

# 704SM Biostatistica

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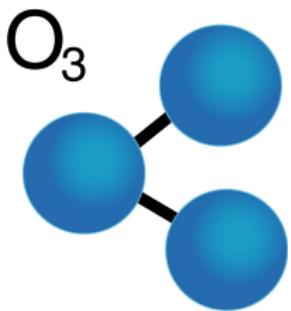
UNIVERSITÀ DEGLI STUDI DI TRIESTE

Dipartimento di Scienze della Vita



SOCIETA' DEI MATEMATICI  
E NATURALISTI DI MODENA  
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# questioni da approfondire



# La regressione multipla

il dataset `airquality`

	Ozone	Solar.R	Wind	Temp	Month	Day
1	41	190	7.40	67	5	1
2	36	118	8.00	72	5	2
3	12	149	12.60	74	5	3
4	18	313	11.50	62	5	4
5	NA	NA	14.30	56	5	5
6	28	NA	14.90	66	5	6
..	..	..	..	..	..	..
152	18	131	8.00	76	9	29
153	20	223	11.50	68	9	30

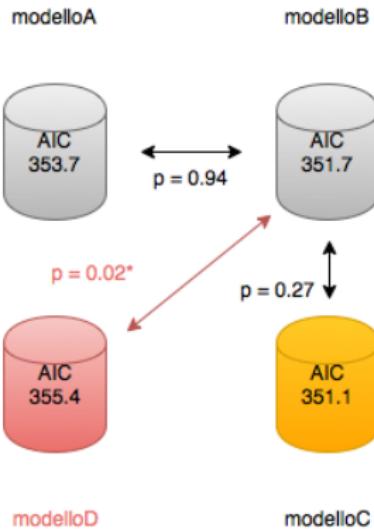
si tratta di una **serie temporale**, non di un design *cross-section*

# questioni da approfondire



domande

come si sceglie il 'migliore' modello statistico?

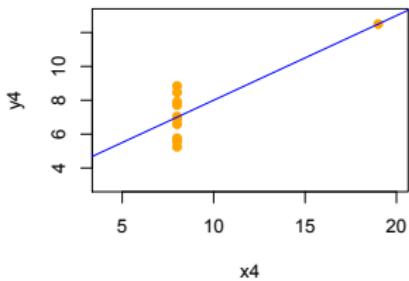
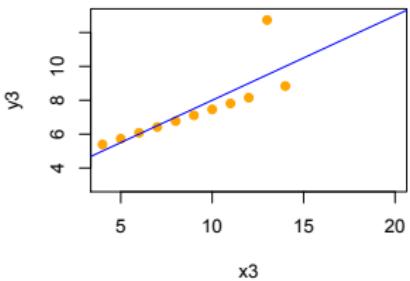
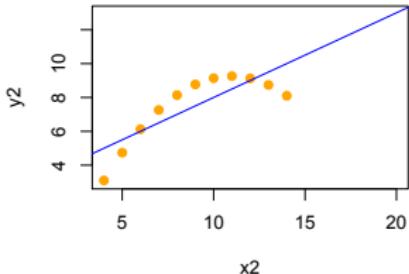
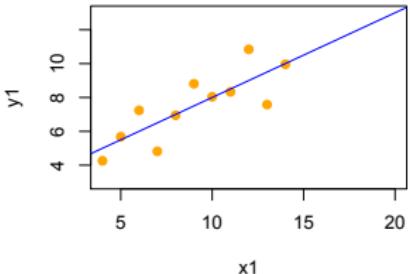


## domande

come si sceglie il 'migliore' modello statistico

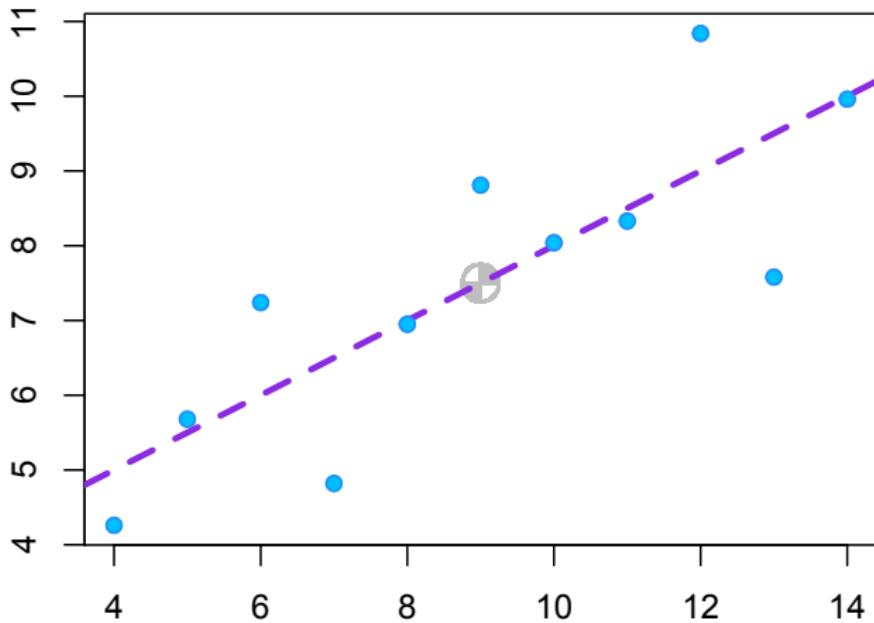
- mediante la **analisi della devianza**
- confrontando i **criteri di informazione**
- simulando dati in base allo ***residual standard error***

# che cosa è la devianza?



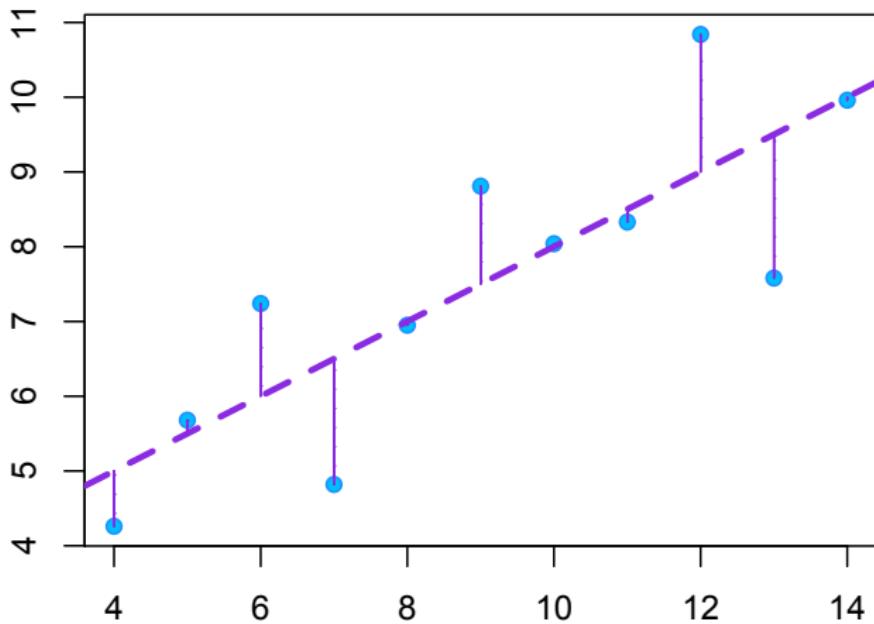
# che cosa è la devianza

$$y = 0.5 x + 3 \text{ (p} = 0.002\text{)}$$



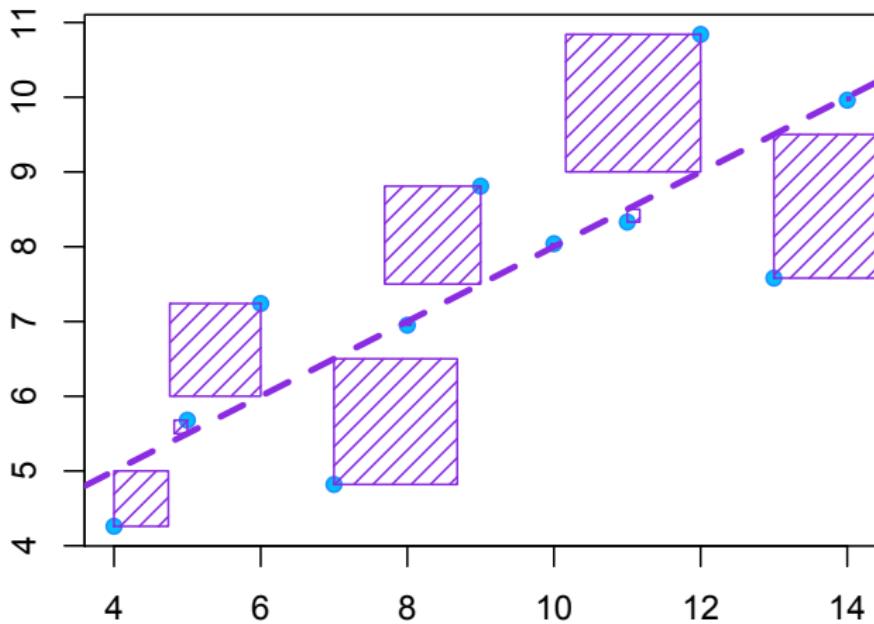
# che cosa è la devianza

**residui**

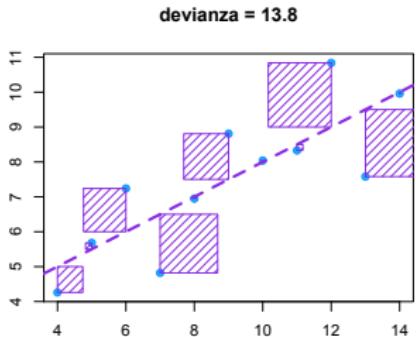


# che cosa è la devianza

**devianza = 13.8**



# analisi della devianza

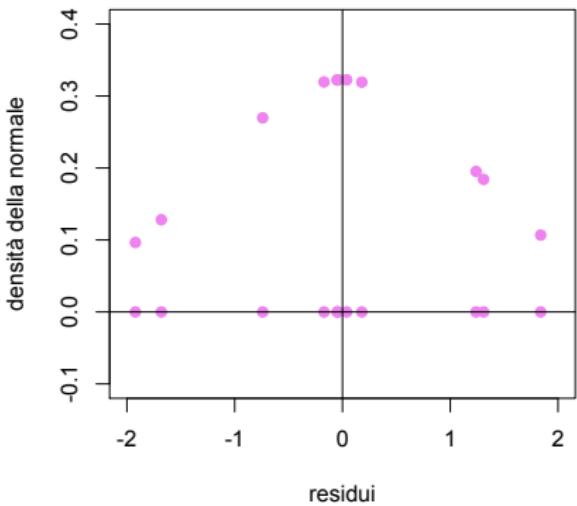
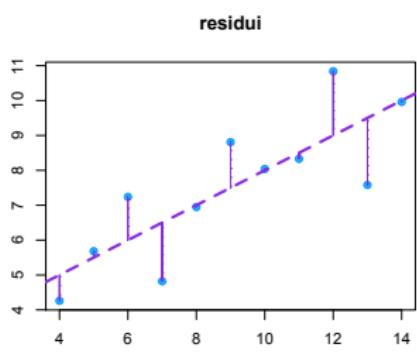


- la somma dei quadrati dei residui (RSS) si comporta approssimativamente come una variabile aleatoria Chi Quadrato
- possiamo testare le RSS dei modelli:**analisi della devianza**

```
anova(modelloA, modelloB)
```

# che cosa sono i criteri di informazione?

che cosa è la log-verosimiglianza?



```
plot(resid(m2), dnorm(resid(m2), 0, sigma))
```

che cosa sono i criteri di informazione?

che cosa è la log-verosimiglianza?

```
> dim(model.matrix(m1))[2]      # intercept + slope
[1] 2
> sigma.ML = sigma*sqrt((11-dim(model.matrix(m1))[2])/11)
> sigma.ML
[1] 1.11855
> sum(log(dnorm(resid(m2), mean = 0, sd = sigma.ML)))
[1] -16.84069
> logLik(m1)
'log Lik.' -16.84069 (df=3)
```

## ^ Definition



Suppose that we have a **statistical model** of some data. Let  $L$  be the maximum value of the **likelihood function** for the model; let  $k$  be the number of estimated **parameters** in the model. Then the AIC value of the model is the following.<sup>[1][2]</sup>

$$\text{AIC} = 2k - 2\ln(L)$$

Given a set of candidate models for the data, the preferred model is the one with the minimum AIC value. AIC rewards goodness of fit (as assessed by the likelihood function), but it also includes a penalty that is an increasing function of the number of estimated parameters. The penalty discourages overfitting.

```
> logLik(m2)
'log Lik.' -16.84069 (df=3)
> 2 * 3 - 2 * logLik(m1)
'log Lik.' 39.68137 (df=3)
> AIC(m2)
[1] 39.68137
```

come si simulano i dati in base allo *residual standard error*?

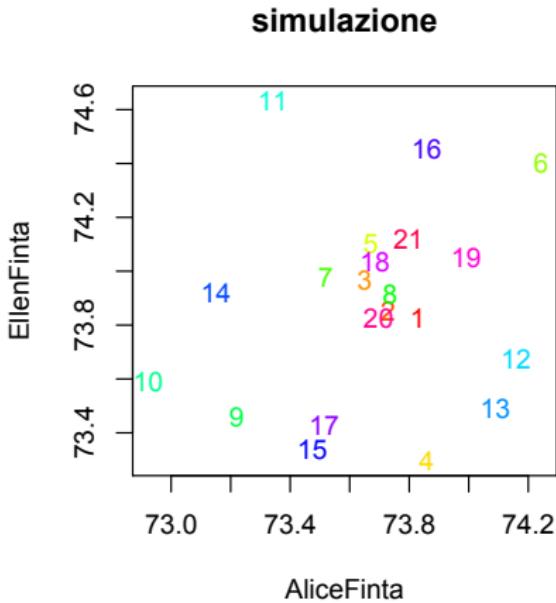
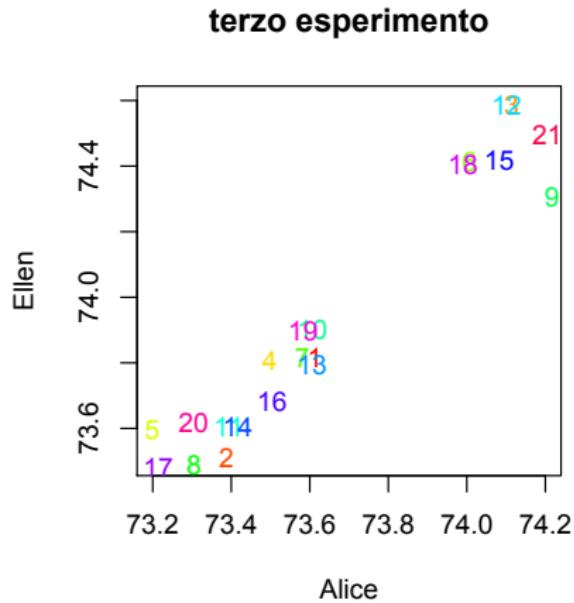
	Alice	Ellen		Alice	Ellen
1	73.60	73.80	12	74.10	74.60
2	73.40	73.50	13	73.60	73.80
3	74.10	74.60	14	73.40	73.60
4	73.50	73.80	15	74.10	74.40
5	73.20	73.60	16	73.50	73.70
6	74.00	74.40	17	73.20	73.50
7	73.60	73.80	18	74.00	74.40
8	73.30	73.50	19	73.60	73.90
9	74.20	74.30	20	73.30	73.60
10	73.60	73.90	21	74.20	74.50
11	73.40	73.60	-	-	-

come si simulano i dati in base allo *residual standard error*?

```
Call:  
lm(formula = peso ~ gemella)  
  
Residuals:  
    Min      1Q  Median      3Q     Max  
-0.4619 -0.3226 -0.1024  0.4179  0.6571  
  
Coefficients:  
            Estimate Std. Error t value Pr(>|t|)  
(Intercept) 73.66190   0.08078 911.915 <2e-16 ***  
gemellaellen 0.28095   0.11424   2.459   0.0183 *  
---  
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

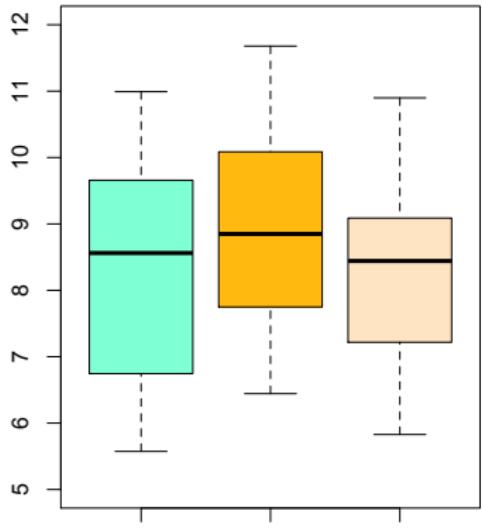
Residual standard error: 0.3702 on 40 degrees of freedom  
Multiple R-squared: 0.1314, Adjusted R-squared: 0.1096  
F-statistic: 6.049 on 1 and 40 DF, p-value: 0.01834

come si simulano i dati in base allo *residual standard error*?

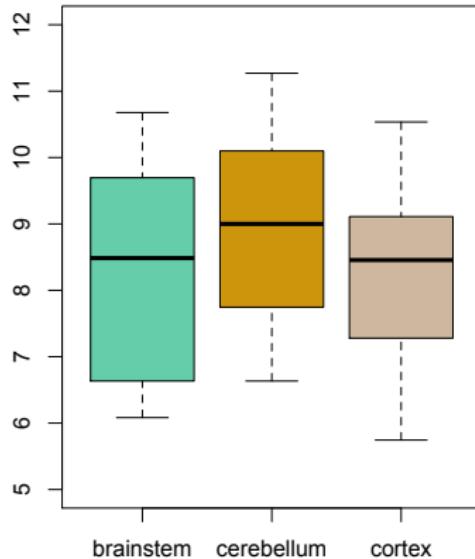


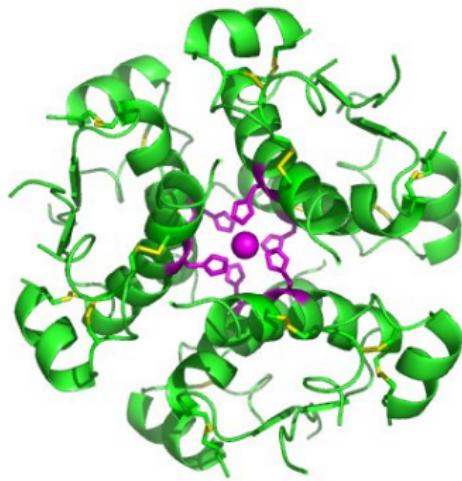
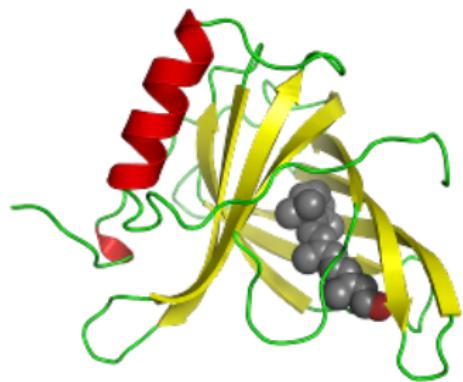
come si simulano i dati in base allo *residual standard error*?

simulazione



Taba



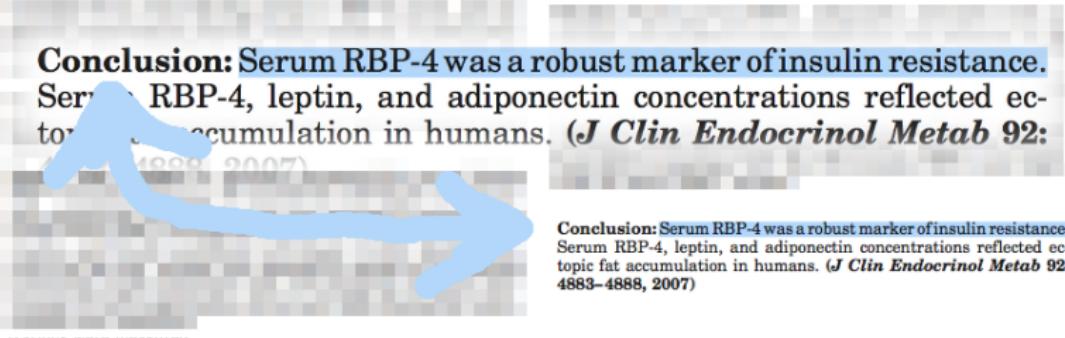


## BRIEF REPORT

### Serum Retinol-Binding Protein-4, Leptin, and Adiponectin Concentrations Are Related to Ectopic Fat Accumulation

REVIEW ARTICLE

**Conclusion:** Serum RBP-4 was a robust marker of insulin resistance. Serum RBP-4, leptin, and adiponectin concentrations reflected ectopic fat accumulation in humans. (*J Clin Endocrinol Metab* 92: 4883–4888, 2007)

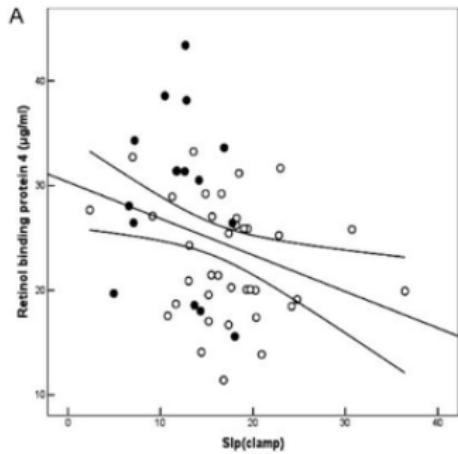
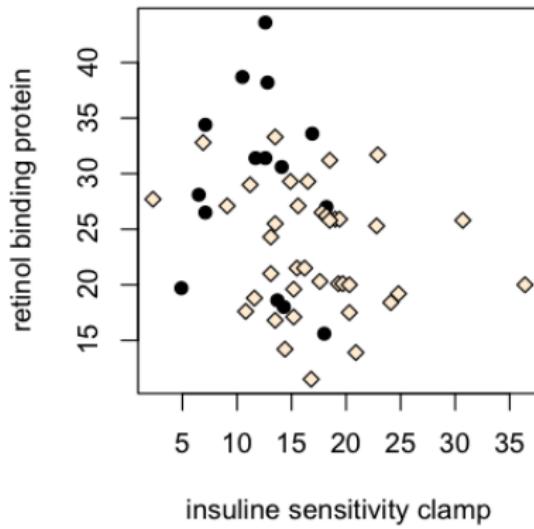


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## il dataset diabete

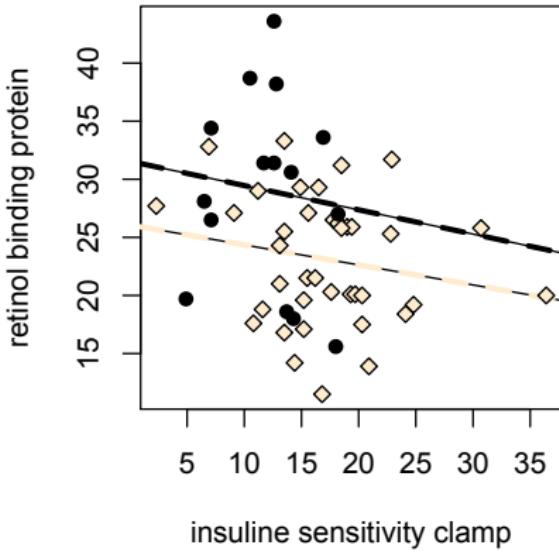
	serumprotein	response	group
1	12.60	43.60	black
2	10.50	38.70	black
3	12.80	38.20	black
4	7.10	34.40	black
5	16.90	33.60	black
6	13.50	33.30	white
...	...	...	...
51	14.40	14.20	white
52	20.90	13.90	white
53	16.80	11.50	white

### RBP vs. SI

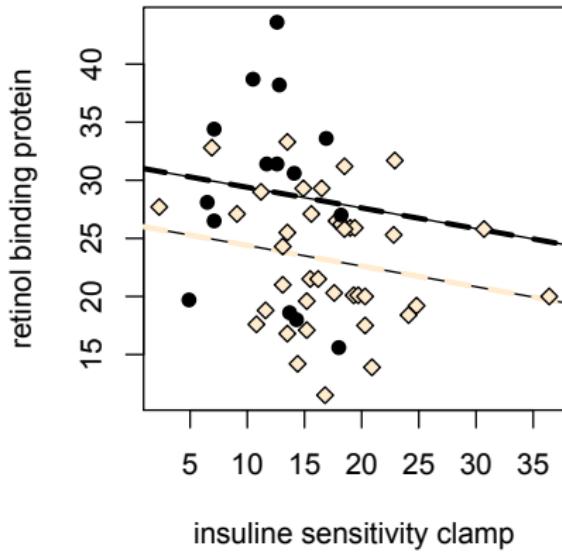


# il dataset diabete

## modello massimale

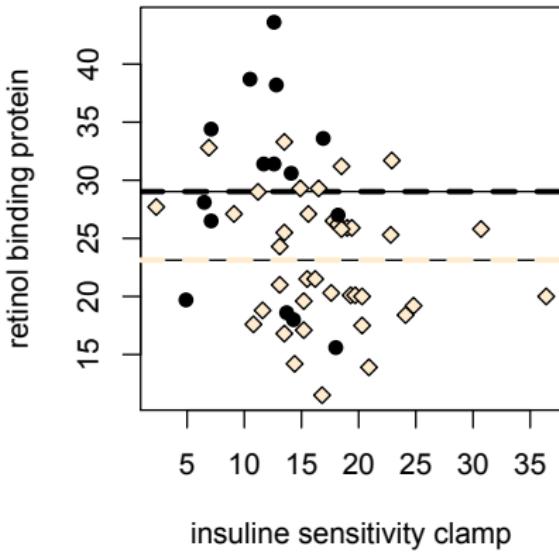


## modello additivo



# il dataset diabete

**minimale adeguato**



## il dataset diabete

$$p = 0.04$$

