Understanding Diffusion with **netdiffuseR**
More on model estimation

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```r
library(netdiffuseR)
data("medInnovationsDiffNet")

# Exposure terms

# Structural equivalence
medInnovationsDiffNet[["seexp"]] <- exposure(
  medInnovationsDiffNet, alt.graph = "se", groupvar="city",
  valued = TRUE
)

# Cohesive
medInnovationsDiffNet[["cohexp"]] <- exposure(medInnovationsDiffNet)

# Attribute weighted
medInnovationsDiffNet[["proage"]][is.na(medInnovationsDiffNet[["proage"]])] <- 0
medInnovationsDiffNet[["cohexp_proage"]] <- exposure(
  medInnovationsDiffNet, attrs="proage", groupvar = "city")

# Creating model
dat <- diffnet.attrs(medInnovationsDiffNet, as.df = TRUE)
dat <- subset(
  dat, per <= toa,
  select=c(id, toa, per, city, attend,
          cohexp, cohexp_proage, seexp, proage))

dat$adopted <- with(dat, per == toa)

mod <- formula(adopted ~ factor(city) + cohexp + cohexp_proage + seexp + I(proage^2) +
      attend*proage)
out <- glm(mod, data=dat, family=binomial(link="logit"))

pander::pander(out)
```

Table 1: Fitting generalized (binomial/logit) linear model: mod

	Estimate	Std. Error	z value	Pr($>$|z|)
factor(city)2	0.1074	0.2669	0.4023	0.6875
factor(city)3	-0.1097	0.2944	-0.3728	0.7093
factor(city)4	-0.1634	0.297	-0.5502	0.5822

	Estimate	Std. Error	z value	Pr(>|z|)
cohexp	2.206	1.614	1.367	0.1717
cohexp__proage	-1.832	1.603	-1.143	0.253
seexp	1.159	0.4193	2.764	0.005712
I(proage^2)	-0.08546	0.04121	-2.074	0.03811
attend	0.4214	0.3632	1.16	0.246
proage	0.8076	0.3002	2.69	0.007138
attend:proage	-0.06668	0.09158	-0.7282	0.4665
(Intercept)	-4.372	0.6136	-7.126	1.036e-12

```
# Likelihood ratio test
# l0 <- update(out, adopted~1)
# library(rms)
# lrm(mod)
```

Computing xxx early adopters, laggards

```
sdclass <- function(x, na.rm=TRUE, breaks=c(-1.5,-1,0,1,1.5)) {
  # Computing sd
  x_sd <- sd(x, na.rm = na.rm)

  # Creating labels
  m <- length(breaks)

  # Computing breaks and classifying
  x_sd <- mean(x, na.rm=na.rm) + x_sd*breaks
  lab <- c(
    sprintf("(-Inf; %.2f)", x_sd[1]),
    sprintf("[%.2f; %.2f)", x_sd[-m], x_sd[-1]),
    sprintf("[%.2f; +Inf)", x_sd[m])
    )

  x <- rowSums(sapply(x_sd, `<`, x))
  x[x==0] <- m + 1
  factor(lab[x+1], lab)
}

x <- sdclass(diffnet.toa(medInnovationsDiffNet))
y <- sdclass(threshold(medInnovationsDiffNet))
```

	(-Inf; -0.01)	[-0.01; 0.20)	[0.20; 0.61)	[0.61; 1.01)	[1.01; 1.22)	[1.22; +Inf)
(-Inf; -0.27)	0	0	0	0	0	0
[-0.27; 2.48)	0	5	4	0	0	0
[2.48; 7.98)	0	15	17	23	0	0
[7.98; 13.47)	0	6	1	16	0	0
[13.47; 16.22)	0	1	1	8	0	0
[16.22; +Inf)	0	1	0	16	0	0