Chapter 18

Effect modification and interactions

18.1 Modeling effect modification



Figure 18.1: Data from an experimental study investigating the effect of the vitamin B intake on the weight of mice.

Figure 18.2: The data of Figure 18.1 with regression lines for male and female mice.

In some applications one is interested in the question how one covariate may affect the effect of another covariate. Figure 18.1 illustrates a typical situation of this type, in which the effect of the vitamin B intake on the weight of mice seems to differ between male and female mice. If we fit regression lines separately for male and female mice (Figure 18.2), it looks like that the vitamin B has only a small effect in female mice, but a large effect in male mice.

Fitting two regression lines, however, does not directly allow to compare the two lines in the sense of assessing the statistical significance of the difference between the two lines. This can

be approached by considering a joint model across the two groups. Introducing the random variables

$$X_1$$
 = Vitamin B intake (in mg)

and

$$X_2 = \begin{cases} 1 & \text{if mouse is male} \\ 0 & \text{if mouse is female} \end{cases}$$

we can describe the situation by two separate regression models:

$$\mu(x_1, x_2) = \begin{cases} \beta_0^A + \beta_1^A x_1 & \text{if } x_2 = 1\\ \beta_0^B + \beta_1^B x_1 & \text{if } x_2 = 0 \end{cases}$$
(*)

with β_1^A denoting the slope in male mice and β_1^B denoting the slope in female mice as the main parameter of interest. However, this description does not have the usual form of a regression model still. This can be approached by regarding X_1 as actually two different covariates, one defined in the male and one defined in the female mice:

$$X_{1}^{A} = \begin{cases} X_{1} & \text{if } x_{2} = 1 \\ 0 & \text{if } x_{2} = 0 \end{cases}$$
$$X_{1}^{B} = \begin{cases} 0 & \text{if } x_{2} = 1 \\ X_{1} & \text{if } x_{2} = 0 \end{cases}$$

We can now consider a regression model with the covariates X_1^A , X_1^B and X_2 which reads

$$\tilde{\mu}(x_1^A, x_1^B, x_2) = \tilde{\beta}_0 + \tilde{\beta}_1^A x_1^A + \tilde{\beta}_1^B x_1^B + \tilde{\beta}_2 x_2$$

Here $\tilde{\beta}_1^A$ denotes the effect of changing X_1 in the male mice, and $\tilde{\beta}_1^B$ describes the effect of changing X_1 in the female mice, and hence it is not surprising that $\tilde{\beta}_1^A = \beta_1^A$ and $\tilde{\beta}_1^B = \beta_1^B$. Indeed, this model is equivalent to the "double" model (*) with the relations

$$\tilde{\beta}_0 = \beta_0^A, \ \tilde{\beta}_1^A = \beta_1^A, \ \tilde{\beta}_1^B = \beta_1^B, \ \text{and} \ \tilde{\beta}_2 = \beta_0^B - \beta_0^A$$

because in the case $x_2 = 0$ we have

$$\mu(x_1, 0) = \beta_0^A + \beta_1^A x_1$$
 and $\tilde{\mu}(x_1^A, 0, 0) = \tilde{\beta}_0 + \tilde{\beta}_1^A x_1^A = \tilde{\beta}_0 + \tilde{\beta}_1^A x_1$

and in the case $x_2 = 1$ we have

$$\mu(x_1, 1) = \beta_0^B + \beta_1^B x_1 \text{ and } \tilde{\mu}(0, x_1^B, 1) = \tilde{\beta}_0 + \tilde{\beta}_1^B x_1^B + \tilde{\beta}_2 = \tilde{\beta}_0 + \tilde{\beta}_2 + \tilde{\beta}_1^B x_1$$

Consequently, if fitting a regression model with the three covariates X_1^A , X_1^B and X_2 to the data of Figure 18.1, we obtain an output like

variable	beta	SE	95%CI	p-value
intercept	47.714	7.845	[25.933,69.495]	0.004
dosemale	0.589	0.158	[0.151,1.026]	0.020
dosefemale	0.143	0.158	[-0.295,0.581]	0.416
sex	2.829	11.094	[-27.974,33.631]	0.811

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and we obtain $\hat{\beta}_1^A = 0.589$ and $\hat{\beta}_1^B = 0.143$ as the slope parameter estimates in males and females, respectively. To assess the degree of effect modification, we will look at the difference between the slopes, i.e.

$$\gamma = \beta_1^B - \beta_1^A$$

and we obtain $\hat{\gamma} = \hat{\beta}_1^B - \hat{\beta}_1^A = 0.589 - 0.143 = 0.446$. By further steps we can obtain a confidence interval of [-0.173, 1.065] and a p-value of 0.116. So the evidence we have in favor for a true difference between male and female mice with respect to the effect of vitamin B intake is limited. However, the large confidence interval suggests that the difference may be substantial. Note that it does not make great sense to look at the p-values of $\hat{\beta}_1^B$ and $\hat{\beta}_1^A$, since it is not the aim of our analysis to assess the question, whether there is an effect in each subgroup, but to assess whether there is a difference in the effect.



Figure 18.3: Data from a clinical trial on an antihypertensive treatment and a visualisation of this data

Figure 18.3 illustrates a second example in which the effect of an antihypertensive treatment is considered to be dependent on sex. We can see that in females the treatment difference can be expressed as an empirical odds ratio of $1.207 = \frac{0.590}{0.489}$, whereas in the males we obtain an odds ratio of $3.331 = \frac{2.045}{0.614}$, i.e. the treatment effect is much bigger in males, as we can also see in the graph of Figure 18.3. We can now use logistic regression to obtain a confidence interval and a p-value for the ratio between these two odds ratios, which describes to which degree sex alters the treatment effect. Introducing the two covariates

$$X_1 = \begin{cases} 1 & \text{if treatment is given to the patient} \\ 0 & \text{if placebo is given to the patient} \end{cases}$$

and

$$X_2 = \begin{cases} 1 & \text{if patient is male} \\ 0 & \text{if patient is female} \end{cases}$$

we can describe the situation again by a double regression model

logit
$$\pi(x_1, x_2) = \begin{cases} \beta_0^A + \beta_1^A & \text{if } x_2 = 1\\ \beta_0^B + \beta_1^B & \text{if } x_2 = 0 \end{cases}$$

and $e^{\beta_1^A}$ is identical with the odds ratio in males, and $e^{\beta_1^B}$ is identical with the odds ratio in females. Consequently, e^{γ} for $\gamma = \beta_1^B - \beta_1^A$ satisfies

$$e^{\gamma} = e^{\beta_1^B - \beta_1^A} = \frac{e^{\beta_1^B}}{e^{\beta_1^A}}$$

i.e. it is the ratio of the odds ratio in males and females.

As above it is equivalent to consider a regression model in the three covariates X_1^A , X_1^B and X_2 and in fitting this model we obtain an output like

variable	beta	SE	95%CI	p-value
intercept	-0.716	0.260	[-1.226,-0.206]	0.006
treatmale	1.204	0.357	[0.504,1.904]	0.001
treatfemale	0.188	0.370	[-0.537,0.912]	0.612
sex	0.227	0.357	[-0.472,0.927]	0.524

The difference $\hat{\gamma} = \hat{\beta}_1^B - \hat{\beta}_1^A = 1.204 - 0.188 = 1.016$ corresponds to the difference we see in Figure 18.3, and by further steps we can obtain a confidence interval of [0.009, 2.024]. By exponentiating the estimate and the confidence interval we obtain 2.763 with a confidence interval of [1.009, 7.568]. Note that 2.763 is exactly the ratio between the two empirical odds ratios 3.331 and 1.207 we have computed above.

The considerations above can be easily extended to categorical covariates. If, for example, a categorical covariate X_2 with three categories A, B, and C modifies the effect of another covariate X_1 , we have just to construct for each category a covariate:

$$X_1^A = \begin{cases} X_1 & \text{if } x_2 = A \\ 0 & \text{if } x_2 \neq A \end{cases}$$
$$X_1^B = \begin{cases} X_1 & \text{if } x_2 = B \\ 0 & \text{if } x_2 \neq B \end{cases}$$
$$X_1^C = \begin{cases} X_1 & \text{if } x_2 = C \\ 0 & \text{if } x_2 \neq C \end{cases}$$

and we proceed as above.



Figure 18.4: The relative frequency of hypertension in dependence on the smoking status and age in an observational study with 1332 subjects. Age is available in years and only grouped into categories for this graph.

It remains to consider the case, in which we are interested in modeling the modifying effect of a continuous covariate on the effect of another covariate. Figure 18.4 illustrates such a situation with the two covariates

$$X_1 = \begin{cases} 1 & \text{subject is a smoker} \\ 0 & \text{subject is no smoker} \end{cases}$$

and

 X_2 = age of subject (in years) ,

and we are interested in how age changes the effect of smoking.

Since X_2 is a continuous covariate, we cannot apply the approach defining a version of X_1 for any value of X_2 . Instead, we have to consider directly the model we are interested in, i.e. a model allowing the effect of X_1 to depend on X_2 . We can write such a model as

logit
$$\pi(x_1, x_2) = \beta_0 + \beta_1(x_2)x_1 + \beta_2 x_2$$
,

i.e. we allow the regression coefficient of X_1 to depend on the value of X_2 . The most simple type of dependence is a linear relation, i.e. we specify the dependence as

$$\beta_1(x_2) = \alpha_0 + \alpha_1 x_2$$

such that α_0 is the effect of X_1 if $x_2 = 0$ and α_1 describes the increase of the effect of X_1 if we increase X_2 by 1.0. If we now insert this in the model above, we obtain

logit
$$\pi(x_1, x_2) = \beta_0 + (\alpha_0 + \alpha_1 x_2) x_1 + \beta_2 x_2$$
,

which we can rewrite as

$$logit \pi(x_1, x_2) = \beta_0 + \alpha_0 x_1 + \alpha_1 x_1 x_2 + \beta_2 x_2 \quad . \tag{**}$$

This is a model we can fit directly to our data. We have just to introduce a new covariate

$$X_3 = X_1 \times X_2$$

variable	beta	SE	95%CI	p-value
intercept	-3.906	0.385	[-4.660,-3.152]	<0.001
smoking	2.955	0.506	[1.963,3.947]	<0.001
age	0.051	0.006	[0.039,0.064]	<0.001
agesmoking	-0.033	0.009	[-0.050,-0.016]	<0.001

and we fit a linear model in the three covariates X_1 , X_2 and X_3 . If we do this for the data of Figure 18.4, we obtain an output like

So we obtain the estimate $\hat{\alpha}_1 = -0.033$, suggesting the the difference between smokers and non smokers with respect to the probability of hypertension (on the logit scale) decreases by 0.033 with each year of age, or by 0.33 with 10 years of age. Or, if one prefers to use odds ratios, that the odds ratio comparing smokers and non smokers decreases by a factor of $e^{-0.33} = 0.72$ with ten years of age.

However, just presenting this result would be a rather incomplete analysis, as we only know, that the difference becomes smaller, but we do not know, how big the effect of smoking is at different ages. Hence it is wise to add estimates of the effect of smoking at different ages, e.g. at the ages of 35 and 75. The effect of smoking at a certain age x_2 is, as mentioned above, $\alpha_0 + \alpha_1 x_2$. According to (**), α_0 is just the coefficient of X_1 in the fitted model, i.e. from the output above we obtain $\hat{\alpha}_0 = 2.955$. So we obtain estimates for the effect of smoking at the age of 35 as

$$\hat{\alpha}_0 + \hat{\alpha}_1 \times 35 = 2.955 + (-0.033) \times 35 = 1.812$$
 or an OR of $e^{1.812} = 6.12$

and at the age of 75 we obtain

$$\hat{\alpha}_0 + \hat{\alpha}_1 \times 75 = 2.955 + (-0.033) \times 75 = 0.506$$
 or an OR of $e^{0.506} = 1.66$.

So the odds ratio for the effect of smoking on hypertension is at the age of 75 only about a fourth of the odds ratio at the age of 35.

Remark: Note that the computation of the effect of smoking at selected ages contributes also to assessing the relevance of the effect modification. In our example, we observe a reduction of the effect of smoking (on the logit scale) from 1.812 at age 35 down to 0.506 at the age of 75. So over the whole range we have a substantial effect of smoking. However, the same estimate of $\hat{\alpha}_1$ will also appear, if the effect of smoking decreases from 0.612 down to -0.694. In this case the effect of smoking vanishes with increasing age and has at the end the opposite sign. Such a qualitative change is much more curios and typically much more relevant than the purely quantitative change seen above.

18.2 Adjusted effect modifications

The adequate assessment of effect modifications may require to take other covariates into account. As an example, let us consider the data shown in Figure 18.5. The effect of alcohol



Figure 18.5: The relative frequency of hypertension (on the logit scale) in dependence on smoking status, alcohol consumption and sex.



Figure 18.6: The relative frequency of hypertension (on the logit scale) in dependence on smoking status and alcohol consumption.

consumption seems to be roughly identical in all four subgroups defined by smoking status and sex. However, if we ignore in our analysis the variable sex (Figure 18.6), it looks like that the effect of alcohol consumption is bigger in smoking subjects. Indeed, if we fit a logistic model to the data of Figure 18.6 allowing different effects of alcohol for smokers and non smokers, we obtain an output like

variable	beta	SE	95%CI	p-value
alcoholsmoker	0.801	0.218	[0.374,1.229]	<0.001
alcoholnosmoker	0.385	0.230	[-0.067,0.836]	0.095
smoking	0.509	0.233	[0.052,0.965]	0.029

suggesting different effects of alcohol consumption for smokers and non smokers. However, if we adjust the analysis for sex, we obtain an output like

variable	beta	SE	95%CI	p-value
alcoholsmoker	0.374	0.235	[-0.086,0.833]	0.111
alcoholnosmoker	0.418	0.244	[-0.061,0.896]	0.087
smoking	0.583	0.247	[0.100,1.067]	0.018
sex	1.390	0.172	[1.053,1.726]	<0.001

with nearly identical effects of alcohol consumption for smokers and non smokers, as suggested by Figure 18.5. The explanation for this striking difference can be found in Figure 18.7, in which we have added the number of subjects in each subgroup. We can see that the subgroup of smokers with high alcohol consumption is dominated by males, whereas in all other subgroups the majority of subjects are females. And as males have in this study a higher risk for hypertension than females, this contributes to the high frequency of hypertension in smokers with high alcohol consumption resulting in the pattern we have seen in Figure 18.6.

Hence this examples illustrates that it is important to adjust for potential confounders in the analysis of effect modifications also.



Figure 18.7: The relative frequency of hypertension (on the logit scale) in dependence on smoking status, alcohol consumption and sex. The numbers indicate the number of subjects behind the relative frequency.

18.3 Interactions

Whenever one starts to model an effect modification one has to be aware of a slight arbitrariness, because we decide in advance that X_1 modifies the effect of X_2 , and not vice versa. However, these two perspectives are equivalent and – in principle – indistinguishable. Let us consider for example Figure 18.4. We have used it to illustrate how age modifies the effect of smoking, but we can also regard it as an illustration that the effect of age is different for smokers and non smokers: The frequency of hypertension increases with age slower for smokers than for non smokers. Similar in Figure 18.3 we may say that each treatment is associated with a sex

effect of its own instead of that sex alters the treatment effect. It may happen that one of the two perspectives sounds more logically but in principle both perspectives are correct.

The symmetry of both perspectives can be also nicely illustrated by our considerations above in the case of continuous covariates. We have shown that modeling the modifying effect of X_2 on the effect of X_1 leads to the expression

$$\beta_0 + (\alpha_0 + \alpha_1 x_2) x_1 + \beta_2 x_2 \\ = \beta_0 + \alpha_0 x_1 + \beta_2 x_2 + \alpha_1 x_1 x_2$$

Now modeling the modifying effect of X_1 on the effect of X_2 leads to

$$\tilde{eta}_0 + \tilde{eta}_1 x_1 + \tilde{eta}_2(x_1) x_2$$

and assuming the $\tilde{\beta}_2(x_1)$ is linear in x_1 we obtain

$$\tilde{\beta}_0 + \tilde{\beta} x_1 + (\tilde{\alpha}_0 + \tilde{\alpha}_1 x_1) x_2$$

= $\tilde{\beta}_0 + \tilde{\beta} x_1 + \tilde{\alpha}_0 x_2 + \tilde{\alpha}_1 x_1 x_2$

where $\tilde{\alpha}_1$ now describes how much the effect $\beta_2(x_1)$ of X_2 increases if we increase X_1 by 1.0. However, in both cases we obtain a linear model in the covariates X_1 , X_2 and X_1X_2 , hence the values of α_1 and $\tilde{\alpha}_1$ are identical. Hence this single number describes both the modifying effect of X_1 on the effect of X_2 as well as the modifying effect of X_2 on the effect of X_1 . Hence choosing only one of these two interpretations is arbitrary.

The statistical literature avoids this problem by introducing the term "interaction", i.e. instead of talking about whether X_1 modifies the effect of X_2 or vice versa, we just say that the two covariates interact. And instead of modeling the modifying effect explicitly as we have done in the previous sections statisticians just add the product X_1X_2 as an additional term to the regression model. This term is called an interaction term, and the corresponding parameter is called an interaction parameter. And we have just seen that this makes perfect sense as this parameter describes the modifying effect from both perspectives.

Adding the product of covariates makes perfect sense also in the case of effect modification by a binary covariate. Let us assume that X_2 is a binary covariate and we start with a model with an interaction:

$$\mu(x_1, x_2) = \tilde{\beta}_0 + \tilde{\beta}_1 x_1 + \tilde{\beta}_2 x_2 + \tilde{\beta}_{12} x_1 x_2 \quad . \tag{(*)}$$

Then

$$\mu(x_1, 0) = \tilde{\beta}_0 + \tilde{\beta}_1 x_1 \text{ and}$$

$$\mu(x_1, 1) = \tilde{\beta}_0 + \tilde{\beta}_1 x_1 + \tilde{\beta}_2 + \tilde{\beta}_{12} x_1 = \tilde{\beta}_0 + \tilde{\beta}_2 + (\tilde{\beta}_1 + \tilde{\beta}_{12}) x_1$$

If we compare this with our explicit modeling of the effect modification

$$\mu(x_1, 0) = \tilde{\beta}_0^A + \tilde{\beta}_1^A x_1 \text{ and} \mu(x_1, 1) = \tilde{\beta}_0^B + \tilde{\beta}_1^B x_1$$

we can observe that

$$\tilde{\beta}_1 = \beta_1^A$$
 and $\tilde{\beta}_1 + \tilde{\beta}_{12} = \beta_1^B$

which implies

$$\tilde{\beta}_{12} = \beta_1^B - \beta_1^A$$

Hence the interaction parameter $\tilde{\beta}_{12}$ is nothing else but the differences of the slopes in the two subgroups defined by X_2 , which we have already previously used to describe the difference between the two subgroups with respect to the effect of X_1 . And of course this fits also to the general interpretation of the interaction parameter: It describes how the effect of X_1 increases if we increase X_2 by 1.0, and if the latter is a binary covariate, a difference of 1.0 means to go from $X_2 = 0$ to $X_2 = 1$.

If we reanalyze the data of Figure 18.1 by a model like (*) with an interaction term, we obtain an output like

variable	beta	SE	95%CI	p-value
intercept	47.714	7.845	[25.933,69.495]	0.004
dose	0.143	0.158	[-0.295,0.581]	0.416
sex	2.829	11.094	[-27.974,33.631]	0.811
dosesex	0.446	0.223	[-0.173,1.065]	0.116

We can see that the estimate $\hat{\beta}_{12} = 0.446$ coincides with the values of $\hat{\gamma}$ we have computed previously. If we want to obtain estimates of the effect of vitamin B intake in the two subgroups, we have just to remember that for females (sex=0) our model reduces to

$$\mu(x_1,0) = \tilde{\beta}_0 + \tilde{\beta}_1 x_1$$

so $\hat{\beta}_1 = 0.143$ is the estimated effect of vitamin B intake in females, and for males it reduces to

$$\mu(x_1, 1) = \tilde{\beta}_0 + \tilde{\beta}_2 + (\tilde{\beta}_1 + \tilde{\beta}_{12})x_1$$

so $\hat{\beta}_1 + \hat{\beta}_{12} = 0.143 + 0.446 = 0.589$ is the estimated effect of vitamin B intake in males.

So using interaction terms in regression models is a general framework which is equivalent to an explicit modeling of effect modifications. Inclusion of interaction terms is directly supported by most statistical packages, whereas the explicit modeling used in the previous sections has to be done usually by hand. Hence the interaction approach is the one typically seen in the literature. However, it is a major drawback of the interaction approach that is does not directly provide effect estimates within subgroups or at selected covariate values, which is essential for the interpretation of interactions. One has to construct such estimates usually by hand, and not all statistical packages support to compute confidence intervals for the constructed estimates. And in my experience this construction is cumbersome and error-prone, especially in models with several interactions or categorical covariates (see the next two sections). Hence I recommend, especially if a researcher starts to investigate effect modifications for the first time, to use an explicit modeling, as this approach is more transparent. However, this is restricted to the case where at least one of the interacting covariates is binary or categorical.

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One may argue that the interaction approach is always the preferable one, as it avoids to select (arbitrarily) a perspective with respect to the effect modification. However, this is in my opinion not a valid argument. As shown above an interpretation of an interaction parameter without taking its actual impact on subgroup specific effects into account will be always incomplete, hence it is dangerous to look only at the value of the interaction parameter. Hence the translation of an interaction parameter into an effect modification is an important step in the analysis. One may now argue that one should always look at both perspectives of effect modification. I agree with this, however, this should not imply that we have to present the results of both perspectives in any paper. It is allowed to select only one of the two perspectives, and typically we are especially interested in one of our covariates, so it makes sense to focus on how the effect of this covariate may depend on other covariates. It is only necessary to keep in mind that there are two perspectives, and to ensure that the perspective neglected is not an important one. As a simple example, let us consider the results of a randomised trial randomising general practitioners (GPs) to an intervention group and a control group. In the intervention group the GPs were informed about recent developments in antidepressant drug treatment and called to use new, effective drugs. To evaluate the study, for each GP the rate of hospitalisation for depression within one year among all patients with a incident diagnosis of depression was computed and averaged over GPs. The following table summarizes the results stratified by practice size:

	practice size		
	small	large	
control group	10.7%	33.4%	
intervention group	27.8%	30.4%	
OR	3.21	0.87	

The above representation suggests that the practice size modifies the intervention effect: A clear deterioration, i.e. increase of hospitalisations in the intervention group in small practices and a slight improvement in large practices. However, a closer look at the table reveals that in the control group reflecting the current situation GPs from small practices are much better in handling patients with depressions than GPs in large practices. If we speculate that the original difference among small and large practices is due to that GPs in small practices have more time to talk with their patients and hence can manage patients suffering from depressions without drug treatment, then we have to conclude that here the intervention modifies the differences between GPs in small and large practices: The focus on drug therapy prevents GPs in the small practices to remain superior to GPs in large practices.

This example illustrates also another problem of using the term "effect modification". It sounds like an action, which really takes place, and that we have a responsible, active actor. However, the only thing we do is to describe a difference of effect (estimates), and we have in any case to think carefully about possible explanations for this. The situation is similar to that of using the term "effect", which we discussed in Section 11.1.

18.4 Modeling effect modifications in several covariates

In some applications one might be interested in investigating the modifying effect of several covariates on the effect of other covariates. As long as we can structure the problem in a way that the effect of a single covariate depends only on one other binary or categorical covariate, one can try the explicit modeling approach of the first section, even if the binary/categorical covariate modifies the effect of several covariates. However, as soon as the effect of one covariate depends on several covariates, this approach becomes cumbersome, and if at least two continuous covariates interact, one is forced to use the interaction term approach by adding an interaction term for each pair of interacting covariates. The interpretation of the interaction terms remain: They describe how the effect of one covariate changes if the value of the other increases by 1.0. In any case one need to compute subgroup specific effects to complete the analysis.

We have seen above, that it can be rather tricky to obtain subgroup specific effects, but there is a simple general strategy to do this. If we are interested in the effects of the other covariates for a specific value x of the covariate X_j , we just have to insert this value into the regression model formula and we obtain a new regression model describing exactly the effect of the other covariates if $X_j = x$. For example, let us assume we are interested in a model with three covariates allowing that X_3 modifies the effect of X_1 and X_2 . Hence we have a model with the interaction terms X_1X_3 and X_2X_3 :

$$\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_{13} x_1 x_3 + \beta_{23} x_2 x_3$$

If we now want to know the effect of X_1 and X_2 if $x_3 = 7.3$, we just have to impute 7.3 for x_3 in the above expression and obtain

$$\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 \times 7.3 + \beta_{13} x_1 \times 7.3 + \beta_{23} x_2 \times 7.3$$

= $(\beta_0 + 7.3 \times \beta_3) + (\beta_1 + 7.3 \times \beta_{13}) x_1 + (\beta_2 + 7.3 \times \beta_{23}) x_2$

So the effect of X_1 is $\beta_1 + 7.3 \times \beta_{13}$ and the effect of X_2 is $\beta_2 + 7.3 \times \beta_{23}$ if $X_3 = 7.3$, and what remains is only to insert the estimates.

Remark: If one is interested in analysing the modifying effect of X_3 and X_2 together on the effect of X_1 , the inclusion of the interaction terms X_1X_2 and X_1X_3 is equivalent to modelling the effect β_1 of X_1 as a linear function of x_2 and x_3 :

$$\beta_0 + \beta_1(x_2, x_3)x_1 + \dots$$

= $\beta_0 + (\alpha_0 + \alpha_2 x_2 + \alpha_3 x_3)x_1 + \dots$
= $\beta_0 + \alpha_0 x_1 + \alpha_2 x_1 x_2 + \alpha_3 x_1 x_3 + \dots$

One can now of course ask, whether there is again an interaction between X_2 and X_3 with respect to the modifying effect. For example if X_2 is age and X_3 is sex, one might be interested in evaluating, whether the effect is especially large in old females. Then one can extend the

above approach to

$$\beta_0 + \beta_1(x_2, x_3)x_1 + \dots$$

= $\beta_0 + (\alpha_0 + \alpha_2 x_2 + \alpha_3 x_3 + \alpha_{23} x_2 x_3)x_1 + \dots$
= $\beta_0 + \alpha_0 x_1 + \alpha_2 x_1 x_2 + \alpha_3 x_1 x_3 + \alpha_{23} x_1 x_2 x_3 + \dots$

i.e. we have to include the product of three covariates. Such interaction terms are called higher order interactions.

18.5 The effect of a covariate in the presence of interactions

Whenever we start to include an interaction term, e.g. X_1X_2 in a regression model, it is our aim to investigate how X_1 modifies the effect of X_2 and vice versa. This implies that we assume a priori that the effect of X_1 varies in dependence on X_2 and vice versa. So it does not make sense to talk about "the effect of X_1 " or "the effect of X_2 ".

Although a sole effect of a covariate involved in an interaction is logically not existing, one can find in the medical literature very frequently that the effect of covariates are reported although they are involved in interactions. There are two reason for this: First many statistical packages report in the analysis of a regression model with interaction terms some estimates which look like effect estimates. Let us look for example again at the output in analysing the data of Figure 18.1 using the interaction term approach.

variable	beta	SE	95%CI	p-value
intercept	47.714	7.845	[25.933,69.495]	0.004
dose	0.143	0.158	[-0.295,0.581]	0.416
sex	2.829	11.094	[-27.974,33.631]	0.811
dosesex	0.446	0.223	[-0.173,1.065]	0.116

To understand the meaning of $\hat{\beta}_1 = 0.143$ and $\hat{\beta}_2 = 2.829$, let us look again at our model:

$$\mu(x_1, x_2) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 x_2 \quad .$$

If we set $x_2 = 0$, we obtain

$$\mu(x_1, 0) = \beta_0 + \beta_1 x_1 \;\;,$$

hence $\hat{\beta}_1$ is just the estimate for the effect of vitamin B in females. And it is completely unjustified to call this the effect of vitamin B intake in general. If we set $x_1 = 0$, we obtain

$$\mu(0, x_2) = \beta_0 + \beta_2 x_2 ,$$

hence $\hat{\beta}_2$ is just the estimate for the effect of sex if we have a vitamin B intake of 0. It is again unjustified to call this the general sex effect and it is moreover an unreliable extrapolation, as the range of vitamin B in the data is from 30 to 70 mg. So it makes no sense to look at these

estimates. We have to regard them usually as nuisance parameters like the intercept parameter. We can only use them as a technical aid in some computations, e.g. for subgroup specific effects.

The second reason is that one can define overall effects of a covariate by taking the average of subgroup specific effects. For example one can in the example above define the overall dose effect as the average of the dose effect in male and female mice, respectively, i.e. as $\frac{1}{2}\beta_1^A + \frac{1}{2}\beta_1^B$, which we can simply estimate by $\frac{1}{2}\hat{\beta}_1^A + \frac{1}{2}\hat{\beta}_1^B$, and we may obtain also confidence intervals and p-values. Some statistical packages provide such estimates and inference in their standard output as "main effects", especially if they are designed to analyse experimental data. There are also subtle differences between different programs with respect to choosing the weights. Some packages give equal weights to the subgroups, some weight the subgroups by their size.

Whether such overall effects are meaningful has to be discussed in each single application. It happens that in spite of a main interest in assessing effect modifications, one still is interested in confirming that a covariate has an effect at all. Then the overall effect provides one reasonable and simple way to answer the question of interest. One has only to be aware of that in the case of a qualitative interaction, i.e. both positive and negative subgroup specific effects, the overall effect may be close to 0 and hence one may fail to demonstrate an overall effect. An alternative is then to perform a test of the null hypothesis

$$H_0: \beta_1^A = 0 \text{ and } \beta_1^B = 0$$
,

i.e. to test whether both subgroup specific effects are 0. If one can reject this null hypothesis, one has also shown that the covariate has some effect. In the case of no qualitative interactions, this test is much less powerful than testing the average effect, so it cannot be recommended in general. Hence we have again here the situation that one typically starts with testing the overall effect, but that in presence of a qualitative interaction one applies post hoc the second test, and has to convince the reader of a paper that this decision is justified.

Remark: The interpretation of the regression parameter of a covariate X_j , which is not involved in any interaction term, is not affected by the presence of interactions terms for other covariates. This parameters describe still the effect of a difference in X_j of 1.0, if we compare two subjects agreeing in all other covariates. This interpretation is obviously independent of how the other covariates may interact together.

18.6 Interactions as deviations from additivity

In the medical literature one can find frequently that interactions are interpreted as deviations from additivity of effects, and one can find the terms synergistic and antagonistic effects for positive or negative interaction terms. The rationale behind this is illustrated at hand of the example in Figure 18.8. In subjects continuing smoking who received only standard antihypertensive treatment we can observe an average decrease of blood pressure by 2.1. In subjects continuing smoking with additional physical exercises we observe an average decrease of 9.5, i.e. physical exercises increase the effect of the standard treatment by 7.4. In subjects quitting



Figure 18.8: Results of a randomised clinical trial in smokers on adding physical exercises to standard antihypertensive treatment, stratified by continuing or quitting smoking

Figure 18.9: The concept of additivity and its relation to the interaction term illustrated at hand of the data of Figure 18.8.

smoking who received only standard antihypertensive treatment we can observe an average decrease of blood pressure by 13.3, so quitting smoking seem to increase the effect of the standard treatment by 11.2. From these numbers we may now expect, that the average decrease in subjects quitting smoking and performing additional physical exercises is 2.1 + 7.4 + 11.2 = 20.7. However, we observe an average decrease in blood pressure of 27.9 in these subjects, i.e. a higher value than we have to expect from the effects of adding additional physical exercises or quitting smoking alone.

This synergistic effect corresponds to a positive interaction term as illustrated in Figure 18.9. Let

 $X_1 = \begin{cases} 1 & \text{physical exercises added to standard treatment} \\ 0 & \text{standard treatment only} \end{cases}$

and

$$X_2 = \begin{cases} 1 & \text{quitting smoking} \\ 0 & \text{continuing smoking} \end{cases}$$

and we consider a regression model with an interaction:

$$\mu(x_1, x_2) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_{12} x_1 x_2 \quad .$$

Then the effect of adding physical exercises to the standard treatment is

$$\mu(1,0) - \mu(0,0) = \beta_1$$

and the effect of quitting smoking under the standard treatment is

$$\mu(0,1) - \mu(0,0) = \beta_2$$

so that in the case of additivity of these two effects we expect

$$\mu(1,1) - \mu(0,0) = \beta_1 + \beta_2$$

but in our model we have

$$\mu(1,1) - \mu(0,0) = \beta_1 + \beta_2 + \beta_{12}$$

such that β_{12} equals the access compared to additivity. Similar, a negative value of β_{12} would correspond to an antagonistic effect, i.e. $\mu(1, 1)$ is smaller than expected.



Figure 18.10: Illustrations of qualitative interactions. Left side: The effect of X_1 is positive if $X_2 = 1$, but negative if $X_2 = 0$ and the effect of X_2 is positive for both values of X_1 . Right side: The effect of X_1 is positive, if $X_2 = 0$, but negative if $X_2 = 1$ and the effect of X_2 is positive, if $X_1 = 0$, but negative if $X_1 = 1$.

It is, however, misleading to interpret any positive interaction parameter as synergy and any negative parameter as antagonism. If, for example, we exchange the values 1 and 0 in one of the covariates in the example above, the interaction parameter will become negative. So it is essential that both covariates have a positive effect in order to associate a positive interaction with synergy. We have already learned that we have to be careful with using the term "effect of a covariate" in the presence of interactions, and it is indeed not enough to look at single effect estimates. Whenever we want to talk about synergistic or antagonistic effects, we have to sort out the situations illustrated in Figure 18.10, where in at least one of the two perspectives of effect modification the modified effect changes its sign. Such situations are often referred to as "qualitative interactions", whereas situation as in Figure 18.8, where we have a positive treatment effect in subjects continuing smoking as well as quitting smoking and a positive effect of quitting smoking in both treatment arms are often referred to as "quantitative interactions". So only if we have the situation of a quantitative interaction and all subgroup specific effects are positive, it makes sense to interpret a positive interaction parameter as synergy and a negative interaction parameter as antagonism.

To check the presence of a quantitative interaction, in the case of two binary covariates we just have to look at the two subgroup specific effects in both perspectives. In the case of continuous covariates we have to define a "natural" range of the covariate and to check, whether the effects have identical signs at both boundaries of the range. However, a small deviation, e.g. an effect of 1.0 at one boundary and an effect of -0.15 at the other boundary may be still regarded as a quantitative interaction, as we make the rather strong assumption that the change of the effect is linear over the whole range. So such a result may be more an indication, that the effect vanishes if we approach the boundary, rather than that the sign of the effect really changes.



Figure 18.11: An artificial dataset

Figure 18.12: The same dataset as in Figure 18.11, now with the outcome on a logarithmic scale on the y-axis.

18.7 Scales and interactions

Figure 18.11 shows the results of an experimental study investigating the effect of two binary covariates X_1 and X_2 on the number of mutations in a cell culture. The mean values suggest that going from $x_1 = 0$ to $x_1 = 1$ doubles the amount of mutated cells in both groups defined by X_2 (5 to 10 if $x_2 = 0$ and 10 to 20 if $x_2 = 1$), so there is no effect modification. However, analysing this data by linear regression, we obtain a highly significant interaction, as we have different differences in the two subgroups: 10-5=5 and 20-10=10. So the absence and presence of an interaction of effect modification depends on whether we consider additive or multiplicative effects. If one views the data on a logarithmic scale (Figure 18.12) for the outcome, the apparent interaction vanishes.

A similar situation occur in the following example, again with two binary covariates, but now with a binary outcome. The (true) model can be described by the following probabilities:

x_1	x_2	$\pi(x_1, x_2)$	logit $\pi(x_1, x_2)$
0	0	0.61	0.45
0	1	0.78	1.27
1	0	0.72	0.94
1	1	0.91	2.31

If we look at the probability values, we have exact additivity: $\pi(1, 0) = \pi(0, 0) + 0.11$, $\pi(0, 1) = \pi(0, 0) + 0.17$, $\pi(1, 1) = \pi(0, 0) + 0.11 + 0.17$. However, on the logit scale we have a distinct interaction, cf. Figure 18.13. Similar, in a Cox model we may have an interaction on the log hazard scale, which correspond to additivity on the hazard scale, or vice versa.



Figure 18.13: Illustrations of a simple model with additivity on the probability scale, but an interaction on the logit scale.

Hence in any interpretation of (quantitative) interactions or effect modification, one has to consider always the choice of the scale as one possible explanation. However, a change in the sign of the effect of a covariate, i.e. a qualitative interaction, is robust against monotone transformations of the scale, so here this explanation cannot be valid.

Remark: In the case of a continuous outcome, one may decide to transform the outcome variable if one feels that the standard scale is inadequate. However, here the same considerations as with transforming the outcome to obtain a better linear fit have to be applied (cf. Section 17.1).

18.8 Ceiling effects and interactions

Many outcome variables cannot be decreased or increased to any degree. There may be biological bounds, e.g. a certain fat intake is necessary for human beings to survive. Many outcome variables are also bounded by the measurement instrument: For example if assessing the quality of life of a patient by scores computed from the marks on a questionnaire, a patient cannot score more than the maximal number of points. If there are now subjects in a study with values close to such a bound, they may be limited in showing a relation to covariates, as they cannot further improve or deteriorate. We then say that a regression analysis may suffer from ceiling (or floor) effects.

Ceiling effects are often a source for interactions, as they may prevent one subgroups of subjects to be sensitive to the covariate of interest. For example we may consider another study in GPs looking at the effect of calling GPS to use more time on counseling in patients suffering from depressions. In such an intervention study we may observe the following result with respect to rates of hospitalisation:

	practio	ce size
	small	large
control group	10.7%	33.4%
intervention group	10.1%	12.4%
OR	0.94	0.28

One may conclude that the intervention is working fine in GPs in large practices whereas in small practices there is no effect. However, it is not allowed to interpret this in the way that GPs in the small practices did not follow the suggestions of the intervention study or lacked compliance in another manner. As visible from the results in the control group GPs in small practice are already today good in handling patients with depressions and the intervention brings the GPs from large practices just up to the level of GPs from small practices. If we assume that 10% of all patients with depression are in general robust against treatment by GPs and can only be managed by hospitalisation, than the GPs in small practices had no chance to improve, and hence no chance to show an effect of the intervention in contrast to the GPs from large practices. So this interaction may be due to a floor effect of GPs in small practices.

So whenever one observes an interaction, one should take a closer look at the data and ask oneself whether it may be due to a ceiling effect. If it can be explained this way, it does not mean that the interaction is invalid or an artefact. It just means that one has to take the ceiling effect into account in the subject matter interpretation of the interaction.

18.9 Hunting for interactions

From a general research methodological point of view it is highly desirable to detect existing interactions. If we use regression models to describe and understand the influence of several covariates X_1, X_2, \ldots, X_p , interactions will make a major contribution to the understanding, as the dependence of the effect of X_1 on X_2 may allow some insights into the mechanism how X_1 influences the outcome. Qualitative interactions are of special importance, as they typically challenge the traditional interpretation of covariates as universal risk factors in the particular setting. So this suggests to look systematically for interactions, whenever we fit a regression model to asses the effect of covariates.

Unfortunately an investigation of interactions or effect modification suffers usually from a poor power. Let us compare the situation of estimating the overall effect β_1 of a covariate X_1 in a model without interactions with estimating the difference between the two subgroup specific effects β_1^A and β_1^B , i.e. an interaction with a binary covariate X_2 . If 50% of our sample shows $X_2 = 1$ and the other half $X_2 = 0$, then each of the two estimates $\hat{\beta}_1^A$ and $\hat{\beta}_1^B$ are based on half of the data. This implies, that their standard errors are inflated by a factor of $\sqrt{2}$ in comparison to the standard error of $\hat{\beta}_1$. And taking the difference $\hat{\beta}_1^B - \hat{\beta}_1^A$ increases the standard error further by a factor of $\sqrt{2}$, such that the standard error of the difference $\hat{\beta}_1^B - \hat{\beta}_1^A$ is hence twice the standard error of $\hat{\beta}_1$. In the situation of a quantitative interaction, we may have $\beta_1^A = 0.5\beta_1$ and $\beta_1^A = 1.5\beta_1$, such that $\beta_1^B - \beta_1^A = \beta_1$, i.e. the parameter of interest is of the same magnitude in both situations. However, if our study has a power of 80% to reject the null hypothesis H_0 : $\beta_1 = 0$, it will have only a power of 29% to reject the null hypothesis H_0 : $\beta_1^A = \beta_1^B$ of no interaction due to the larger standard error of $\hat{\beta}_1^B - \hat{\beta}_1^A$. If we want to have a similar power for the detection of a difference in the sub group specific effects, we have to assume that the difference between β_1^B and β_1^A is twice as β_1 , i.e. a rather extreme effect modification. And in most applications of regression models we are typically glad to have a sample size allowing to estimate the effect of the covariates with sufficient precision to prove that they have an effect, such that we cannot expect a large power to detect interactions.

The second problem with a systematic investigation of interactions is multiplicity. If we have 5 covariates, we have already 10 pairs of covariates, i.e. 10 interaction terms we can add (or even more, if some of the covariates are categorical). So if we just look at the resulting p-values, we cannot regard the significance of an interaction as a reliable indicator for its existence. One can find nevertheless sometimes the results of such a search in medical publications without any attempt to take the multiplicity problem into account, just reporting typically one significant interaction out of 10 or 20 tested. This is of no great value, and it is one example of the bad tradition of "hunting for p-values".

So whenever one starts to think about investigating interactions systematically, one should be aware of that one tries something which has only a very limited chance to produce any reliable result. We have a rather low power to detect true interactions and simultaneously a high chance to produce false signals. To reduce the multiplicity problem the first step should be to define a (small) subset of all possible interactions or effect modifications, which are a priori of special interest or likely to indicate effect modifications of interest. There are three major sources to identify such interactions:

- a) We may find hints on interactions in the literature. These may be due that authors have already investigated effect modification or that studies varying in important population characteristics vary with respect to their effect estimates of a covariate. Personal communications with experienced researchers in the field of interest may be a similar source, as they may have experienced that some traditional factors are of limited value in some subjects.
- b) Certain effect modifications may be more plausible than others. Subject matter reasons may suggest that a factor has different meanings in different subgroups. For example in looking at the association between physical occupation and back pain as considered in

Exercise 8.6, it will not be very surprising that the four categories of physical occupation may show a different effect in males and females due to differences in the physiology and biomechanics between women and men. In contrast, an interaction between social class and sex might be more difficult to explain.

c) If a study focus on a particular covariate, then interactions with this covariate are of higher interest than interactions among other covariates.

Once we have identified a very few of such interactions, we should include them as primary hypotheses in the study protocol, and if we succeed in confirming these hypothesis in the present study, we can include this as a result in our publication without being accused for extensive hunting for p-values. In addition, as a hypotheses generating part of the analysis, one may look systematically at all possible interactions.

In any case, any investigation of interactions should focus on the relevance of the implied effect modifications, not only just on the p-values of the interaction parameters. So a basis for the systematic investigation may be a table structured like that shown in Table 18.1.

effect		effect of covariate					
modifying		age	sex		occupation		
covariate		β_{age}	β_{sex}	$\hat{\delta}_{ ext{blue vs. white}}$	$\hat{\delta}_{ ext{blue vs. others}}$	$\hat{\delta}_{ ext{white vs. others}}$	
	effect at	_					
	age of 30		[,]	[,]	[,]	[,]	
age	effect at	_					
	age of 70		[,]	[,]	[,]	[,]	
	difference	_					
			[,]	[,]	[,]	[,]	
	effect		_				
	in males	[,]	—	[,]	[,]	[,]	
sex	effect		_				
	in females	[,]	—	[,]	[,]	[,]	
	difference		_				
		[,]	_	[,]	[,]	[,]	
	effect for			_	_	_	
	blue collar	[,]	[,]				
	effect for			_	_	_	
occupation	white collar	[,]	[,]				
	effect for			_	_	_	
	others	[,]	[,]				
	p-value			_	_	_	

Table 18.1: A proposal for a tabular presentation of relevant results for a systematic investigation of interactions.

18.10 How to analyse effect modification and interactions with Stata

We start with the example of Figure 18.1:

- . clear
- . use vitaminB
- . list

	+		+
	dose	sex	weight
1.	30	1	73
2.	30	0	51
3.	40	1	67
4.	40	0	56
5.	50	1	81
6.	50	0	53
7.	70	1	93
8.	70	0	58
	+		+

We define the two version of the covariate dose, one for the males and one for the females:

- . gen dosemale=dose*(sex==1)
- . gen dosefemale=dose*(sex==0)

Now we can put this into a regression model:

. regress weight dosemale dosefemale sex

SS	df	MS	Number of obs =	8
			F(3, 4) =	22.57
1472.97143	3	490.990476	Prob > F =	0.0057
87.0285714	4	21.7571429	R-squared =	0.9442
			Adj R-squared =	0.9024
1560	7	222.857143	Root MSE =	4.6645
	SS 1472.97143 87.0285714 1560	SS df 1472.97143 3 87.0285714 4 1560 7	SS df MS 1472.97143 3 490.990476 87.0285714 4 21.7571429 1560 7 222.857143	SS df MS Number of obs = 1472.97143 3 490.990476 F(3, 4) = 87.0285714 4 21.7571429 R-squared = 1560 7 222.857143 Root MSE =

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weight		Coef.	Std.	Err.		t	P>	t	[9	5% Con	f. I	nterva	[]
dosemale dosefemale sex _cons	 - - 2 4	5885714 1428571 2.828571 47.71429	.157 .157 11.0 7.84	6874 6874 9429 4848	3. 0. 0. 6.	73 91 25 08	0.0 0.4 0.8 0.0	 20 16 11 04	.1 2 -27 2	507611 949532 .97412 5.9335		1.02638 .580663 33.6312 69.4950	32 75 26 97

We obtain directly the two sex specific effect estimates of the vitamin B intake. To assess the difference between the two effect estimates, we can use the lincom command.

. lincom dosemale-dosefemale

```
(1) dosemale - dosefemale = 0
```

weight	Coef.	Std. Err.		P> t	[95% Conf.	Interval]
(1)	.4457143	.2230036	2.00	0.116	173443	1.064872

If we assume that we are also interested in showing that the vitamin B intake has any effect, we can perform the strategy discussed in Section 18.5 and look on the average dose effect:

. lincom 0.5*dosemale+0.5*dosefemale

```
( 1) .5*dosemale + .5*dosefemale = 0
```

weight	Coef.	Std. Err.	t	P> t	[95% Conf.	Interval]
(1)	.3657143	.1115018	3.28	0.031	.0561356	.6752929

So we have evidence for an effect of the dose. For illustrative purposes we also perform the alternative strategy to test the null hypothesis of no effect in both male and female mice:

. test dosemale dosefemale

- (1) dosemale = 0
- (2) dosefemale = 0

F(2, 4) = 7.38 Prob > F = 0.0455

Note that the p-value is bigger, reflecting the lower power of this approach.

If we want to follow the approach to add interaction terms, we can define the product of the covariates dose and sex explicitly

. gen dosesex=dose*sex

and add it to the regression model:

. regress weight dose sex dosesex

Source	SS	df	MS		Number of obs	= 8
	+				F(3, 4)	= 22.57
Model	1472.97143	3 490.	990476		Prob > F	= 0.0057
Residual	87.0285714	4 21.7	571429		R-squared	= 0.9442
	+				Adj R-squared	= 0.9024
Total	1560	7 222.	857143		Root MSE	= 4.6645
weight	Coef.	Std. Err.	t	P> t	[95% Conf.	Interval
doco	+	1576074	0 01	 ۵ /16	2040522	E 006675
uose	.14205/1	.15/00/4	0.91	0.410	2949552	. 3000073
sex	2.828571	11.09429	0.25	0.811	-27.97412	33.63126
dosesex	.4457143	.2230036	2.00	0.116	173443	1.064872
_cons	47.71429	7.844848	6.08	0.004	25.9335	69.49507

Note that the results for dosesex agree with those of the first lincom command above.

To obtain the slope estimates within the two sex groups we have just to realize that within the females (sex==0) our model reads

$$\mu(x_1,0) = \tilde{\beta}_0 + \tilde{\beta}_1 x_1$$

such that the effect of the vitamin B intake in females is equal to the effect of dose in the output above. Within males (sex==1) the model reads

$$\mu(x_1, 1) = \tilde{\beta}_0 + \tilde{\beta}_1 x_1 + \tilde{\beta}_2 + \tilde{\beta}_{12} x_1$$
(18.1)

$$= \tilde{\beta}_0 + \tilde{\beta}_2 + (\tilde{\beta}_1 + \tilde{\beta}_{12})x_1 \quad . \tag{18.2}$$

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such that the slope estimate for the males (sex==1) can be computed as

. lincom dose+dosesex
(1) dose + dosesex = 0
weight | Coef. Std. Err. t P>|t| [95% Conf. Interval]
(1) | .5885714 .1576874 3.73 0.020 .1507611 1.026382

The tests about any effect of the vitamin B intake can be performed by

. lincom 0.5*dose + 0.5*(dose+dosesex)

```
(1) dose + .5*dosesex = 0
```

weight	Coef.	Std. Err.	t	P> t	[95% Conf.	Interval]
(1)	.3657143	.1115018	3.28	0.031	.0561356	.6752929

and by

. test dose dosesex

(1) dose = 0
(2) dosesex = 0
F(2, 4) = 7.38
Prob > F = 0.0455

One can also use Stata's xi: construct to add the product of the covariates to the regression model:

. xi: regress we	eight i.sex*	dose					
i.sex	_Isex_0-1		<pre>(naturally coded; _Isex_0 omitted)</pre>				
i.sex*dose _IsexXdose_#		(coded as above)					
Source	SS	df	MS	Number of obs =	8		

	+-						F(3,	4)	=	22.57
Model	Ι	1472.97143	3	490.	990476		Prob) > F		=	0.0057
Residual	L	87.0285714	4	21.7	7571429		R-so	quare	d	=	0.9442
	+-						Adj	R-sq	uared	=	0.9024
Total	L	1560	7	222.	857143		Root	: MSE		=	4.6645
weight		Coef.	Std.	Err.	t	P> t	 ا	 [95% (Conf.	In	terval]
Isex1		2.828571	11.09	429	0.25	0.811	-2	27.97	412	3	3.63126
dose	Ι	.1428571	.1576	874	0.91	0.416		2949	532		5806675
_IsexXdose_1	Ι	.4457143	.2230	036	2.00	0.116	-	173	443	1	.064872
_cons	I	47.71429	7.844	848	6.08	0.004		25.9	335	6	9.49507

Note however that this does not work if both covariates are continuous.

We now consider the example of Figure 18.4.

. use hyper

. list in 1/10

	+			+
	id	age	smoking	hyper
1.	1	47	0	0
2.	2	53	1	1
3.	3	50	1	1
4.	4	40	1	1
5.	5	33	1	0
6.	6	47	0	0
7.	7	54	1	1
8.	8	38	0	0
9.	9	59	0	1
10.	10	67	0	1
	+			+

and would like to investigate the effect of *smoking* as a function of *age*. Since age is a continuous covariate, we have to follow the interaction approach:

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```
. gen agesmoking=age*smoking
```

```
. logit hyper age smoking agesmoking
           log likelihood = -877.28077
Iteration 0:
Iteration 1: log likelihood = -795.08929
Iteration 2: log likelihood = -793.22769
Iteration 3: log likelihood = -793.22413
Iteration 4: log likelihood = -793.22413
                                      Number of obs=1332LR chi2(3)=168.11Prob > chi2=0.0000Pseudo R2=0.0958
Logistic regression
Log likelihood = -793.22413
 _____
    hyperCoef.Std. Err.zP>|z|[95% Conf. Interval]
_____
   age | .0512461 .0064305 7.97 0.000 .0386426 .0638497
smoking | 2.955036 .5061917 5.84 0.000 1.962918 3.947153
 agesmoking | -.0326584 .0087536 -3.73 0.000 -.0498152 -.0155016
     _cons | -3.905869 .3847093 -10.15 0.000 -4.659885 -3.151852
 _____
```

Now we can assess the change of the effect of smoking over 10 years

. lincom agesmoking*10

```
(1) 10*[hyper]agesmoking = 0
```

hyper	Coef.	Std. Err.	Z	P> z	[95% Conf.	Interval]
(1)	3265839	.0875364	-3.73	0.000	4981521	1550156

and we can use lincom's or option to obtain the result as the factor corresponding to the increase of the odds ratio:

- . lincom agesmoking*10, or
- (1) 10*[hyper]agesmoking = 0

hyper		Odds Ratio	Std.	Err.	Z	P> z	[95% C	onf.	Interval]
(1)	+-	.7213839	.0631	474	-3.7	3 0.000	.60765	25	.8564018

Now we look at the effect of smoking at age 35 and age 75:

```
. lincom _b[smoking] + 75 * _b[agesmoking]
```

```
(1) [hyper]smoking + 75*[hyper]agesmoking = 0
```

h	yper	Coef.	Std. Err.	Z	P> z	[95% Conf.	Interval]
	(1)	.5056565	.2059231	2.46	0.014	.1020546	.9092584
. lincom (1) [_b[smok hyper]sm	ing] + 35 * oking + 35*	_b[agesmoki [hyper]agesm	ng] oking =	0		
h	yper	Coef.	Std. Err.	 Z	P> z	[95% Conf.	Interval]
	(1)	1.811992	.2217385	8.17	0.000	1.377393	2.246591

Finally, we take a look at how to perform likelihood ratio tests. (Which are again slightly more powerful.) First we test the null hypothesis of no interaction by comparing the model above with a model without an interaction:

```
. estimates store A
```

```
. logit hyper age smoking
```

Iteration	0:	log	likelihood	=	-877.28077
Iteration	1:	log	likelihood	=	-801.10435
Iteration	2:	log	likelihood	=	-800.2788
Iteration	3:	log	likelihood	=	-800.27872

Logistic regression

Number of obs	=	1332
LR chi2(2)	=	154.00
Prob > chi2	=	0.0000

Log likelihood = -800.27872					Pseudo R2 =			
hyper	Coef.	Std. Err.	Z	P> z	[95%	Conf.	Interval]	
age smoking _cons . lrtest A	.0344195 1.139242 -2.936872	.0043207 .1214511 .2597851	7.97 9.38 -11.31	0.000 0.000 0.000	.0259 .901 -3.446	511 202 6042	.0428878 1.377281 -2.427703	
Likelihood-ratio test (Assumption: . nested in A)					LR chi2(Prob > c	(1) = hi2 =	14.11 0.0002	

Next we test the null hypothesis of "no effect of smoking at all" by comparing the full model with the model in which all terms involving smoking are omitted:

. logit hyper age Iteration 0: log likelihood = -877.28077 Iteration 1: log likelihood = -846.18595 Iteration 2: log likelihood = -846.07003 Iteration 3: log likelihood = -846.07002 Number of obs = 1332 LR chi2(1) = 62.42 Prob > chi2 = 0.0000 Logistic regression Log likelihood = -846.07002Pseudo R2 = 0.0356 _____ hyper | Coef. Std. Err. z P>|z| [95% Conf. Interval] age | .0320192 .0041419 7.73 0.000 .0239012 _cons | -2.278813 .2361742 -9.65 0.000 -2.741706 .0401373 -1.81592 _____ . lrtest A Likelihood-ratio test LR chi2(2) = 105.69Prob > chi2 = 0.0000 (Assumption: . nested in A)

18.11 Exercise Treatment interactions in a randomised clinical trial for the treatment of malignant glioma

The dataset gliom includes data from a randomised clinical trial comparing a mono chemotherapy (BCNU) with a combination therapy (BCNU + VW 26) for the treatment of malignant glioma in adult patients. The variable time includes the survival time (in days) after chemotherapy (if died==1), or the time until the last contact with the patient (if died==0).

- a) It has been claimed that the benefit from the combination therapy depends on the performance status of the patient. The variable ps divides the subjects into those with poor performance status (ps==0) and those with good performance status (ps==1). Try to clarify the claim based on the available data. Try to support the results of your analysis by appropriate Kaplan Meier curves.
- b) Some people have even raised doubt about that the combination therapy is of any benefit for the patients. Try to clarify this question based on the available data.
- c) It has been claimed that the benefit from the combination therapy depends on the age of the patient. Try to clarify this claim based on the available data. Try to support the results of your analysis by appropriate Kaplan Meier curves.
- d) The dataset includes besides the variable ps also a variable karnindex, which divides the subjects into three groups according to their Karnofsky index, a more detailed measurement of the performance status. Try to reanalyse a) again using this variable. Try to support the results of your analysis by appropriate Kaplan Meier curves.