

Install package on your own R:

DO NOT DO THIS NOW!

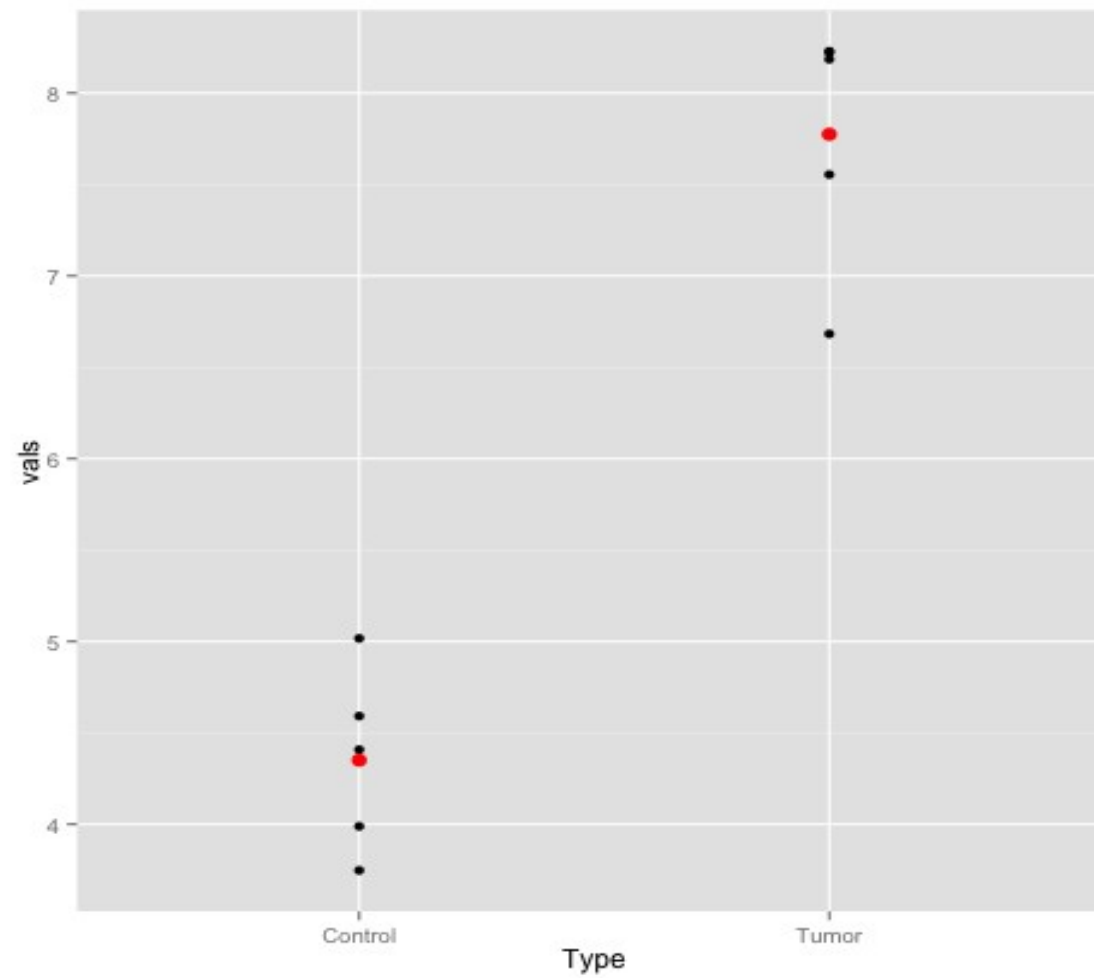
- Install R-3.2.1
- `source("http://bioconductor.org/biocLite.R")`
- `biocLite(c("affycoretools", "BiocStyle", "devtools"))`
- `library(devtools)`
- `install_github("jmacdon/MacDonaldBioC2015",
 build_vignettes = TRUE)`
- `library(MacDonaldBioC2015)`
- `openVignette()`

	Type	TypeControl	TypeTumor
1	Tumor	0	1
2	Tumor	0	1
3	Tumor	0	1
4	Tumor	0	1
5	Tumor	0	1
6	Control	1	0
7	Control	1	0
8	Control	1	0
9	Control	1	0
10	Control	1	0

Tumor	=	0*TypeControl	+	1*TypeTumor
Tumor	=	0*TypeControl	+	1*TypeTumor
Tumor	=	0*TypeControl	+	1*TypeTumor
Tumor	=	0*TypeControl	+	1*TypeTumor
Tumor	=	0*TypeControl	+	1*TypeTumor
Control	=	1*TypeControl	+	0*TypeTumor
Control	=	1*TypeControl	+	0*TypeTumor
Control	=	1*TypeControl	+	0*TypeTumor
Control	=	1*TypeControl	+	0*TypeTumor
Control	=	1*TypeControl	+	0*TypeTumor

OR

Tumor = TypeTumor + error
Control = TypeControl + error



Tumor	=	1*Intercept	+	1*TypeTumor
Tumor	=	1*Intercept	+	1*TypeTumor
Tumor	=	1*Intercept	+	1*TypeTumor
Tumor	=	1*Intercept	+	1*TypeTumor
Tumor	=	1*Intercept	+	1*TypeTumor
Control	=	1*Intercept	+	0*TypeTumor
Control	=	1*Intercept	+	0*TypeTumor
Control	=	1*Intercept	+	0*TypeTumor
Control	=	1*Intercept	+	0*TypeTumor
Control	=	1*Intercept	+	0*TypeTumor

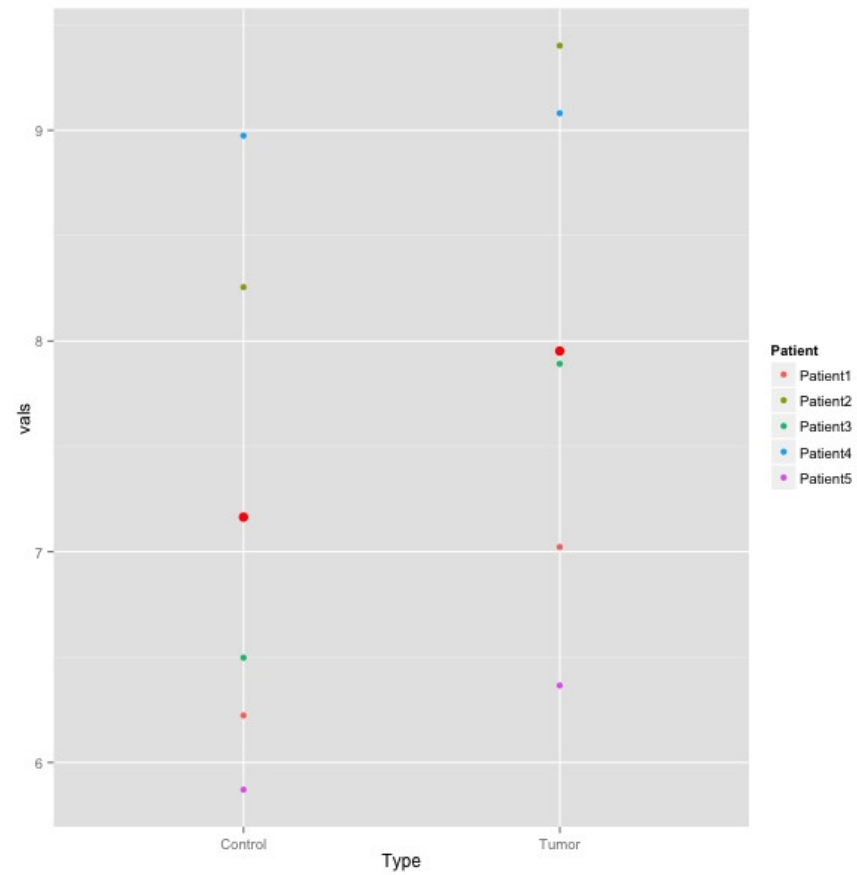
Or

Tumor = Intercept + TypeTumor
Control = Intercept

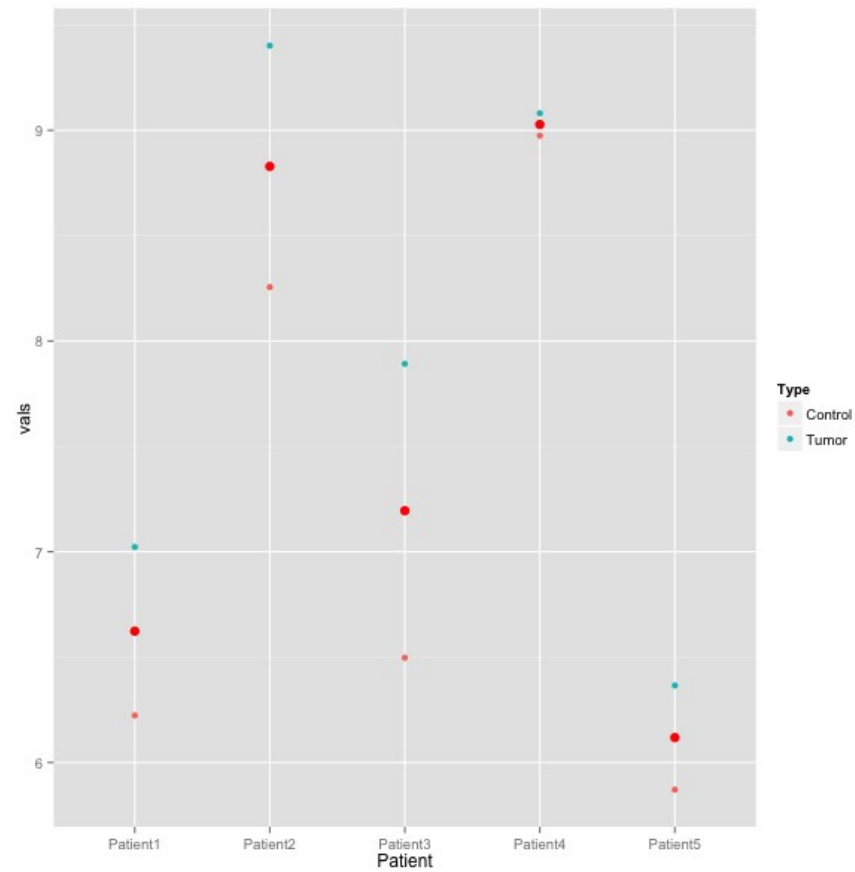
Or

Intercept = Control
Tumor = Control + TypeTumor \Rightarrow TypeTumor = Tumor - Control

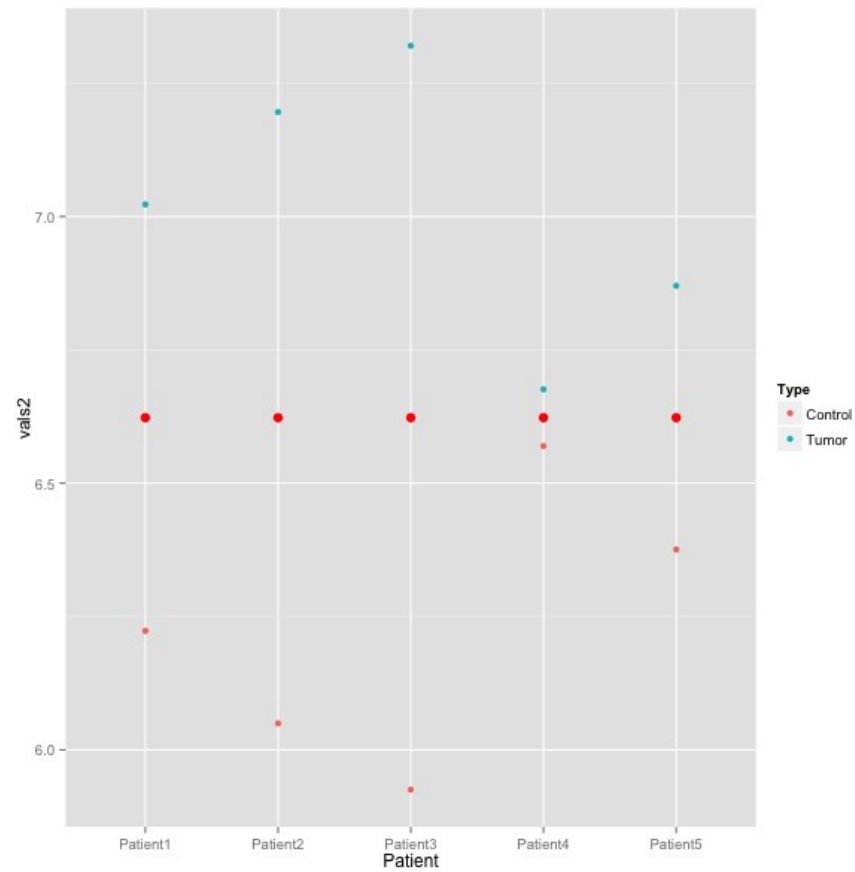
Paired samples, ignoring pairing



Paired samples, by patient



Paired samples, adjusted for patient batch effect



Comparison of batch-controlled paired samples

