

**The analysis of an individually
randomised clinical trial of back
pain with clustering effect due
to group sessions and repeated
measures**

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A multicentred randomised controlled trial of a primary care-based cognitive behavioural programme for low back pain. The Back Skills Training (BeST) trial

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Executive summary

Health Technology Assessment 2010; Vol. 14; No. 41
DOI: 10.3310/hta14410

Health Technology Assessment
NIHR HTA programme
www.hta.ac.uk



OVERVIEW

- BeST (Back Skills training Trial) with two complex interventions
- In a literature review (Bauer et al., 2008; Roberts and Roberts (2005)) these types of designs are more popular than cluster-randomised and equally popular to the parallel group design.

CURRENT METHODOLOGY (Bauer et al., 2008)

Intercept Model:

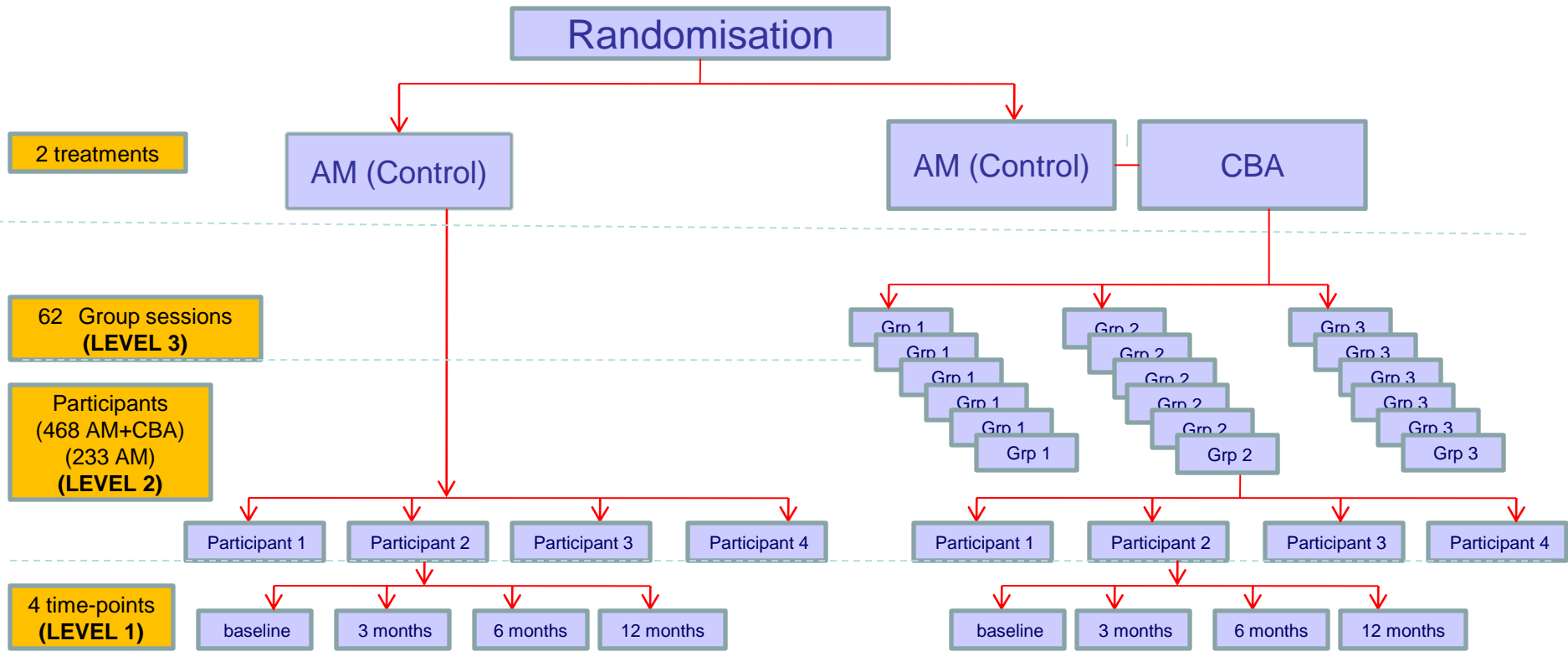
- At level 1 (patient) we can write: $Y_{ij} = \beta_{0j} + \beta_{1j} \textit{treatment}_{ij} + \varepsilon_{ij}$
- At level 2 (group) we can write: $\beta_{0j} = b_{00} + u_{0j} \quad \beta_{1j} = b_{10}$

Heterogeneity across the groups (each participant is a sole member of his own group in the individual arm)

- At level 1 (patient) we can write: $Y_{ij} = \beta_{0j} + \beta_{1j} \textit{treatment}_{ij} + \varepsilon_{ij}$
- At level 2 (group) we can write: $\beta_{0j} = b_{00}$ $\beta_{1j} = b_{10} \textit{treatment} + u_{1j} \textit{treatment}$

Back Skills Training Trial (BeST)

(701 participants with primary outcome response: ROLAND MORRIS QUESTIONNAIRE SCORE)



Multi-level model (with 3 levels)

Level 1 model (time):

$$RMQ_{tj} = \pi_{0ij} + \pi_{1ij} \textit{time} + \varepsilon_{tj}$$

Time profile for each participant

we derive:

- π_{0ij} are the participant specific intercepts
- π_{1ij} are the time slopes and represent the rate of change for a participant across time
- ε_{tj} are the residuals based on the each time t , patient i and group session j

Multi-level model (with 3 levels)

Selecting a variance-covariance structure for the residuals

- The distribution of the residuals associates with repeated observation on same patient is:

$$\varepsilon_{tjj} = \begin{pmatrix} \varepsilon_{1ij} \\ \varepsilon_{2ij} \\ \varepsilon_{3ij} \end{pmatrix} \approx N(0, R_{tjj})$$

- Variance-covariance matrix R_{tjj} for the residuals is defined using unstructured, compound symmetry and autoregressive

$$R_{tjj} = \begin{pmatrix} \text{var}(\varepsilon_{1ij}) & \text{cov}(\varepsilon_{1ij}, \varepsilon_{2ij}) & \text{cov}(\varepsilon_{1ij}, \varepsilon_{3ij}) \\ \text{cov}(\varepsilon_{2ij}, \varepsilon_{1ij}) & \text{var}(\varepsilon_{2ij}) & \text{cov}(\varepsilon_{2ij}, \varepsilon_{3ij}) \\ \text{cov}(\varepsilon_{3ij}, \varepsilon_{1ij}) & \text{cov}(\varepsilon_{3ij}, \varepsilon_{2ij}) & \text{var}(\varepsilon_{3ij}) \end{pmatrix}$$

Multi-level model (with 3 levels)

Level 2 model (participant) clustering one arm of the treatment

$$\pi_{0ij} = \beta_{000} + \beta_{01j} \text{treatment} + r_{0ij} \text{treatment} + \beta_{020} \text{RMQ_b} \quad r_{0ij} \approx N(0, \sigma_{r_{0ij}}^2)$$

$$\pi_{1ij} = \beta_{100} + \beta_{11j} \text{treatment} + r_{1ij} \text{treatment} + \beta_{120} \text{RMQ_b} \quad r_{1ij} \approx N(0, \sigma_{r_{1ij}}^2)$$

- β_{000} overall mean RMQ score over time for all participants in the AM arm
- β_{01j} difference in the mean RMQ for group j, within AM+CBA arm and the overall mean in AM arm
- r_{0ij} the random departure from the overall difference for every participant in his group
is the fixed baseline RMQ parameter

Multi-level model (with 3 levels)

Level 3 model (group) clustering one arm of the treatment

$$\beta_{000} = \gamma_{000} \quad \beta_{01j} = \gamma_{010} + u_{01j} \quad \beta_{020} = \gamma_{020} \quad u_{01j} \approx N(0, \sigma_{u_{01j}}^2)$$

$$\beta_{100} = \gamma_{100} \quad \beta_{11j} = \gamma_{110} + u_{11j} \quad \beta_{120} = \gamma_{120} \quad u_{11j} \approx N(0, \sigma_{u_{11j}}^2)$$

- γ_{000} overall mean RMQ score for all participants in the AM arm (as before)
- γ_{010} difference between the overall treatment mean
- u_{01j} is the deviation of each group mean from this mean in the AM+CBA arm

Multi-level model (with 3 levels)

$$\begin{aligned}
 RMQ_{tij} = & \gamma_{000} + \gamma_{100}time + \gamma_{100}treatment_{ij} + \gamma_{020}RMQ + \\
 & \gamma_{110}time * treatment + \gamma_{120}time * RMQ + \\
 & r_{0ij}treatment + r_{1ij}treatment * time + \\
 & u_{01j}treatment + u_{11j}treatment * time + \\
 & \mathcal{E}_{tij}
 \end{aligned}
 \left. \begin{array}{l} \\ \\ \\ \\ \end{array} \right\} \begin{array}{l} \text{fixed} \\ \\ \text{random} \end{array}$$

Multi-level model (with 3 levels)

Reduction of the model – selecting a structure for the random effects

- RANDOM EFFECT : To preserve the hierarchy test the significance of random effects at level 2 using change in REML , i.e.

$$H_0 : \sigma_{r1ij}^2 = 0$$

$$H_A : \sigma_{r1ij}^2 > 0$$

$$H_0 : \sigma_{u11j}^2 = 0$$

$$H_A : \sigma_{u11j}^2 > 0$$

- FIXED EFFECT : Test the significance of the fixed terms using change in -2 Max LL

Results

<i>NULL(H₀)</i>	<i>ALTERNATIVE (H₁)</i>	<i>NESTED MODEL</i>	<i>REFERENCE MODEL</i>	<i>CHANGE</i>
$\sigma_{r1ij}^2 = 0$	$\sigma_{r1ij}^2 > 0$	Model1 - $r_{1ij} = 0$ (REML =8063.4)	Model 1 (REML=8063.4)	Negligible
$\sigma_{u11j}^2 = 0$	$\sigma_{u11j}^2 > 0$	Model 1- $u_{11j} = \text{Model 2}$ (REML=8063.8)	Model 1- r_{1ij} (REML=8063.4)	0.4 P=0.2635
$\gamma_{110} = 0$ Treatment* time	$\gamma_{110} \neq 0$	Model 2- $\gamma_{110} = \text{Model 3}$ (ML=8038.4)	Model 2 (ML= 8035.7)	2.7 P=0.0502
$\gamma_{120} = 0$ Treatment*baseline	$\gamma_{120} \neq 0$	Model 4 (ML=8038.4)	Model 3- γ_{120} =Model 4 (ML=8038.4)	Negligible
$\sigma_{t1}^2 = \sigma_{t2}^2 = \sigma_{t3}^2 = 0$ Constant residual variance	$\sigma_{t1}^2 \neq \sigma_{t2}^2 \neq \sigma_{t3}^2 \neq 0$	Model 4: CS (AIC=8066.2) Model 4 with UN (AIC=8052.5) Model 4: AR (AIC = 8057.3)		

Multi-level model (with 3 levels)

$$RMQ_{tjj} = \gamma_{000} + \gamma_{100}time + \gamma_{100}treatment_{ij} + \gamma_{020}RMQ + \quad \left. \vphantom{RMQ_{tjj}} \right\} \text{ fixed}$$

$$r_{0ij}treatment + u_{01j}treatment + \varepsilon_{tjj} \quad \left. \vphantom{r_{0ij}treatment} \right\} \text{ random}$$

Results

<i>MODEL</i>	<i>Intercept</i>	<i>Baseline RMQ</i>	<i>Mean Treatment difference</i>	<i>Time-point</i>	<i>P-value for mean treatment difference</i>
Longitudinal model	-0.46 (0.32)	0.78 (0.03)	1.24 (0.30)	0.028 (0.15) 0.04 (0.15)	0.0001
Random effects longitudinal model	-0.11 (0.33)	0.76 (0.03)	1.21 (0.30)	0.15 (0.02)	0.0001

Conclusion

- Power of the study is important in fitting these model
- Results of the longitudinal analysis and hierarchical model very similar
- **FOOD FOR THOUGHT:**
- Implication of clustering effects → increase sample size → more patients to recruit
- If clustering effects are negligible, then (a) is it right to spend large amounts of tax-payers recruiting more patients and (b) and therefore is it ethical to randomise more patient unnecessarily into trials?

Acknowledgements:

- **NIHR Health and Technology Assessment Funding Body (NIHR HTA)**
- **Birmingham Science City Alliance**
- **BeST (Back Skills Training trial) Team**

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