Polytomous Models		Polytomous Models	Ŵ
		Polytomous Models	
		extension to more than two response categories $h = 0, 1, \dots$	., m
		nominal responses (multidimensional):	
Part 8: Polytomous Models		The Polytomous Multidimensional RM	
Partial Credit Model (PCM) and Rating Scale Model (RSM)	)	$P(X_{vi} = h   \theta_{vh}, \beta_{ih}) = \frac{\exp(\theta_{vh} - \beta_{ih})}{1 + \exp(\theta_{vh} - \beta_{ih})}$	
		there are $h$ latent dimensions	
		$X_{vi} \dots$ person $v$ scores in category $h$ of item $i$ $\theta_{vh} \dots$ location of person $v$ on latent trait $h$ $\beta_{ih} \dots$ location of item $i$ on $h$ -th latent trait	
Psychometric Methods 2010/11		Psychometric Methods 2010/11	
Polytomous Models		Polytomous Models	ių,
ordinal responses (unidimensional):		ICCs for the PCM	
Partial Credit Model (PCM; Masters, 1982)		ICC plot for item 12	
$P(X_{vih} = 1) = \frac{\exp[h\theta_v - \beta_{ih}]}{\sum_{l=0}^{m_i} \exp[l\theta_v - \beta_{il}]}$ introducing the restrictions $\theta_{vh} = h\theta_v$ $\beta_{ih}$ 's describe item-category combinations number of categories may vary across items $(m_i)$ alternative formulation: $P(W_{ih} = 1) = \frac{\exp[h(\theta_v - \beta_i) + \omega_{hi}]}{\exp[h(\theta_v - \beta_i) + \omega_{hi}]}$		Acobastic ul disposicional di category 1 Category 1 Category 2 Category 3 Category 3 Category 3	
$P(X_{vi} = h) = \frac{\sum_{l=0}^{m_i} \exp[l(\theta_v - \beta_i) + \omega_{li}]}{\sum_{l=0}^{m_i} \exp[l(\theta_v - \beta_i) + \omega_{li}]}$ $\omega_{hi} \text{ are category parameter, have also interpretation as cumultive thresholds}$	a-	-4 -2 0 2 4 Latent Dimension	
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#### Polytomous Models

independent

# ۲ **Derivation of the PCM (cont'd)** how about hierarchical dependence? RM requires one parameter for each item and probabilities being

alternative view of  $\beta$ :

instead of ordered level difficulty it can be seen as difficulty of each successive step

- third step, e.q., is from level 2 to level 3
- difficulty of this step governs probability to complete this step (to level 3)
- i.e., the probability of making 3 rather than 2 (once having reached 2)

it says nothing about other steps, they depend on  $\theta$  and the other  $\beta$ 's

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Polytomous Models

### The Rating Scale Model (RSM)

derived in a different context (Andrich, 1978) can be seen as special case of the PCM

if we simplify the PCM by  $\omega_{hi} = \omega_h$  for all *i* and  $m_i$  is m

$$\pi_{vih} = \frac{\exp[h(\theta_v - \beta_i) + \omega_h]}{\sum_{l=0}^{m_i} \exp[l(\theta_v - \beta_i) + \omega_l]}$$

this is sometimes called 'equidistant' scoring we assume, that the distances between the categories are equal across all items used for 'Likert Scales' often too restrictive cannot detect possible violation of 'ordinality'

Polytomous Models

## **Threshold Formulation**

 $\beta_{ii}$  can be rewritten as  $h\beta_i + \omega_{ih}$  giving

$$\pi_{vih} = \frac{\exp[h\theta_v - \beta_{ih}]}{\sum_{l=0}^{m_i} \exp[l\theta_v - \beta_{il}]} = \frac{\exp[h(\theta_v - \beta_i) + \omega_{ih}]}{\sum_{l=0}^{m_i} \exp[l(\theta_v - \beta_i) + \omega_{il}]}$$

 $\omega$ 's can be interpreted as category 'difficulty' parameters

when using

$$\phi_{vij} = \frac{\exp[\theta_v + \tau_{ij}]}{j + \exp[\theta_v + \tau_{ij}]} = \frac{\exp[\theta_v - (\beta_i + \tau_j)]}{j + \exp[\theta_v + (\beta_i + \tau_j)]}$$

in the derivation of the model and normalise  $\tau$  as  $\sum \tau_i = 0$  then  $-\beta_i$  is mean of the threshold locations  $-\tau_i$  are the distances to the thresholds

 $\omega$ 's are cumulative  $\tau$ 's, i.e.,  $\omega_{ih} = \sum_{j=1}^{h} \tau_{ij}$ 

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Polytomous Models





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Polytomous Models		Polytomous Models	Ø	
R commands		PCM Example		
main functions concerning fit of polytomous models:		Data: Eurobarometer 71.1 (Jan/Feb 2009)		
<ul> <li>PCM(data) fits the PCM and generates object of class Rm</li> <li>RSM(data) fits the RSM and generates object of class Rm</li> <li>thresholds(rmobj) displays the itemparameter estimates as thresholds</li> <li>all other functions are the same as previously presented (except for plotjointICC())</li> </ul>		Question Q20: 6 Items on satisfaction with aspects of everyday life qa20_1: HOUSING qa20_2: AREA qa20_3: LIVING STANDARD qa20_4: STATE OF HEALTH qa20_5: MEDICAL SERVICES qa20_6: JOB OPPORTUNITIES		
		responses recoded (for this example): (0) not at all satisfactory(3) very satisfactory		
		Italian subsample, $n = 1009$ (NAs removed)		
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Polytomous Models		Polytomous Models	Ŵ	
PCM Example		Analysis using eRm		
ASK ALL         QA20       I am now going to read out different aspects of everyday life. For each, could you tell me if this aspect of your life is very satisfactory, fairly satisfactory, not very satisfactory or not at all satisfactory?         (SHOW CARD WITH SCALE - ONE ANSWER PER LINE)         ISHOW CARD WITH SCALE - ONE ANSWER PER LINE)         I (READ OUT)       Very Fairly satisfactor satisfactor satisfactor y y         y       Not very y       Not at all DK         I (READ OUT)       Very Fairly satisfactor satisfactor y       Not at all DK         I Your house or flat       1       2       3       4       5         (335)       I hequility of life in the area       1       2       3       4       5         (336)       3       Yery       Site of health       1       2       3       4       5         (336)       3       Yery       3       4       5         (336) <th cols<="" td=""><td></td><td><pre># data load(file="zacatI.Rdata") # pM&lt;-PCM(zacatI[,1:6]) thresholds(pM) plotPImap(pM) # # check the model LRtest(pM) # items 1, 3, 4 inappropriate response patterns # let's have a look at the distribution of the response patterns apply(zacatI[,1:6],2,table) # response distribution # # rawscores r&lt;-rowSums(zacatI[,1:6]) median(r) mean(r) attach(zacatI) table(r,QA20_1) # suggests to split: &lt;=8,&gt;8</pre></td><td></td></th>	<td></td> <td><pre># data load(file="zacatI.Rdata") # pM&lt;-PCM(zacatI[,1:6]) thresholds(pM) plotPImap(pM) # # check the model LRtest(pM) # items 1, 3, 4 inappropriate response patterns # let's have a look at the distribution of the response patterns apply(zacatI[,1:6],2,table) # response distribution # # rawscores r&lt;-rowSums(zacatI[,1:6]) median(r) mean(r) attach(zacatI) table(r,QA20_1) # suggests to split: &lt;=8,&gt;8</pre></td> <td></td>		<pre># data load(file="zacatI.Rdata") # pM&lt;-PCM(zacatI[,1:6]) thresholds(pM) plotPImap(pM) # # check the model LRtest(pM) # items 1, 3, 4 inappropriate response patterns # let's have a look at the distribution of the response patterns apply(zacatI[,1:6],2,table) # response distribution # # rawscores r&lt;-rowSums(zacatI[,1:6]) median(r) mean(r) attach(zacatI) table(r,QA20_1) # suggests to split: &lt;=8,&gt;8</pre>	

Polytomous Models	۲	Polytomous Models	
Analysis using eRm (cont'd)		Analysis using eRm (cont'd)	
<pre># look at possible split values for other items table(r,QA20_3) # 'too good' to split table(r,QA20_4) # either at 6, 7 or 8 # # let's try sex lrs&lt;-LRtest(pM,splitcr=SEX) lrs # # let's try age lra&lt;-LRtest(pM,splitcr=AGE) # significant lra # again inappropriate response patterns # # now Item 1 table(QA20_1,AGE) # no cat 1 response for youngest category # collapse age categories age3&lt;-ifelse(AGE&gt;1,AGE-1,AGE) lra3&lt;-LRtest(pM,splitcr=age3) # still significant lra</pre>		<pre># plot estimates beta3&lt;-as.matrix(as.data.frame(lra\$betalist)) beta3<beta3 #="" difficulty="" parameters<br="">pairs(beta3, lower.panel=panel.smooth, upper.panel=panel.smooth) # # one with value very large value table(age3,QA20_6) # few responses in category 3 # # check if RSM is possible rM&lt;-RSM(zacatI[,1:6]) devdiff&lt;-2*(pM\$loglik-rM\$loglik) dfdiff&lt;-pM\$par =rM\$npar 1-pchisq(devdiff,dfdiff) # no # # further steps can be taken by collapsing categories, covariate = # detach(zacatI) # don't forget</beta3></pre>	Levels,
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