pos  
745 1.174 39 neg  
746 0.488 46 neg  
747 0.358 27 pos  
748 1.096 32 neg  
749 0.408 36 pos  
750 0.178 50 pos  
751 1.182 22 pos  
752 0.261 28 neg  
753 0.223 25 neg  
754 0.222 26 pos  
755 0.443 45 pos  
756 1.057 37 pos  
757 0.391 39 neg  
758 0.258 52 pos  
759 0.197 26 neg  
760 0.278 66 pos  
761 0.766 22 neg  
762 0.403 43 pos  
763 0.142 33 neg  
764 0.171 63 neg  
765 0.340 27 neg  
766 0.245 30 neg  
767 0.349 47 pos  
768 0.315 23 neg

#made descriptive table summary  
  
logistic\_model <- glm(diabetes\_5y ~ glucose\_mg\_dl + pregnancy\_num + age + bmi,  
 data = diabetes, family = binomial())

#created logistic regression model  
library(haven)  
library(gtsummary)  
  
# Assuming 'diabetes' is your dataset  
library(gtsummary)  
  
  
  
tbl\_regression(  
 logistic\_model,  
 exponentiate = TRUE,  
 label = list(  
 glucose\_mg\_dl ~ "Glucose concentration (mg/dl)",  
 pregnancy\_num ~ "Number of Pregnancies",  
 age ~ "Age (yrs)",  
 bmi ~ "BMI"  
 ),  
  
 tidy\_fun = broom.helpers::tidy\_parameters )

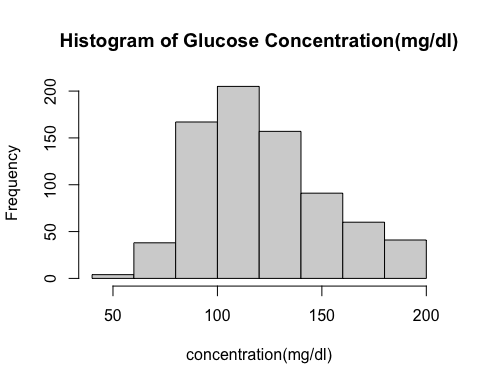
Table printed with `knitr::kable()`, not {gt}. Learn why at  
https://www.danieldsjoberg.com/gtsummary/articles/rmarkdown.html  
To suppress this message, include `message = FALSE` in the code chunk header.

| **Characteristic** | **OR** | **95% CI** | **p-value** |
| --- | --- | --- | --- |
| Glucose concentration (mg/dl) | 1.04 | 1.03, 1.04 | <0.001 |
| Number of Pregnancies | 1.12 | 1.05, 1.19 | <0.001 |
| Age (yrs) | 1.01 | 0.99, 1.03 | 0.2 |
| BMI | 1.10 | 1.07, 1.13 | <0.001 |

str(diabetes)

'data.frame': 768 obs. of 9 variables:  
 $ pregnancy\_num : num 6 1 8 1 0 5 3 10 2 8 ...  
 $ glucose\_mg\_dl : num 148 85 183 89 137 116 78 115 197 125 ...  
 $ dbp\_mm\_hg : num 72 66 64 66 40 74 50 NA 70 96 ...  
 $ triceps\_mm : num 35 29 NA 23 35 NA 32 NA 45 NA ...  
 $ insulin\_microiu\_ml: num NA NA NA 94 168 NA 88 NA 543 NA ...  
 $ bmi : num 33.6 26.6 23.3 28.1 43.1 25.6 31 35.3 30.5 NA ...  
 $ pedigree : num 0.627 0.351 0.672 0.167 2.288 ...  
 $ age : num 50 31 32 21 33 30 26 29 53 54 ...  
 $ diabetes\_5y : Factor w/ 2 levels "neg","pos": 2 1 2 1 2 1 2 1 2 2 ...

hist(diabetes$glucose\_mg\_dl,  
 main = "Histogram of Glucose Concentration(mg/dl)",  
 xlab = "concentration(mg/dl)")



str(diabetes$glucose\_mg\_dl)

num [1:768] 148 85 183 89 137 116 78 115 197 125 ...

rangers <- function(x){  
 max(x)-min(x)  
}  
  
x<- diabetes$glucose\_mg\_dl  
x<-na.omit(x)  
result<- rangers(x)  
print(result)

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