Index of Lecture 3b: Introduction to logistic regression & Prediction for presentation (revised on page 17)

Practical Information

Logistic regression:

- binary (0/1, dichotomous) outcomes, possibly grouped to binomial outcomes (e.g., 3 positive out of 10 animals),
- first of several regression-type models without normal distribution assumptions,
  - sometimes called generalised linear models (glm's),
  - model building from the predictors is similar to linear regression,
  - but some common features in their analysis that distinguish them from linear regression analysis.

This lecture:

- follow-up from Lecture 3a (Javier),
- review of simple logistic regression (one predictor) and its relation to known analyses, in particular 2×2-table analysis; using Stata to illustrate,
- more on predictions, in particular using `margins` command (Stata).

VER/MER textbooks:

- today: $16.1-5, 8$ with some omissions (included in next lecture),
- maybe also check PSLS Chapter 28 (the VHM 801 textbook; at Moodle).

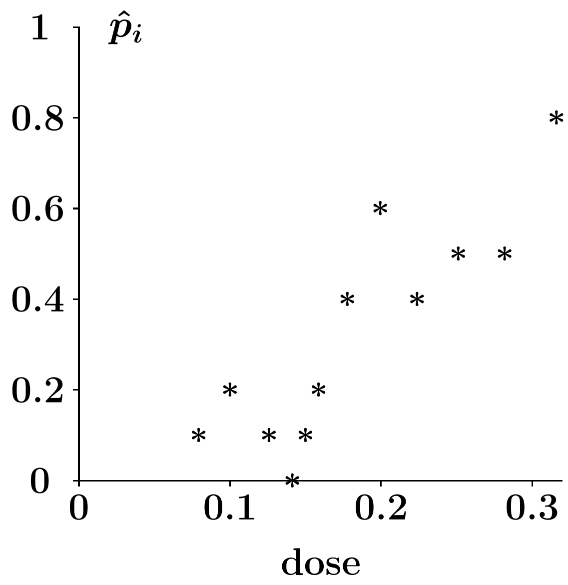
Preparation for Friday: the Model-building exercise (VER 15).

Example Dataset MICE

Toxicity study of dose-response curve (Woodward 1941, from RC textbook):

- lethality of different doses of chloracetic acid, measured as the mortality among 10 mice subjected to each dose,

group i	dose x_i	# died r_i	# total N_i	prop. died $\hat{p}_i = r_i/N_i$	logit$(\hat{p}_i)$
1	0.0794	1	10	0.1	-2.197
2	0.1000	2	10	0.2	-1.386
3	0.1259	1	10	0.1	-2.197
4	0.1413	0	10	0.0	undef.
5	0.1500	1	10	0.1	-2.197
6	0.1588	2	10	0.2	-1.386
7	0.1778	4	10	0.4	-0.405
8	0.1995	6	10	0.6	0.405
9	0.2239	4	10	0.4	-0.405
10	0.2512	5	10	0.5	0
11	0.2818	5	10	0.5	0
12	0.3162	8	10	0.8	1.386



- grouped binary data,
- statistical model: $r_i \sim \text{Bin}(N_i, p_i)$, and $r_1, \ldots, r_{12}$ independent,
- parameters: $p_1, \ldots, p_{12}$ (probability of death in dose groups),
- question: how to use the doses?

Why not Linear Regression?

Regression for binary outcomes ($Y_i = 0$ or $Y_i = 1$),

$$Y_i = \beta_0 + \beta_1 x_{1i} + \ldots + \beta_k x_{ki} + \varepsilon_i,$$

conflicts with the model assumptions:

(1) the errors ε_i are far from normally distributed (can only take two possible values[1]),

(2) with $p_i = P(Y_i = 1)$, we have $\text{Var}(Y_i) = p_i(1 - p_i)$, which is not constant when p_i is modelled by predictors,

(3) both Y_i and p_i are bounded (do not go beyond 0 and 1) but linear predictions by the x-variables can easily give predictions outside the interval (0,1).

Regression for grouped binary outcomes (proportions r_i/N_i):

- same problems (1)–(3), although (1) is less severe,
- transformation is a possibility, usually with the variance-stabilising transformation: $Y_i = \arcsin(\sqrt{r_i/N_i})$ (slide 1aL–12) — however, not recommended unless
  - the denominators N_i are all "large" and approximately the same,
  - the proportions r_i/N_i are not too extreme (close to 0 or 1),

  and usually offers no advantages over logistic regression.

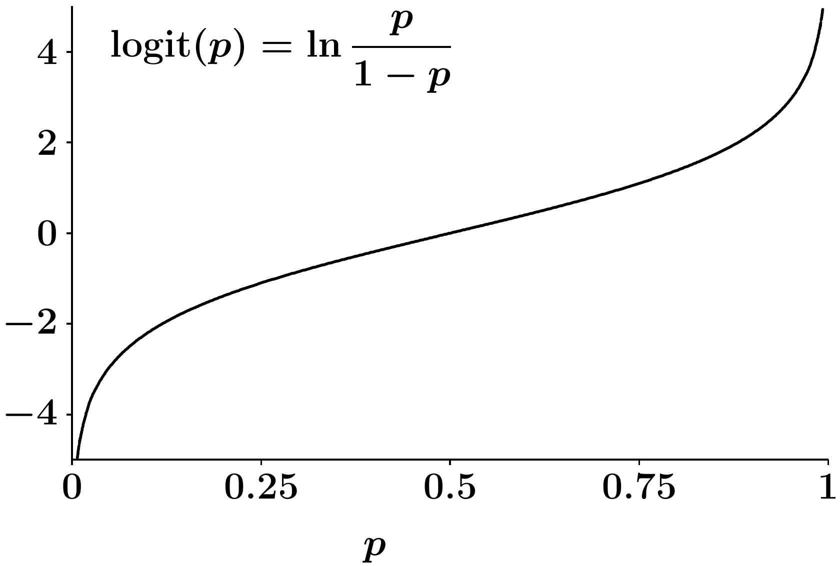
[1] Possible values for the error of obs. i are: $\varepsilon_i = 1 - (\beta_0 + \beta_1 x_{1i} + \ldots + \beta_k x_{ki})$, and $\varepsilon_i = -(\beta_0 + \beta_1 x_{1i} + \ldots + \beta_k x_{ki})$.

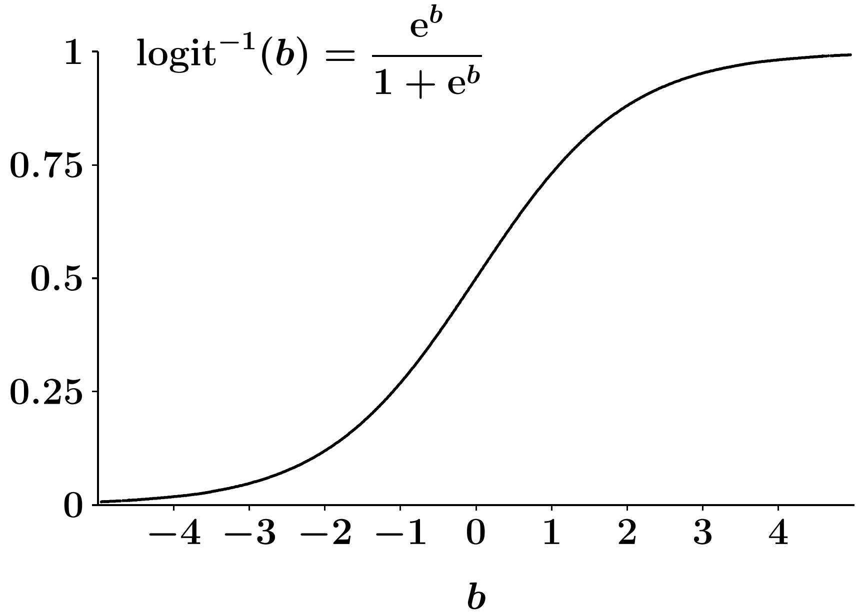
Logit Transformation

Define for $0 < p < 1$ and any b,

$$\text{logit}(p) = \ln\left(\frac{p}{1-p}\right) \quad \text{and} \quad \text{logit}^{-1}(b) = \frac{e^b}{1+e^b} = \frac{1}{1+e^{-b}},$$

- the logit function stretches the interval (0,1), excluding endpoints!, onto the entire real axis (from $-\infty$ to ∞),
- $\text{logit}(\frac{1}{2}) = 0$, and $\text{logit}(p)$ is increasing in p,
- with $\text{odds}(p) = \frac{p}{1-p}$, we have $\text{logit}(p) = \ln(\text{odds}(p))$,
- logit and inverse logit functions:





Logistic Regression Model

= a different transformation approach:

- keep observations (binary/grouped binary) untransformed,
- transform probability parameter p by logit function to logit scale where linear modelling takes place, e.g.

$$\ln\left(\frac{p_i}{1-p_i}\right) = \text{logit}(p_i) = \beta_0 + \beta_1 x_{1i} \quad \text{for } i = 1, \ldots, n,$$

where $Y_i = \begin{cases} 1 & \text{“success”} \\ 0 & \text{“failure”} \end{cases}$, $p_i = \mathrm{P}(Y_i{=}1)$, and x_i = predictor value for obs. i.

Model assumptions:

- independence of all the observations (Y_i's),
- linearity in modelling equation (above) on logit scale.[2]

Grouped binary data (with N_i replicates in ith group):

- same modelling equation for p_i = probability of “success” in group i,
- same model as if set up as binary data (with $n = \sum_i N_i$).

Multiple logistic regression model for predictors $x_1, \ldots, x_k$:

$$\text{logit}(p_i) = \beta_0 + \beta_1 x_{1i} + \ldots + \beta_k x_{ki}.$$

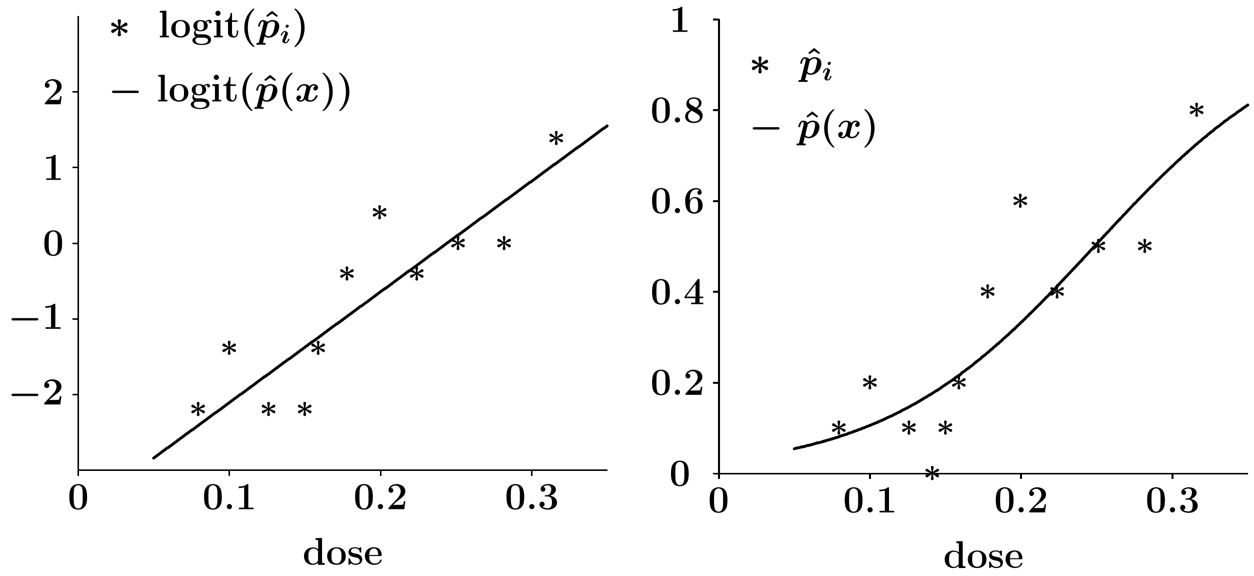
[2] For a single predictor model, the linearity assumption applies only to the case where x_1 is continuous.

Logistic Regression for Mice Data

Estimates (with SE):
$\hat{\beta}_0 = -3.57\,(0.71)$,
$\hat{\beta}_1 = 14.64\,(3.33)$.

Estimated line:
$\hat{\beta}_0 + \hat{\beta}_1 \cdot \text{dose}$
– on logit-scale.

Estimated curve $\hat{p}(x)$:
$\text{logit}^{-1}(\hat{\beta}_0 + \hat{\beta}_1 \cdot \text{dose})$
– on probability-scale.



Test of H_0: $\beta_1 = 0$:

$$z = \hat{\beta}_1/\text{SE}(\hat{\beta}_1) = 4.39 \sim \text{ very significant in N}(0,1) \;\Rightarrow\; \text{strong effect of dose.}$$

Interpretation of $\hat{\beta}_1$: change in dose of a units $\Rightarrow$

- change in logit(p) of $a\hat{\beta}_1$ units,
- change in odds(p) by factor $\exp(a\hat{\beta}_1)$ (= odds-ratio), where odds(p) = $p/(1-p)$.

Test of model: (Pearson goodness-of-fit test)

$$X^2 = 8.74,\; P = 0.56 \quad\Rightarrow \text{no lack of fit (model ok).}$$

2×2—Table Analysis

Mice data: outcome = mortality, explanatory = dichotomous version of dose (for illustration only):

	dose2 = (dose> 0.16)		
dead	1	0	Total
1	32	7	39
0	28	53	81
Total	60	60	120

Statistical model (with binary dose predictor): two binomial distributions $\text{Bin}(60, p_1)$ and $\text{Bin}(60, p_0)$ — analyzed in VHM 801 by computing:

$$\begin{aligned}
\hat{p}_1 &= 32/60 = 0.533, \quad \text{SE}(\hat{p}_1) = \sqrt{\hat{p}_1(1-\hat{p}_1)/60} = 0.0644, \\
\hat{p}_0 &= 7/60 = 0.117, \quad \text{SE}(\hat{p}_0) = \sqrt{\hat{p}_0(1-\hat{p}_0)/60} = 0.0414, \\
\hat{p}_1 - \hat{p}_0 &= 0.533 - 0.117 = 0.417, \quad \text{SE}(\hat{p}_1 - \hat{p}_0) = \sqrt{0.0644^2 + 0.0414^2} = 0.077.
\end{aligned}$$

Alternative ways of comparing the probabilities $\hat{p}_1$ and $\hat{p}_0$:

$$\begin{aligned}
\text{relative risk}: \ \text{RR} &= \hat{p}_1/\hat{p}_0 = 0.533/0.117 = 4.57, \\
\text{odds-ratio}: \ \text{OR} &= \text{odds}(\hat{p}_1)/\text{odds}(\hat{p}_0) = [\hat{p}_1/(1-\hat{p}_1)] \,/\, [\hat{p}_0/(1-\hat{p}_0)] \\
&= [0.533/(1-0.533)] \,/\, [0.117/(1-0.117)] = 1.143/0.132 = 8.653.
\end{aligned}$$

Advantages of the ratio statistics (over the simple $\hat{p}_1 - \hat{p}_0$):

- multiplicative effects are more meaningful than additive effects for proportions bounded by 0 and 1,
- when both probabilities are “close” to zero (clearly not the case here): OR $\approx$ RR,
- both statistics more useful than $(\hat{p}_1 - \hat{p}_0)$ when multiple factors studied together.

2×2—Table and Logistic Regression

Mice data: (same as on previous slide):
outcome = mortality, predictor = `dose2`
(dichotomous version of dose):

	`dose2` = (`dose`> 0.16)		
`dead`	1	0	Total
1	32	7	39
0	28	53	81
Total	60	60	120

Logistic regression model with `dose2` as predictor:

$$\text{logit}(p_i) = \beta_0 + \beta_1 \texttt{dose2}_i,$$

gives the estimates

$$\hat\beta_1 = 2.158 = \ln(8.653) = \ln(\text{OR}),$$
$$\hat\beta_0 = -2.024 = \text{logit}(0.117) = \text{logit}(\hat p_0).$$

Interpretations (valid also in multiple logistic regression):

- odds-ratio for effect of `dose2` $= e^{\hat\beta_1} = e^{2.158} = 8.653$,
- baseline probability $= \text{logit}^{-1}(\hat\beta_0) = \text{logit}^{-1}(-2.024) = 0.117$.

Summary: the 2×2-table analysis and the logistic regression analysis are equivalent (also, the P-values are similar[3]).

[3] The likelihood-ratio tests (next lecture) for the effect of `dose2` are identical in the two models.

GOODNESS-OF-FIT TESTS

New feature compared to normal distribution models[4]:

- formal statistic test for whether the agreement between observed and expected values is "acceptable",
  - in the sense of corresponding to the distribution assumed (e.g. binomial), because the variance of that distribution determines bounds for "acceptable" differences between observed and expected,[5]
- different tests exist (discussed later in course), but the most intuitive one is the Pearson goodness-of-fit test.

For grouped binary (binomial) data, the Pearson test takes the form,

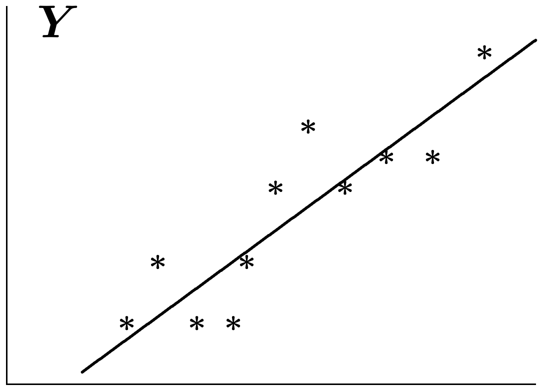
$$X^2 = \sum_i \frac{(Y_i - N_i\hat{p}_i)^2}{N_i\hat{p}_i(1-\hat{p}_i)} \approx \chi^2(I-1-k),$$

where $\hat{p}_i = \text{logit}^{-1}(\hat{\beta}_0 + \hat{\beta}_1 x_{1i} + \ldots + \hat{\beta}_k x_{ki})$ is the predicted probability for the ith group, and $i = 1, \ldots, I \sim$ groups. The approximate reference chi-square distribution is valid[6] under the assumed logistic regression model ($\sim$ null hypothesis), and large values of X^2 indicate departures from the model.

[4] Such tests do not work for a normal distribution because of its separate dispersion parameter (σ).
[5] For example, in a binomial distribution (N, p) the standard deviation equals $\sqrt{Np(1-p)}$.
[6] The approximation may be poor if the denominators $N_i\hat{p}_i(1-\hat{p}_i)$ are too low.

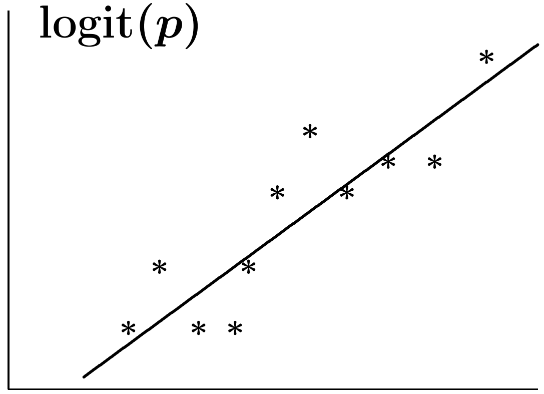
Linear versus Logistic Modelling

Linear regression



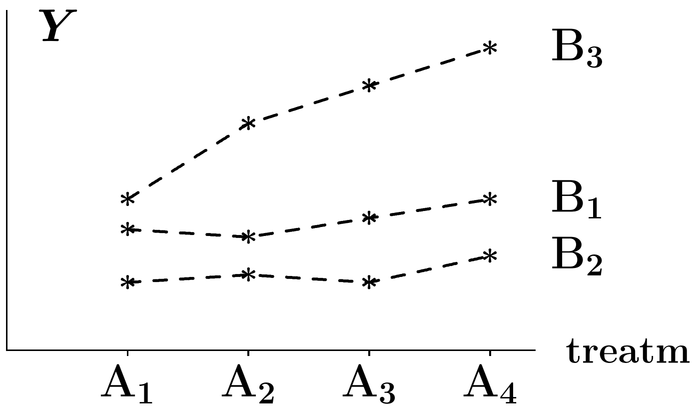
Model: $Y_i = \beta_0 + \beta_1 x_i + \varepsilon_i$
where ε_i's $\sim$ N$(0,\sigma^2)$

Logistic regression



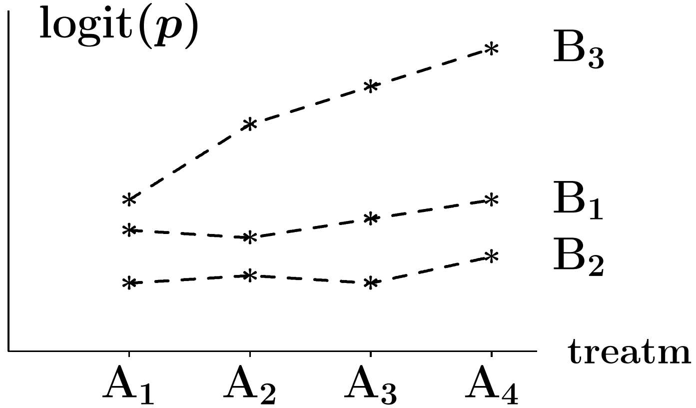
Model: $\text{logit}(p_i) = \beta_0 + \beta_1 x_i$
where $p_i = \text{P}(Y_i = 1)$

Factorial design



Model: $Y_{ij} = \mu + \alpha_i + \beta_j + \varepsilon_{ij}$
where ε_{ij}'s $\sim$ N$(0,\sigma^2)$

Logistic factorial design



Model: $\text{logit}(p_{ij}) = \mu + \alpha_i + \beta_j$
where $p_{ij} = \text{P}(Y_{ij} = 1)$

Computing Predictions in Linear Models

We distinguish between two types of predictions (or purposes):

i) for individual observations: "real" prediction,

ii) for purposely selected combinations of predictor values: "illustrative" prediction.

All software packages for linear models offer predictions of type i), directly for observed predictor patterns, and also for new predictor patterns:

- Stata/SAS: add extra observations to data with missing outcome,
- Minitab/R: specify new observations in separate columns/dataset,
- Stata/SAS: special commands (`lincom`/`estimate`) produce estimates for linear combinations of regression coefficients.

Fully specified predictions of type ii): may (in principle) be done using methods for type i) (perhaps tedious).

Some software offer both fully and partially specified predictions of type ii):

- Stata: the `margins` command (R: `emmeans` library),
- Minitab/SAS: least squares means[7]; i.e., all predictors not included in the prediction are set at their average value or as equally distributed across categories.

[7] The term "least squares means" originates from experimental designed studies/data, where factors are often balanced by design.

Stata: the `margins` Command

- very flexible command (from version 12) with a wide range of options and setups; so flexible that caution is needed to not use it wrongly. . . ,
- strongly recommended to always check your predictions with simpler methods (in a few examples) — if you don't know what is computed, how can others know. . .
- linkage to the `marginsplot` command allows easy plotting of predicted values; in particular, this is the easiest way to generate an interaction plot,
- mainly intended for "illustrative" predictions, and uses predictions from the `predict` command behind the scenes to come up with the requested predictions,
- the online help is pretty confusing ⇒ recommended to work from well-established examples, and to avoid use of numerous extra "fancy" options.

Coverage in course: worked examples (from simple to more complex) illustrating the basic features of command:

- 1-predictor settings (categorical and continuous),
- 2-predictor settings, and the questions arising from omitting a predictor from a prediction,
- VER 14.16 worked example,
- plots and transformations as needed.

Simplest Examples: 1 Predictor

(1a) categorical: simple means, with model-based SE,

```
regress wpc i.herd
margins herd
lincom _cons+2.herd
```

(1b) continuous: predictions at specified set of values, with subsequent plot by `marginsplot`:

```
regress wpc milk120
margins , at( milk120=(1400(1000)5400) )
marginsplot
lincom _cons+milk120*3400
```

note: flexible format of "atspec"; e.g., $1400(1000)5400 = 1400, 2400, \ldots, 5400$, but list can also include statistics (e.g., mean and percentiles) and the special names "asobserved" and "asbalanced",

(1c) continuous with quadratic effect: predictions as above, but need to use factor notation for quadratic term:

```
regress wpc c.milk120##c.milk120
margins , at( milk120=(1400(1000)5400) )
marginsplot
```

(1d) backtransformation from transformed scale: can be specified by formula, but note CI problems,[8]

```
regress lnwpc milk120
margins , at( milk120=(1400(1000)5400))
margins , at( milk120=(1400(1000)5400)) expression(exp(predict(xb)))
marginsplot
```

[8] The correct CIs are obtained by backtransformation, but the method used by the `margins` command is based on an approximate SE (from the so-called "delta method") on original scale.

Examples with 2 Categorical Predictors

(2a) additive model: predictions require decision about how to weight contributions from the other predictor, e.g.:

- equally/balanced (∼ standard of least squares means),
- total data weights (default choice of `margins`),
- choices corresponding to specific prediction settings,

```
regress wpc i.rp i.vag_disch
margins rp vag_disch
table rp vag_disch
lincom _cons+1.rp+1.vag_disch*82/1574 /* rp=1 */
margins rp vag_disch, asbalanced
lincom _cons+1.rp+1.vag_disch*0.5 /* rp=1 */
margins rp, over(vag_disch) /* same as: at(vag_disch=(0 1)) */
lincom _cons+1.rp+1.vag_disch /* rp=1, vag_disch=1 */
```

(2b) model with interaction: combined effect ∼ simple means and the interaction plot; separate effects require decision about how to weight contributions from the other predictor (as above for the additive model),

```
regress wpc rp##vag_disch
margins rp#vag_disch
marginsplot, noci /* this is the interaction plot! */
marginsplot, noci x(vag_disch) /* x() to control variable on x */
marginsplot, noci x(rp) /* same as default */
margins rp
lincom _cons+1.rp+(1.vag_disch+1.rp#1.vag_disch)*82/1574 /* rp=1 */
margins rp, asbalanced
lincom _cons+1.rp+(1.vag_disch+1.rp#1.vag_disch)*0.5  /* rp=1 */
```

Examples with 2 Predictors (continued)

Categorical + continuous predictor:

(2c) similar to single continuous predictor, with multiple groups (intercepts and lines),

```
regress wpc i.dyst milk120
margins dyst, at( milk120=(1400(1000)5400))
marginsplot, noci
lincom _cons+1.dyst+milk120*3400 /* dyst=1, milk120=3400 */
margin dyst, atmeans
lincom _cons+1.dyst+milk120*3215.096
* interaction model
regress wpc dyst##c.milk120
margins dyst, at( milk120=(1400(1000)5400))
marginsplot, noci /* this is the interaction plot! */
lincom _cons+1.dyst+(c.milk120+1.dyst#c.milk120)*3400 /* dyst=1, milk120=3400 */
```

Two continuous predictors:

(2d) need values (possibly lists) for both predictors ⇒ predictions usually fully specified (no averaging/weighting),

```
regress wpc parity milk120
margins , at( parity=(1(1)6) milk120=(1400(1000)5400))
marginsplot, noci
margins , at( milk120=(1400(1000)5400) parity=(1(1)6) )
marginsplot, noci /* changing roles in plot */
margins , at( milk120=(1400(1000)5400) (median)parity)
marginsplot
lincom _cons+milk120*1400+parity*2 /* milk120=1400, parity=2 */
margins, atmeans
lincom _cons+milk120*3215.096+parity*2.73628 /* both at means */
```

Prediction in Multivariable Models

Main challenge/thing to remember: predictions need values or weights for all predictor terms in model $\Rightarrow$ no software can do this automatically (so that it always makes sense)!

Some issues to consider when setting up predictions:

- the purpose (e.g., "real" versus "illustrative"),
- should the prediction correspond to an average instead of a real situation? (e.g., when using weights for categorical predictors, the predictions will not correspond to real situations),[9]
- is the predictor distribution in the observed data representative for the population or the targeted setting? [9]
- are the predictor distributions independent enough to set the values for different predictors independently? [9]
- for categorical predictors, are predictions intended to facilitate pairwise comparisons beyond comparisons with baseline? (perhaps the main motivation of least squares means),
- if modelling is carried out on transformed scale, should any weighting take place on transformed or original scale? (as they will lead to different results).

[9] Beware that using `margins` with its default settings implies that your answer to this question is "yes".

Predictions for VER Example 14.16

Model summary:
- outcome: wpc, on square-root transformed scale,
- categorical predictors: aut_calv, twin, dyst, rp##vag_disch,
- continuous predictors: parity and herd_size with quadratic term.

Some possible prediction aims:

1) illustrate combined effect of diseases (rp,dyst,vag_disch) on wpc,

2) illustrate interaction rp#vag_disch (effectively included under 1),

3) illustrate effect of herd_size on wpc.

1): Prediction/Estimates for combinations of disease, with backtransformed means ∼ median wpc-values:

Estimates*		$\sqrt{\text{wpc}}$ (mean)		wpc (median)	
rp	vag_d	dyst=0	dyst=1	dyst=0	dyst=1
0	0	7.328	7.870	53.70	61.94
0	1	7.315	7.857	53.51	61.73
1	0	7.717	8.260	59.56	68.22
1	1	9.195	9.737	84.55	94.82

* at: parity=1, twin=0, herd_size=234, aut_calv=0 (∼ mean herd size, most frequent categories)

3): Prediction/Estimates for the 7 observed herd sizes:

Estimates*	herd sizes						
scale	125	185	201	235	263	294	333
$\sqrt{\text{wpc}}$	7.092	7.013	7.079	7.448	7.674	8.177	9.002
wpc	50.29	49.19	50.11	53.85	58.90	66.86	81.03

* at: parity=1, twin=0, aut_calv=0, all diseases=0