

Generalised multinomial logit models for assessing scale heterogeneity in patient preferences: an example using HIV treatment preferences

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BACKGROUND

- Patient preference weights may be subject to 'scale' heterogeneity whereby some individuals make more random choices compared to others.
- Generalised multinomial logit (GMNL) models have recently been developed to deal with such heterogeneity [1].
- Objectives: To compare GMNL, scale heterogeneity multinomial logit model (SMNL) and mixed logit (MIXL) models.

METHODS

- A prospective, multi-country, web-based survey was set up to collect data from European HIV patients currently treated with anti-retroviral therapy (ART). A steering committee consisting of clinicians, nurses, pharmacists, patient group representatives, and academics guided the initial survey design. HIV patient organisations provided feedback on the pilot survey which was tested by patients.
- Data for this analysis is from the UK survey and discrete choice experiment (DCE) [2-3] which took place from June to October 2014. The survey methodology, a summary of patient characteristics and key results have been presented elsewhere [4].
- The DCE consisted of 12 scenarios of two hypothetical drugs with five treatment attributes. For each of the 12 scenarios, patients chose the option they preferred (A or B).
- The response patterns were analysed in STATA v13.1 using generalised multinomial logit models [1,5].
 - In a MIXL model, the attribute coefficients are assumed to be randomly distributed, meaning that heterogeneity in responses are due to an individual having a strong preferences for some attributes compared to other respondents (preference heterogeneity).
 - In the SMNL model, it is assumed that for some patients, their responses in general are more random compared to others, such that, with attribute coefficients fixed, preference heterogeneity is assumed to be due to differences in the scale of the idiosyncratic error term (scale heterogeneity).
 - The GMNL model is a more general case that nests MIXL and SMNL models, and allows for both preference and scale heterogeneity.
 - Model fit was assessed by Bayesian and Akaike information criteria.
 - Willingness to pay (WTP) in GBP was used as a metric to quantify the strength of preference for each attribute.

RESULTS

- Responses were analysed for 278 HIV patients who are currently receiving ART:
 - 72.7% of the respondents are men who have sex with men and 14.7% are female.
 - The (median) duration of treatment is 5 (range 0-27) years, age is 44 (range 21-66) years, and time since diagnosis is 8 years (range 0-30).
 - 56.8% of the patients reported that they occasionally miss one or more doses of their ART treatment; 36% were on a single tablet regimen (STR), 9% were taking five tablets or more per day.
- Across the models, the attribute rankings are similar, though the range of WTP was more extreme for some models than others (Figure 1).
- The best fitting model was the GMNL with random correlated attributes followed by GMNL with random correlated attributes with two respondent-level covariates (disease duration and on STR) and MIXL model (Figure 1).
- Both the MIXL model and SMNL model provide a better fit than the fixed-effect multinomial logit model, however the SMNL model provides less extreme WTP than the MIXL model (Figure 1).

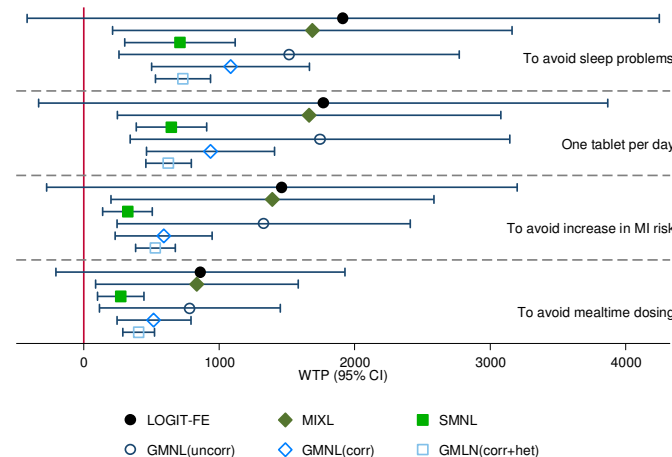


Figure 1: Comparison of WTP for HIV treatment attribute and model fit across 6 MNL models

Model	LL	df	AIC	BIC
LOGIT-FE	-1932.56	7	3879.13	3921.91
MIXL	-1572.68	14	3173.36	3258.94
SMNL	-1905.01	8	3826.01	3874.91
GMNL(uncorr)	-1605.07	16	3242.13	3351.02
GMNL(corr)	-1470.31	37	3014.63	3240.79
GMNL(corr+het)	-1479.78	39	3037.55	3275.94

LOGIT-FE, fixed effect, multinomial logit; MIXL, mixed logit, SMNL, scale heterogeneity fixed effect, multinomial logit; GMNL, generalised multinomial logit; (un)corr, (un)correlated attribute coefficients; het, with heterogeneity parameters (disease duration and on STR); LL, log likelihood; df, degrees of freedom; AIC, Akaike information criteria; BIC, Bayesian information criteria

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RESULTS (continued)

- By examining the respondents' individual log-likelihoods (Figure 2), we can see that respondents can be split into three types [1].
 - Subgroup 1 are responders who make more random choices such that the attribute coefficients are closer to zero (see Figure 3).
 - Subgroup 3 responders have very strong preferences for certain attributes which is reflected in more extreme attribute coefficients (see Figure 3).
 - Subgroup 2 reflects the typical respondents with more 'average' choice behaviour (see Figure 3).
- The SMNL model fits the subgroup 1 and subgroup 3 responders better than the MIXL model (Figure 2) meaning that this model is better equipped to deal with extreme choice behaviour.
- It may be necessary to constrain the full GMNL model to improve convergence [5].

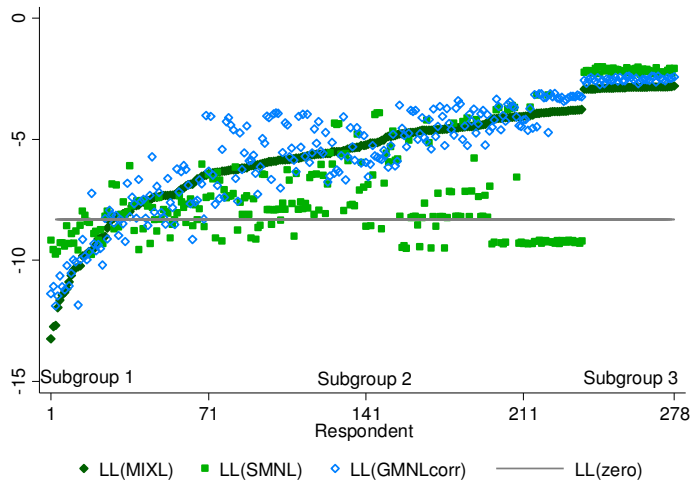


Figure 2: Respondents in order of log-likelihood from MIXL model compared with log-likelihood from SMNL and GMNL(corr) model

LL, log likelihood; MIXL, mixed logit, SMNL, scale heterogeneity fixed effect, multinomial logit; GMNL, generalised multinomial logit; corr, correlated attribute coefficients

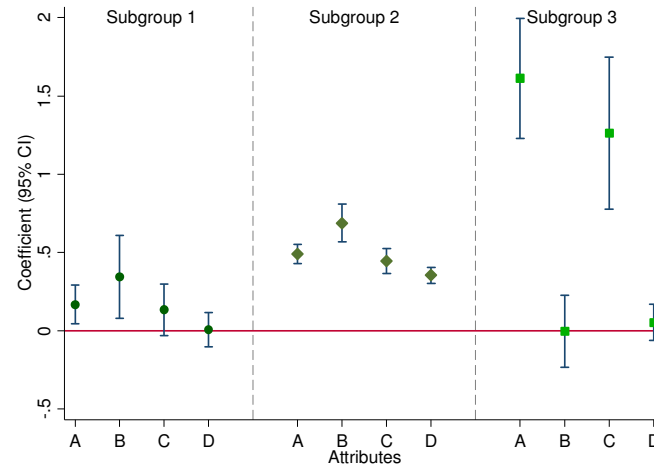


Figure 3: Attribute coefficients estimated from a fixed effect, multinomial logit model with HIV responders split into three subgroups

Subgroup 1: make more random choices (Figure 2, N = 1 to 28); Subgroup 2: display average choice behaviour (Figure 2, N = 29 to 209); Subgroup 3: have strong preferences for selected attributes (Figure 2, N = 210 to 278)
A, avoid sleep problems; B, one tablet per day; C, avoid increase risk in MI; D, avoid mealtime dosing. CI, confidence interval

CONCLUSIONS

- Overall GMNL models provide a flexible framework for analysing preference data taking into account both scale and preference heterogeneity.
- SMNL models have advantages over LOGIT-FE and MIXL models.

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