

Analysis of Stable Matchings in R: Package `matchingMarkets`

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Abstract

R package `matchingMarkets` implements structural estimators to correct for the sample selection bias from observed outcomes in matching markets. This includes one-sided matching of agents into groups as well as two-sided matching of students to schools. The package also contains algorithms to find stable matchings in the three most common matching problems: the stable roommates problem, the college admissions problem, and the house allocation problem.

Keywords: market design, stable matching, matching algorithms, selection models, Bayesian methods, econometrics, R.

1. Introduction

Social scientists are often interested in understanding the outcomes of interactions. Applications range from the success of entrepreneurial teams or management boards (Hoogendoorn, Oosterbeek, and Van Praag 2013) to the performance of bank mergers or credit groups (Klein 2015a). More generally, these questions are at the core of diversity debates on race and gender composition (Herring 2009).

In the economics literature, the markets that describe these interactions are referred to as matching markets. Matching is concerned with who transacts with whom, and how. Economists further distinguish between one-sided and two-sided matching markets. The former are concerned with, for example, who forms a workgroup with whom. Two-sided matching markets consider problems such as who works at which job or which students go to which school, and so on. The empirical analysis of matching markets is naturally subject to sample selection problems. If agents match on characteristics unobserved to the analyst but correlated with both the exogenous variable and the outcome of interest, regression estimates will generally be biased.

In response, Klein (2015a) and Sørensen (2007a) present sample selection models to correct for this bias in one-sided and two-sided matching contexts, respectively. The identifying exclusion restriction in these models is that the characteristics of all agents in a market affect who matches with whom, but the outcome of a match is determined only by its own members. This exogenous variation is similar to an instrumental variable.

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The aim of this paper is to describe the R¹ package `matchingMarkets` (Klein 2015b) that contains Java code for matching algorithms and C++ code for the estimation of structural models that correct for the sample selection bias of observed outcomes in both one-sided and two-sided matching markets. Specifically, the `matchingMarkets` package contains

1. *Bayes estimators.* The estimators implemented in function `stabit` and `stabit2` correct for the selection bias from endogenous matching. The current package version provides solutions for two commonly observed matching processes: (i) the *group formation problem* with fixed group sizes and (ii) the *college admissions problem*. These processes determine which matches are observed – and which are not – and this is a sample selection problem.
2. *Post-estimation tools.* Function `mfx` computes marginal effects from coefficients in binary outcome and selection equations and `khb` implements the Karlson-Holm-Breen test for confounding due to sample selection (Karlson, Holm, and Breen 2012).
3. *Design matrix generation.* The estimators are based on characteristics of all feasible – i.e. observed and counterfactual – matches in the market. Generating the characteristics of all feasible matches from individual-level data is a combinatorial problem. The package returns design matrices based on pre-specified transformations to generate counterfactual matches.
4. *Algorithms.* The package also contains three matching algorithms that can be used to simulated matching data. `hri`: A constraint model (Prosser 2014) for the *stable marriage* and *college admissions* problem, a.k.a. hospital/residents problem (see Gale and Shapley 1962). `sri`: A constraint model for the *stable roommates problem* (see Gusfield and Irving 1989). `ttc`: The top-trading-cycles algorithm for the *housing market problem*. These can be used to obtain stable matchings from simulated or real preference data (see Shapley and Scarf 1974).
5. *Data.* In addition to the `baac00` dataset from borrowing groups in Thailand's largest agricultural lending program, the package provides functions `stabsim` and `stabsim2` to simulate one's own data from one-sided and two-sided matching markets.

Frequently Asked Questions

- *Why can I not use the classic Heckman correction?*

Estimators such as the Heckman (1979) correction (in package `sampleSelection`) or double selection models are inappropriate for this class of selection problems. To see this, note that a simple first stage discrete choice model assumes that an observed match reveals match partners' preferences over each other. In a matching market, however, agents can only choose from the set of partners who would be willing to form a match with them and we do not observe the players' relevant choice sets.

- *Do I need an instrumental variable to estimate the model?*

Short answer: No. Long answer: The characteristics of other agents in the market serve as the source of exogenous variation necessary to identify the model. The identifying exclusion restriction is that characteristics of all agents in the market affect the

¹The R project for statistical computing (R Core Team 2016) at <http://www.r-project.org/>.

matching, i.e., who matches with whom, but it is only the characteristics of the match partners that affect the outcome of a particular match once it is formed. No additional instruments are required for identification (Sørensen 2007a).

- *What are the main assumptions underlying the estimator?*

The approach has certain limitations rooted in its restrictive economic assumptions.

1. The matching models are *complete information* models. That is, agents are assumed to have a perfect knowledge of the qualities of other market participants.
2. The models are *static equilibrium* models. This implies that (i) the observed matching must be an equilibrium, i.e., no two agents would prefer to leave their current partners in order to form a new match (definition of pairwise stability), and (ii) the equilibrium must be unique for the likelihood function of the model to be well defined (Bresnahan and Reiss 1991).
3. Uniqueness results can be obtained in two ways. First, as is common in the industrial organization literature, by imposing suitable *preference restrictions*. A necessary and sufficient condition for agents' preferences to guarantee a unique equilibrium is alignment (Pycia 2012). In a group formation model, pairwise preference alignment requires that any two agents who belong to the same groups must prefer the same group over the other. A second means to guarantee uniqueness is by assigning matches based on matching algorithms that produce a unique stable matching, such as the well-studied Gale and Shapley (1962) deferred acceptance algorithm.
4. Finally, the models assume *bivariate normality* of the errors in selection and outcome equation. If that assumption fails, the estimator is generally inconsistent and can provide misleading inference in small samples (Goldberger 1983).

The remainder of the paper is structured as follows. Section 2 outlines the multi-index sample selection problem, develops the structural model and discusses the identification strategy. Section 3 presents Monte-Carlo evidence of the robustness of the estimator in small samples. Section 4 provides replication code and data for an application of the method in microfinance group formation (see Klein 2015a).

2. Multi-index sample selection

This section develops a structural empirical model to estimate the direct (or causal) effect of the independent variables, net of sorting bias. Technically, the equilibrium groups constitute a self-selected sample.² Heckman (1979) proposes a two-stage correction that estimates selection and outcome equations simultaneously and explicitly models the dependence structure of the error terms. The selection problem at hand, however, differs substantially from that in Heckman.

2.1. Problem statement

The first-stage selection mechanism that determines which player groups are observed (and which are not) is a one-sided matching game and not a simple discrete choice as in the

²Wooldridge (2002, Chapter 17) provides a comprehensive textbook treatment of sample selection models.

Heckman model. A discrete choice model assumes that an observed match reveals group partners' preferences over each other. However, the observed matching is the outcome of complex interactions and conflicts of interest between the players in the market.

To make this point clearer, consider a four-player example where any player strictly prefers matching with partner A or B over C or D . Assume we observe the match of agents C and D in a market of four players A , B , C and D . With a discrete choice model, we would infer that C 's choice of partner D suggests that $u_{C,D} > u_{C,A}$. This restriction on the latent match valuations can then be used to derive the likelihood. However, such a conclusion has potential flaws in matching markets. In such markets, players B , C and D compete over a match with player A . If player A prefers to match with B instead of C , then we observe the match CD from the example although it may well hold that $u_{C,A} > u_{C,D}$. In particular, players can only choose from the set of partners who would be willing to form a match with them. However, we do not observe the players' relevant choice sets. This makes direct inference based on a discrete choice model impossible, even if it accounts for social interactions such as the models in Brock and Durlauf (2007) and Ciliberto and Tamer (2009).

In response to this problem, Sørensen (2007b) generalises the single-index Heckman sample selection model to multi-index sample selection models that allow for selection based on game theoretical models by relaxing the index property. The index property requires that two matches, such as AB and CD , that have the same probability of being observed also have the same conditioning of unobserved characteristics. This requirement fails in matching markets. Here, for safe types A and B the unobserved characteristics are truncated from *below* since they would be unable to match with a safe type if their unobserved characteristics were low. Following the same logic, for risky types C and D the unobserved characteristics are truncated from *above*.

In matching markets, therefore, the index property is violated and a multi-index selection model is called for. This model is a system of two equations. The first equation determines when the outcome is observed, while the second equation determines the outcome.

2.2. Structural empirical model

The first part of the structural model is the selection equation. The selection process can be written as the following system of match equations

$$V_G = W_G \alpha + \eta_G. \quad (1)$$

There are $|\Omega|$ equations, where Ω is the set of feasible groups in the market. $V \in \mathbb{R}^{|\Omega|}$ is a vector of latents and $W \in \mathbb{R}^{|\Omega| \times k}$ a matrix of k characteristics for all feasible groups. $\alpha \in \mathbb{R}^k$ is a parameter vector and $\eta \in \mathbb{R}^{|\Omega|}$ a vector of random errors. Whether a group, and therefore its outcome Y_G , is observed in equilibrium is indicated by $D_G = 1[V_G \in \Gamma_\mu]$. This is an indicator function with $D_G = 1$ if Y_G is observed, and 0 otherwise. Y_G is observed iff a group is part of the equilibrium matching μ in the market. That is, its group valuation is in the set of valuations Γ_μ that satisfy the equilibrium condition.³ This set of valuations is the link between the structural empirical model and the equilibrium characterisations derived in Klein (2015a) (for non-transferable utility) and Proposition A.1 (for transferable utility) in Appendix A. With $V \in \mathbb{R}^{|\Omega|}$, the vector of all valuations in the market, the equilibrium

³The classical Heckman (1979) model is a special case where $D_G = 1[V_G \geq 0]$ and the set of feasible valuations is simply $\Gamma = [0, +\infty)$.

condition can be written as a collection of inequalities that give upper and lower bounds on the match valuations as follows

$$V \in \Gamma_\mu \Leftrightarrow [V_G < \overline{V}_G \ \forall G \notin \mu] \Leftrightarrow [V_G > \underline{V}_G \ \forall G \in \mu]. \quad (2)$$

Substitution of the match valuations in Eqn 1 into the equilibrium condition above, allows us to state the condition on the error terms

$$\mu \text{ is stable} \Leftrightarrow \eta \in \Gamma_\mu - W\alpha. \quad (3)$$

The likelihood of the matching model is then

$$L(\mu; \alpha) = \mathbb{P}(\eta \in \Gamma_\mu - W\alpha) = \int 1[\eta \in \Gamma_\mu - W\alpha] dF(\eta), \quad (4)$$

where $1[\cdot]$ is the indicator function and estimates for α could, in principle, be obtained by maximising this function. When several independent matching markets are observed, the likelihood is the product over these markets. To normalise parameter level, the constant term is excluded from W .

The second part of the model is the outcome equation. The binary outcome is given as $Y_G = 1[Y_G^* > 0]$, where the latent group outcome variable Y_G^* is

$$Y_G^* = X_G\beta + \varepsilon_G, \quad (5)$$

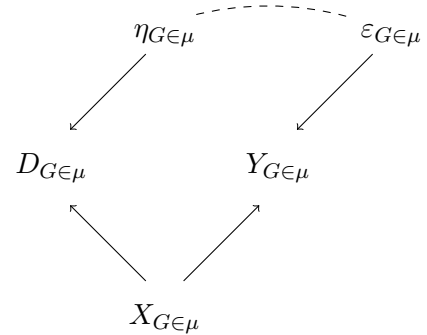
with $\varepsilon_G := \delta\eta_G + \zeta_G$, where ζ_G is a random error. This specification allows for a linear relationship between the error terms in the selection and outcome equation with covariance δ . The design matrices $X \in \mathbb{R}^{|\mu|}$ and $W \in \mathbb{R}^{|\Omega|}$ do not necessarily contain distinct explanatory variables.

2.3. Distribution of error terms

Figure 1 summarises the structural model. If there are unobservables, captured in the error term, that determine both match valuation (the decision who matches with whom in the market) and the outcome, then η and ε are correlated and we have an endogeneity problem.

Figure 1: The structural empirical model.

- $X_{G \notin \mu}$ characteristics of non-equilibrium groups
- $X_{G \in \mu}$ characteristics of equilibrium groups
- $D_{G \in \mu}$ equ. indicator
- $Y_{G \in \mu}$ equ. outcome
- η, ε correlated latents



The joint distribution of ε_G and η_G is assumed bivariate normal with mean zero, and constant covariance δ .

$$\begin{pmatrix} \varepsilon_G \\ \eta_G \end{pmatrix} \sim N\left(0, \begin{bmatrix} \sigma_\xi^2 + \delta^2 & \delta \\ \delta & 1 \end{bmatrix}\right) \quad (6)$$

Here, the variance of the error term of the outcome equation σ_ε^2 is $\text{var}(\delta\eta + \xi) = \delta^2 + \sigma_\xi^2$. To normalise parameter scale, the variance of η and ζ is set to 1, which simplifies σ_ε^2 to $1 + \delta^2$ in the estimation. If the covariance δ were zero, the marginal distributions of ε_G and η_G would be independent and the selection problem would vanish. That is, the observed outcomes would be a random sample from the population of interest.

2.4. Identification

The structural model allows for correlation between ε and η , and imposes necessary equilibrium conditions on the valuations of both observed and unobserved groups. The interaction in the market makes estimation computationally involved but overcomes the identification problem.

Identification requires exogenous variation. In this model, it is the characteristics of the other agents in the market that provide the exogenous variation. To illustrate, recall the four-player example. The characteristics in the outcome equation of group AB are simply $X = (X_{AB})$. The characteristics in the selection equation are $W = (X_{AB}, X_{CD}, X_{AC}, X_{AD}, X_{BC}, X_{BD})$, and the independent elements of W are then $W' = (X_{CD}, X_{AC}, X_{AD}, X_{BC}, X_{BD})$. The identifying assumption is thus that the characteristics of agents outside the match (those comprised in W') are exogenous, i.e., uncorrelated with the error terms. Put differently, the exclusion restriction is that D (which groups are observed in equilibrium) depends the characteristics of all agents in the market, while the outcome of the equilibrium groups only depends on the characteristics of the members of those groups.

In particular, other agents' characteristics are not used as instruments in a traditional sense. Rather than entering the selection equation directly, they pose restrictions on the match valuations by determining the bounds in the estimation.

2.5. Estimation

In the estimation, I follow [Sørensen \(2007a\)](#), who uses Bayesian inference with a Gibbs sampling algorithm that performs Markov Chain Monte Carlo (MCMC) simulations from truncated normal distributions. The latent outcome and valuation variables, Y^* and V , are treated as nuisance parameters and sampled from truncated Normal distributions that enforce sufficient conditions for the draws to come from the equilibrium of the group formation game. For the posterior distributions, see [Klein \(2015a\)](#). For an illustration of the simulation of the posteriors, see [Appendix B](#).

The conjugate prior distributions of parameters α , β and δ are Normal and denoted by $N(\bar{\alpha}, \Sigma_\alpha)$, $N(\bar{\beta}, \Sigma_\beta)$ and $N(\bar{\delta}, \sigma_\delta^2)$. In the estimation, the prior distributions of α and β have mean zero and variance-covariance matrix $\Sigma_\beta = (\frac{1}{|\mu|} X'X)^{-1}$ and $\Sigma_\alpha = (\frac{1}{|\Omega|} W'W)^{-1}$. This is the widely studied and used g-prior ([Zellner 1986](#)). For δ , the prior distribution has mean zero and variance 10. For this parameter, the prior variance is at least 40 times larger than the posterior variance in all estimated models. This confirms that the prior is fairly uninformative.

Under the assumption of transferable utility, estimation is computationally complex due to the valuation of the equilibrium bounds. Here, estimation does not simply involve a maximisation of a given set of valuations as in [Klein \(2015a\)](#). Instead, the bounds in [Eqns 9 and 10](#) derived in [Appendix A](#) require a maximisation over the set of all feasible matchings in the market – rather than only the matches. This involves solving a partitioning linear program (see [Quint](#)

1991).

3. Monte Carlo experiments

The first part of this section presents a simple simulation study of sorting bias. The second part presents Monte Carlo evidence of the correction method proposed in Klein (2015a) (see Section 2) and implemented in R package **matchingMarkets**. It further provides Monte Carlo studies on the robustness of the proposed estimator in small samples.

3.1. A simple example

I first provide a brief overview of the basic functionality of the **matchingMarkets** package and introduce the model specification used in the Monte Carlo experiments.

Individual-level data

The `stabsim` function simulates individual-level, independent variables. The code below generates data for `m=200` markets with `gpm=2` groups per market and group size `ind=5`.

```
R> ## Simulate individual-level, independent variables
R> library(matchingMarkets, quietly = TRUE)
R> idata <- stabsim(m=200, ind=5, seed=123, gpm=2)
R> head(idata)
  m.id g.id      wst  R
1    1    1 -0.56047565 NA
2    1    1 -0.23017749 NA
3    1    1  1.55870831 NA
4    1    1  0.07050839 NA
5    1    1  0.12928774 NA
6    1    2  1.71506499 NA
```

The resulting data frame contains a market and group identifiers `m.id` and `g.id` and the independent variable $wst \sim N(0, 1)$. The dependent variable `R` depends on the error terms and is still undefined at this stage.

Group-level data

Next we apply the function `stabit` that serves three purposes.

- First, it specifies the list of variables to be included in `selection` and `outcome` equations and generates group-level variables based on group members' individual characteristics. For example, the operation `add="wst"` produces the average of variable `wst` for all group members.
- Second, if `simulation="NTU"`, it draws standard normal, group-level unobservables `eta` and `xi` to enter selection and outcome equation and selects equilibrium groups based on the group formation game with non-transferable utility, assuming pairwise aligned preferences as in Klein (2015a). In the case of two groups per market, this selection

rule results in one dominant group with the maximum group valuation and one group comprised of the residual agents.

- Third, the argument `method="model.frame"` specifies that only the group-level model matrices be generated. Other options are estimators using "NTU" for selection correction using non-transferable utility matching as selection rule or "outcome" for estimation of the outcome equation only.

```
R> ## Simulate group-level variables
R> mdata <- stabit(x=idata, simulation="NTU", method="model.frame",
+               selection = list(add="wst"),
+               outcome   = list(add="wst"))
```

The resulting object `mdata` is a list containing data for selection and outcome equations in `SEL` and `OUT`, respectively. `SEL` contains 252,000 rows, one for each of $\binom{5}{10} = 252$ feasible groups in each of the 200 markets. A group's valuation is given by $V = +1*wst.add + eta$. The variable `D` indicates which groups are observed in equilibrium `D=1` and which are not `D=0`.

```
R> head(mdata$OUT, 4)
  m.id g.id intercept    wst.add      R      xi  epsilon
1    1   1         1  0.3698086  1.5670690 -0.8497043  1.5670690
2    1   2         1 -0.2205573 -2.4953827 -1.1373036 -2.4953827
3    2   1         1  0.7198747  1.3680982 -1.1198997  1.3680982
4    2   2         1 -0.3026307  0.3707344 -0.7822018  0.3707344
```

The outcome data in `OUT` contains 400 rows, one for each of 2 equilibrium groups per market. The group outcome is given by $R = 0*wst.add + epsilon$ with $epsilon = eta + xi$.

```
R> head(mdata$SEL, 4)
  m.id g.id reg.id    wst.add D      V      eta
1    1   1     2  0.3698086  1  2.786582  2.4167734
2    1   2     1 -0.2205573  1 -1.578636 -1.3580791
3    1   3    128  0.1935703  0 -0.150347 -0.3439172
4    1   4    129  0.2221432  0  1.820652  1.5985088
```

Bias from sorting

Now, estimating the outcome equation of this model with OLS yields upward biased estimates of the slope coefficient β (see Figure 2a).

```
R> ## Naive OLS estimation
R> lm1 <- lm(R ~ wst.add, data=mdata$OUT)
R> summary(lm1)
```

Call:


```
lm(formula = R ~ wst.add, data = mdata$OUT)

Residuals:
    Min       1Q   Median       3Q      Max
-4.6304 -1.1023 -0.0448  1.2038  4.6228

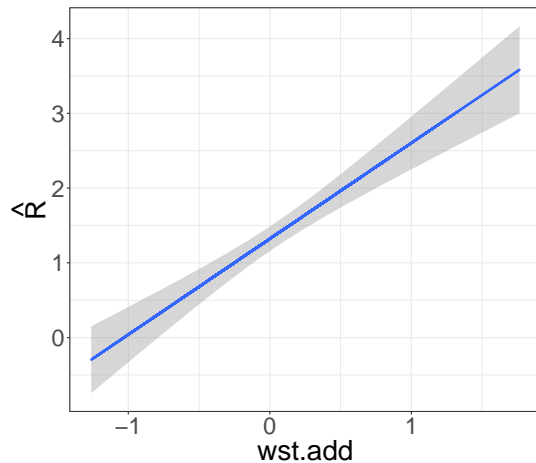
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.32169    0.08377  15.777 < 2e-16 ***
wst.add      1.28172    0.16387   7.822 4.73e-14 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.673 on 398 degrees of freedom
Multiple R-squared:  0.1332, Adjusted R-squared:  0.1311
F-statistic: 61.18 on 1 and 398 DF,  p-value: 4.731e-14
```

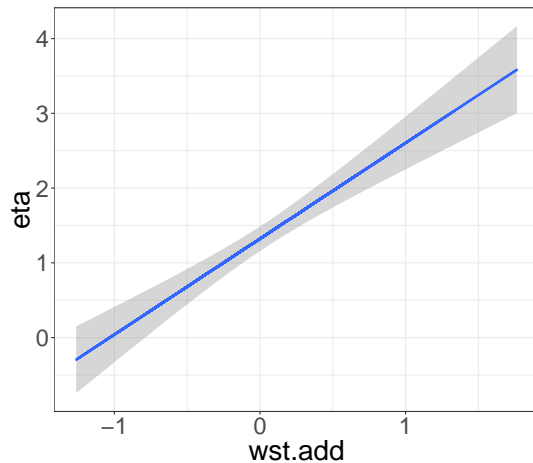
The source of this bias is the positive correlation between `epsilon` and the exogenous variable `wst.add` (see Figure 2b).

Figure 2: Matching on unobservables

(a) Positive sorting bias of the independent variable



(b) Correlation of independent variable with eta



```
R> ## epsilon is correlated with independent variables
R> with(mdata$OUT, cor(epsilon, wst.add))
[1] 0.3650137
```

The intuition behind this bias is given a formal treatment in [Klein \(2015a\)](#). We know that $\epsilon = \delta \cdot \eta$. Thus, conditional on η , the unobservables in the outcome equation are independent of the exogenous variables (because ξ does not enter the selection equation).

```
R> ## xi is uncorrelated with independent variables
R> with(mdata$OUT, cor(xi, wst.add))
[1] 0.001335074
```

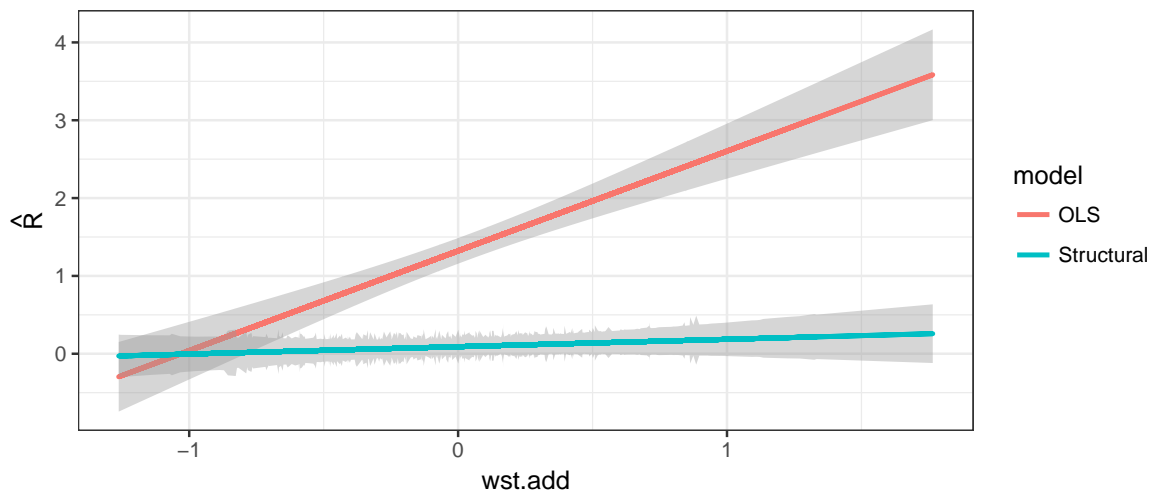
Correction of sorting bias

The selection problem is resolved when the residual from the selection equation, η , is controlled for in the outcome equation (see the horizontal, lower line in Figure 3).

```
R> ## 1st stage: obtain fitted value for eta
R> lm.sel <- lm(V ~ -1 + wst.add, data=mdata$SEL); lm.sel$coefficients
wst.add
1.006372
R> eta <- lm.sel$resid[mdata$SEL$D==1]
R> ## 2nd stage: control for eta
R> coefficients( lm(R ~ wst.add + eta, data=mdata$OUT) )
(Intercept)    wst.add      eta
0.09072970  0.09468869  0.94626877
```

The figure below plots the bias from sorting against the independent variable, for the naive OLS and the selection-correction from the structural model.

Figure 3: Sorting bias corrected: Relative magnitudes of sorting bias and the direct effect.



In most real-world applications, however, the match valuations V are unobserved. The solution is to estimate the selection equation by imposing equilibrium bounds (as derived in Proposition A.1) on the latent match valuations and this is the procedure I follow in the Monte Carlo experiments below.

```
R> ## 4. Run Gibbs sampler
R> fit1 <- stabit(x=idata, method="NTU", simulation="NTU", censored=1, niter=2000,
+               selection = list(add="wst"), outcome = list(add="wst"))
```

```
R> summary(fit1)
```

Coefficients for multi-index sample selection model.

Method: Klein (2015), one-sided matching market

Call:

```
stabit(x = idata, selection = list(add = "wst"), outcome = list(add = "wst"),
      simulation = "NTU", method = "NTU", censored = 1, niter = 2000)
```

Selection equation:

	Estimate	StdErr	t.value	p.value
wst.add	1.15188	0.41565	2.7713	0.005846 **

Outcome equation:

	Estimate	StdErr	t.value	p.value
intercept	0.0733179	0.3871956	0.1894	0.84991
wst.add	-0.0083934	0.4812529	-0.0174	0.98609
delta	0.9632351	0.2999799	3.2110	0.00143 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

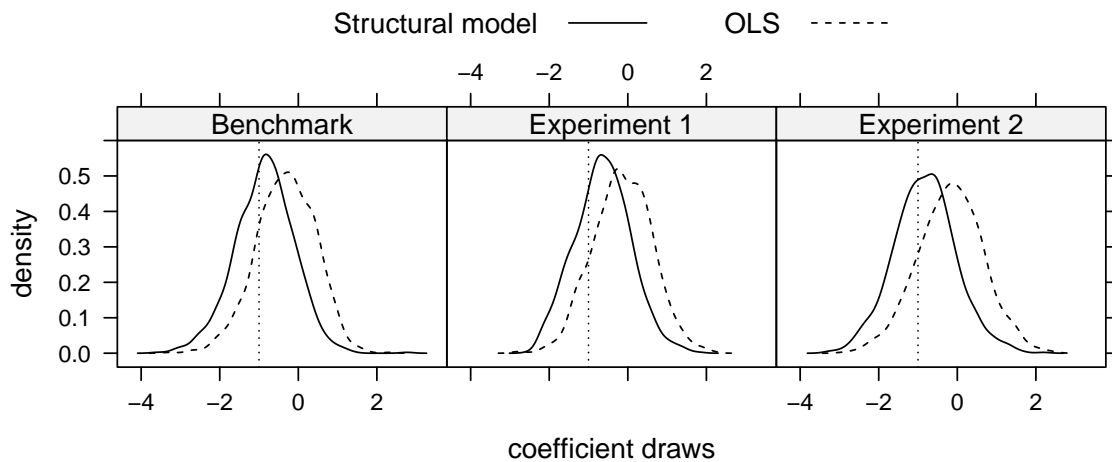
3.2. Simulation results

The Monte Carlo experiments are designed to test for the validity of the estimator. I continue to use the variable `wst.add` from the original model. The true parameters are defined as seen in the first row of Table 1. The table is composed of three blocks, each representing a different market setting and sampling strategy. The first block gives the results of a benchmark experiment that aims to see whether the structural model can reduce the bias of standard OLS estimates. Experiment 1 tests the robustness of the estimator when applied to a random sample of the groups' members. Experiment 2 works with the full population of group members but uses random samples from the counterfactual groups to reduce the computational burden arising from the combinatorics of large groups. I discuss motivation, set-up, implementation and results of each experiment in turn.

Table 1: Monte Carlo results for 40 two-group markets (based on 1,000 draws). True values are given in the first row.

Parameters	α	(Intercept)	β	δ	σ_{ξ}^2
True values	1	0	-1	0.5	1
Benchmark: All group members (5/5); all counterfactual groups (250/250)					
5/5; 250/250 OLS	–	0.304	-0.282	–	1.501
Structural	0.958	-0.112	-0.802	0.469	1.072
Experiment 1: 5 randomly sampled group members; all counterfactual groups					
5/6; 250/250 OLS	–	0.377	-0.242	–	1.676
Structural	0.748	-0.108	-0.642	0.570	0.973
Experiment 2: All group members; 250 randomly sampled counterfactual groups					
6/6; 250/922 OLS	–	0.365	-0.121	–	1.695
Structural	1.052	0.048	-0.707	0.567	0.978

Figure 4: Posterior distributions of parameters for benchmark simulations with 1,000 draws. True values are given by vertical, dotted lines.



Benchmark study

The following steps replicate the results of the benchmark experiment in Table 1. The R code for replication is available in the documentation of function `mce`.

Implementation:

1. Following the nature of the data in the BAAC 2000 survey, I simulate individual-level, independent variables for 40 two-group markets with groups of size five.

```
R> idata <- stabsim(m=40, ind=5, seed=123, gpm=2)
```

2. Repeat the following steps for $i=1$ to 1000.

- a) Draw group-level unobservables ξ and η that determine both (i) which groups are observed in equilibrium and (ii) the equilibrium group outcomes.

```
R> mdata <- stabit(x=idata, selection=list(add="wst"), outcome=
+ list(add="wst"), simulation="NTU", method="model.frame", seed=i)
```

- b) Obtain parameter estimates using (i) OLS and (ii) the structural model.

```
R> ols <- stabit(x=mdata, method="outcome", niter=400000)
R> fit <- stabit(x=mdata, method="NTU", niter=400000)
```

Interpretation: The results for the benchmark study in Table 1 confirm the upward bias in the OLS estimates of the slope coefficient β . It is seen that the structural model successfully reduces the bias resulting from endogenous matching into groups. Note that the modes of the simulated posterior distributions in the first row of Figure 4 correspond to the true values in the first row of Table 1.

The benchmark study works with the full population of borrowers. The two experiments below investigate the robustness of the estimator for the practically more relevant case of working with random samples from the population of interest.

Experiment 1: randomly sampled group members

While group sizes at Grameen Bank, for example, have evolved to five members, self-help group and village lending schemes operate with up to 30 members. Surveys, such as the BAAC survey (Townsend 2000), are often restricted to a random sample of the groups' members.

Set-up: I continue to work with a sample of five borrowers per group but take original group sizes to be six borrowers. This means that one group member is dropped at random.

Implementation:

1. Simulate group-level, independent variables for all $\binom{2n}{n}$ feasible groups of size $n = 6$ in two-group markets.
2. Repeat the following steps 1,000 times.
 - a) Draw group-level unobservables ξ and η that determine both (i) which groups are observed in equilibrium and (ii) the equilibrium group outcomes.
 - b) Randomly drop one member per equilibrium group.
 - c) Generate new group-level, independent variables from the reduced sample of group members (leaving the equilibrium group indicator, D , and group outcomes, R , unchanged).
 - d) Obtain parameter estimates using (i) OLS and (ii) the structural model.

Interpretation: The results for Experiment 1 in Table 1 display clear evidence of attenuation bias (see Wooldridge 2002, Chapter 4.4.2) in both the OLS and structural estimates. The random sampling of group members induces measurement error in the group-level, independent variables that biases the slope estimates towards zero.

Experiment 2: randomly sampled counterfactual groups

While data on the full population of group members solves the attenuation problem encountered in Experiment 1, it creates another problem for statistical analysis. The BAAC 1997 survey (Townsend 1997), for example, comprises data from two-group markets with up to 20 members resulting in $\binom{40}{20} \approx 137.85$ billion feasible groups per market which renders the analysis computationally intractable.

Set-up: As in Experiment 1, the original group size is taken to be six members. In two-group markets, this results in $\binom{12}{6} - 2 = 922$ counterfactual groups, from which 250 groups are sampled at random for the analysis.

Implementation:

1. Simulate group-level, independent variables for all $\binom{2n}{n}$ feasible groups of size $n = 6$ in two-group markets.
2. Repeat the following steps 1,000 times.
 - a) Draw group-level unobservables ξ and η that determine both (i) which groups are observed in equilibrium and (ii) the equilibrium group outcomes.
 - b) Randomly draw 250 groups from the set of counterfactual groups.
 - c) Obtain parameter estimates using (i) OLS and (ii) the structural model.

Interpretation: The results for Experiment 2 in Table 1 suggest that working with a random sample of counterfactual groups does not affect the mode of the posterior distribution of the coefficients. However, the standard deviation of the posterior distribution of β increases from $\hat{\sigma}_{\hat{\beta}} = 0.75$ to 0.79 (not reported in Table 1). A possible explanation is that the random sampling relaxes the equilibrium bounds which results in increased uncertainty in the parameter estimates.

4. Application in microfinance

This section contains R code to replicate the results of the structural model in Table 3 of Klein (2015a). To begin with, load the individual-level data contained in the `matchingMarkets` package (Klein 2015b) and standardise the variables. The 292 borrowers, are nested within 68 groups and 39 markets.

```
R> ## 1. Load individual-level data
R> library("matchingMarkets")
R> data(baac00)
```

In the next step, specify variables and variable transformations for selection and outcome equation. The function `stabit` generates the group-level design matrix and runs the Gibbs sampler with 800,000 iterations to obtain the results of the structural model.

```
R> ## 2-a. Run Gibbs sampler
R> klein15a <- stabit(x=baac00, method="NTU",
+   selection = list(inv="pi",ieq="wst"),
+   outcome   = list(add="pi",inv="pi",ieq="wst",
+     add=c("loan_size","loan_size2","lngroup_agei")),
+   offsetOut=1, binary=TRUE, gPrior=TRUE, marketFE=TRUE, niter=800000
+ )
```

Alternatively, the results can be loaded directly from the package.

```
R> ## 2-b. Load data and get marginal effects
R> data(klein15a)
R> summary(klein15a, mfx=TRUE)
```

Marginal effects for multi-index sample selection model.
Method: Klein (2015), one-sided matching market

Call:

```
stabit(x = baac00, selection = list(inv = "pi", ieq = "wst"),
      outcome = list(add = "pi", inv = "pi", ieq = "wst", add = c("loan_size",
        "loan_size2", "lngroup_agei")), method = "NTU", binary = TRUE,
      offsetOut = 1, marketFE = TRUE, gPrior = TRUE, niter = 8e+05)
```

Selection equation:

	Estimate	StdErr	t.value	p.value
pi.inv	-0.77847	0.92793	-0.8389	0.200771
wst.ieq	0.35601	0.12091	2.9445	0.001624 **
1	-1.50222	4.95863	-0.3029	0.380970
2	-1.30149	1.11601	-1.1662	0.121793
3	-1.59527	1.59147	-1.0024	0.158101
4	-1.36959	1.22883	-1.1145	0.132547
5	-0.31606	3.54283	-0.0892	0.464459
6	-2.96855	4.64408	-0.6392	0.261356
7	-0.35463	1.75609	-0.2019	0.419985
8	-2.48748	2.40423	-1.0346	0.150445
9	-2.09251	1.64972	-1.2684	0.102355
10	-2.79001	2.08429	-1.3386	0.090380 .
11	-2.40204	1.79948	-1.3349	0.090990 .
12	-0.60385	1.65920	-0.3639	0.357959
13	1.41919	1.11175	1.2765	0.100912
14	0.59920	1.50133	0.3991	0.344914

Outcome equation:

	Estimate	StdErr	t.value	p.value
pi.inv	1.571275	1.811454	0.8674	0.1950163
wst.ieq	-0.586014	0.244073	-2.4010	0.0101374 *

```

loan_size.add      0.970321  0.358950  2.7032  0.0047343 **
loan_size2.add    -0.186674  0.078058 -2.3915  0.0103740 *
lngroup_agei.add -0.394577  0.109675 -3.5977  0.0003786 ***
0                  0.479393  0.234757  2.0421  0.0233291 *
1                 -0.040554  0.661055 -0.0613  0.4756688
2                 -0.371607  0.627348 -0.5923  0.2781996
3                  0.203108  0.499668  0.4065  0.3430962
4                 -0.047750  0.553615 -0.0863  0.4658128
5                 -0.073989  0.643599 -0.1150  0.4544777
6                  0.265238  0.582763  0.4551  0.3255307
7                 -0.317368  0.541243 -0.5864  0.2801874
8                 -0.158900  0.614637 -0.2585  0.3985526
9                  0.425090  0.548776  0.7746  0.2211832
10                -0.202136  0.558342 -0.3620  0.3594600
11               -0.056927  0.545283 -0.1044  0.4586439
12                0.420381  0.710406  0.5917  0.2783984
13                0.164946  0.699621  0.2358  0.4073091
delta              0.511696  0.128398  3.9852  0.0001142 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

The results on the attenuation bias in Experiment 1, Section 3, suggests that the difference in the parameter estimates of the Probit and the structural model underestimate the true confounding effect of endogenous matching. Specifically, the selection problem arising from endogenous group formation – while already strongly significant – is still likely to be under-rated because attenuation results in an *underestimation* of the positive Probit coefficient and, at the same time, an *overestimation* of the negative coefficient from the structural model.

The first half of all 800,000 draws are discarded as burn-in draws. The remaining 400,000 draws are used in approximating the posterior means and the posterior standard deviations based on the distributions in Figure 5.

The function `khb` implements the statistical test for confounding in Probit models proposed in [Karlson *et al.* \(2012\)](#). The function takes as arguments the data frame of independent variables $X=X$, the dependent variable $y=R$, and the name of the confounding variable $z="eta"$.

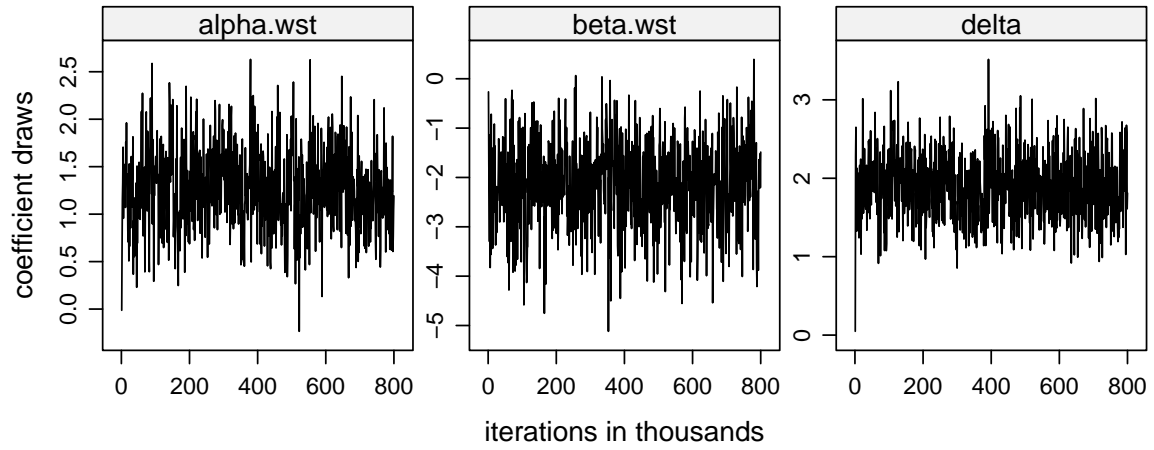
```

R> ## 3. Test for confounding from sample selection (KHB test)
R> with(klein15a$variables, head(khb(X=X, y=Y, z="eta"),5))

Karlson-Holm-Breen method
Null hypothesis: Change in coefficient is not attributable to confounding by z.
      p.value
pi.inv 0.5581
wst.ieq 0.0480
loan_size.add 0.9034
loan_size2.add 0.0442
lngroup_agei.add 0.0412

```


Figure 5: Posterior draws of key parameters in the microfinance application.



The procedure tests for differences in probit and structural model coefficients. It confirms that the probit estimates for variables `wst.ieq`, `loan_size2.add` and `lngroup_agei` are significantly confounded as a result of endogenous matching.

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A. Equilibrium characterisation

Under transferable utility, agents can write binding contracts that specify how to share the total pay-off generated by the collective of all players in the market. As a result, the coordinated efforts of borrowers lead to a matching that maximises the total market pay-off. This pay-off is then shared between the players according to the binding contracts.

A.1. Stability and uniqueness

The group formation game under transferable utility is a special case of the [Kaneko and Wooders \(1982\)](#) partitioning game. A partitioning game consists of a finite set of N players $\mathcal{N} = \{1, \dots, N\}$ and a characteristic function V that assigns a value to each group of players, $G \subset \mathcal{N}$. In the partitioning game, only certain coalitions – so-called *basic coalitions* – can create value. These coalitions are subsets of \mathcal{N} . In the group formation game, the basic coalitions are all groups of size n . The collection of these basic coalitions Ω is the set of feasible matches, i.e. borrowing groups. It can be written as $\Omega = \{G \subset \mathcal{N} : |G| = n\}$.⁴

For the partitioning game, [Quint \(1991\)](#) shows that the equilibrium⁵ coincides with the set of optimal solutions to the dual of a linear programming problem.

A.2. Equilibrium characterisation

Let M denote the set of feasible matchings (or group constellations μ) in the sense that each agent is matched exactly once. This set comprises both the observed group constellation in village t and all unobserved group constellations.⁶ The latter contain equally sized, alternative groups in the same village composed of borrowers from the observed groups. Using this definition, the objective function of the PLP can be rewritten as below. An *optimal partitioning* is a matching μ that maximises the total valuation in the market. This matching is such that it solves the following maximisation problem.

$$\max_{\mu \in M} \sum_{G \in \mu} V_G \quad (7)$$

The equilibrium condition for a coalition-wise (or core) stable matching is given by the following inequality, where $M \setminus \tilde{\mu}$ gives the set of feasible deviations from the equilibrium matching $\tilde{\mu}$.

$$\sum_{G' \in \tilde{\mu}} V_{G'} > \max_{\mu \in M \setminus \tilde{\mu}} \sum_{G \in \mu} V_G \quad (8)$$

The condition can be restated in two simple inequalities that impose upper bounds for non-equilibrium matchings and lower bounds for the equilibrium matchings. [Proposition A.1](#)

⁴In the empirical context of this paper, the set of feasible groups is obtained by generating all k -for- k borrower swaps across two groups in the same village. The total number of swaps in a village with two groups of five borrowers is given by $5 \times 5 = 25$ 1-for-1 swaps, $10 \times 10 = 100$ 2-for-2 swaps, $10 \times 10 = 100$ 3-for-3 swaps and $5 \times 5 = 25$ 4-for-4 swaps (= 250 in total).

⁵Specifically, the set of feasible allocations that cannot be improved upon. This is also referred to as the ‘core’ in the matching literature.

⁶In a context with two groups per market, the number of feasible matchings $|M|$ is half the number of feasible matches $|\Omega|$.

summarises the conditions for pairwise stability based on the bounds \overline{V}_G^* and \underline{V}_G^* derived below.

Proposition A.1 *The matching μ is stable iff $V_G < \overline{V}_G^* \ \forall G \notin \mu$. Equivalently, the matching μ is stable iff $V_G > \underline{V}_G^* \ \forall G \in \mu$.*

Proof A.1 *A matching is stable if deviation is unattractive. Alternative matchings are therefore bound to have lower valuations than observed ones. This naturally leads to upper bounds $V_G < \overline{V}_G^*$ for the valuation of matches $G \in \mu$, not contained in the equilibrium matching $\tilde{\mu}$.*

$$V_G < \sum_{G' \in \tilde{\mu}} V_{G'} - \max_{\mu \in M \setminus \tilde{\mu}} \sum_{G'' \in \mu \setminus G} V_{G''} =: \overline{V}_G^* \quad (9)$$

The upper bounds \overline{V}_G^ are increasing in the valuation of the equilibrium matching $\tilde{\mu}$ (first term on RHS of the inequality in Eqn 9), and decreasing in the valuation of the optimal group constellation of all remaining borrowers not contained in G (second term). It is possible to invert the inequalities to obtain a lower bound $V_G > \underline{V}_G^*$ for the valuation of the equilibrium match $G \in \tilde{\mu}$.*

$$V_G > \max_{\mu \in M \setminus \tilde{\mu}} \sum_{G' \in \mu} V_{G'} - \sum_{G'' \in \tilde{\mu} \setminus G} V_{G''} =: \underline{V}_G^* \quad (10)$$

The lower bound \underline{V}_G^ is increasing in the valuation of the most attractive non-equilibrium matching (first term on RHS of the inequality in Eqn 10) and decreasing in the valuations of the other equilibrium matches without G (second term).*

These conditions are equivalent, but both are important for estimation as they impose different bounds on the latent valuation variables. These inequalities are used in the econometric model to truncate the valuations of feasible groupings.

B. Simulation of posterior distribution

The Bayesian estimator uses the data augmentation approach (proposed by [Albert and Chib 1993](#)) that treats the latent outcome and valuation variables as nuisance parameters. The following four steps illustrate the first iteration of the estimator for the first-stage matching model.

B.1. Match valuations for unobserved groups

The algorithm starts by simulating the latent match valuations for unobserved groups conditional on the data and parameters. In the first iteration illustrated here, the slope parameter α (blue asterisk) and the match valuations of the equilibrium groups (red asterisks) are initially set to zero and match valuations for unobserved groups (black circles) are drawn from a normal distribution with mean zero. For the observed groups to be in equilibrium, the match valuation of the unobserved groups must be lower than the maximum equilibrium group valuation. The draws from the normal are therefore censored from above (gray shades).

B.2. Match valuations for first observed group

In the next step, the match valuation is drawn from a normal distribution with mean zero (conditional mean given by the dashed line). The equilibrium condition holds because the valuation of the second equilibrium group is larger than that of any non-equilibrium group (indicated by the yellow shades). Thus the valuation can be drawn from an uncensored normal.

B.3. Match valuations for second observed group

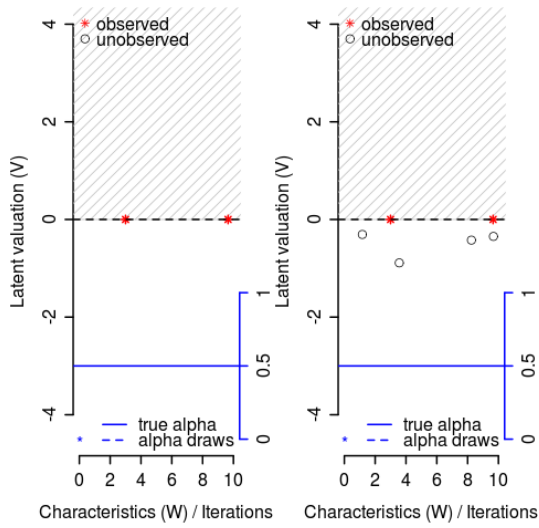
Same procedure as in step 2.

B.4. Alpha slope parameter

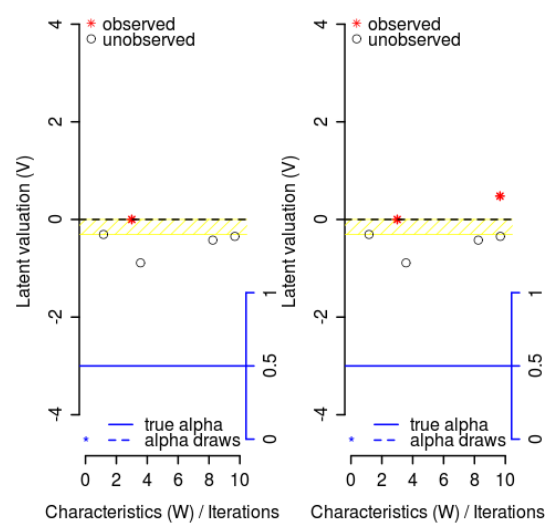
Fit a regression based on the given valuations and data (solid line) and draw α (dashed blue line) from a normal distribution with mean and standard deviation of the estimated slope parameter. Use the new α draw in the next iteration to simulate the latent match valuations, etc etc.

Table 2: Simulation of posterior distribution: Conditional Draws for match valuations and model parameters

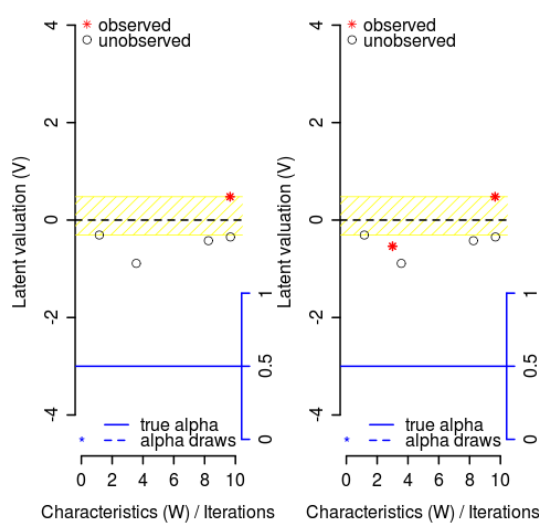
1. Match valuations for unobserved groups before. after.



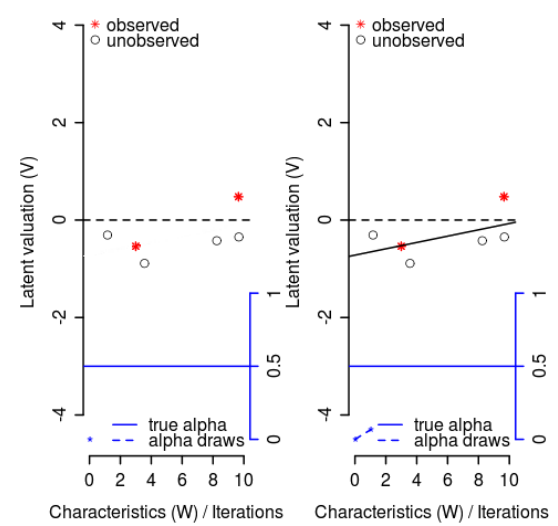
2. Match valuation for 1st observed group before. after.



3. Match valuation for 2nd observed group before. after.



4. Alpha slope parameter before. after.



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