# Likelihood comparison

If the true model is

$$
\begin{aligned}
y_1 &= X(\beta_1 + \Gamma_1(\alpha_1' x)) + X b_1 + \epsilon \\
y_2 &= X(\beta_2 + \Gamma_2(\alpha_2' x)) + X b_2 + \epsilon
\end{aligned}
\tag{1}
$$

If we assume they share the same $\alpha$, the two models are

$$
\begin{aligned}
y_1 &= X(\beta_1 + \Gamma_1(\alpha' x)) + X b_1 + \epsilon \\
y_2 &= X(\beta_2 + \Gamma_2(\alpha' x)) + X b_2 + \epsilon
\end{aligned}
\tag{2}
$$

$\mathrm{df} = 3$

Let's compare the log likelihood calculated from the LME, by using the $\hat{\alpha}$ estimated from

- purity method 1 (coefficient),
- purity method 2 (outcome),
- likelihood method 1 ($f(\theta; y|x)$),
- likelihood method 2 ($f(\theta; y)$),
- likelihood method 3 ($E(\theta)$)

Besides, if we simulate the drug and placebo dataset with different $\alpha$, let's test whether there are significant difference between estimating with one shared $\alpha$ or not.

```
fit_pbo_est_full = lmer(y ~ tt + I(tt^2) + w_pbo + w_pbo * tt + w_pbo * I(tt^2) +
                        (tt + I(tt^2) |subj),
                    data = dat_pbo, REML = FALSE)
fit_drg_est_full = lmer(y ~ tt + I(tt^2) + w_drg + w_drg * tt + w_drg * I(tt^2) +
                        (tt + I(tt^2)|subj),
                    data = dat_drg, REML = FALSE)

l0 = summary(fit_pbo_est_full)$logLik + summary(fit_drg_est_full)$logLik
l0
```

```
## 'log Lik.' -6094.255 (df=13)
```

```
fit_pbo_est_0 = lmer(y ~ tt + I(tt^2) + w0 + w0 * tt + w0 * I(tt^2) +
                        (tt + I(tt^2) |subj),
                    data = dat_pbo, REML = FALSE)
fit_drg_est_0 = lmer(y ~ tt + I(tt^2) + w0 + w0 * tt + w0 * I(tt^2) +
                        (tt + I(tt^2)|subj),
                    data = dat_drg, REML = FALSE)
l00 = summary(fit_pbo_est_0)$logLik + summary(fit_drg_est_0)$logLik
l00
```

```
## 'log Lik.' -6098.291 (df=13)
```

```
fit_pbo_est_1 = lmer(y ~ tt + I(tt^2) + W1 + W1 * tt + W1 * I(tt^2) +
                        (tt + I(tt^2) |subj),
                    data = dat_pbo, REML = FALSE)
```

```r
fit_drg_est_1 = lmer(y ~ tt + I(tt^2) + W1 + W1 * tt + W1 * I(tt^2) +
                       (tt + I(tt^2)|subj),
                     data = dat_drg, REML = FALSE)
fit_pbo_est_2 = lmer(y ~ tt + I(tt^2) + W2 + W2 * tt + W2 * I(tt^2) +
                       (tt + I(tt^2) |subj),
                     data = dat_pbo, REML = FALSE)
fit_drg_est_2 = lmer(y ~ tt + I(tt^2) + W2 + W2 * tt + W2 * I(tt^2) +
                       (tt + I(tt^2)|subj),
                     data = dat_drg, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge with max|grad| = 0.00203211 (tol = 0.002, component 1)
```

```r
fit_pbo_est_3 = lmer(y ~ tt + I(tt^2) + W3 + W3 * tt + W3 * I(tt^2) +
                       (tt + I(tt^2) |subj),
                     data = dat_pbo, REML = FALSE)
fit_drg_est_3 = lmer(y ~ tt + I(tt^2) + W3 + W3 * tt + W3 * I(tt^2) +
                       (tt + I(tt^2)|subj),
                     data = dat_drg, REML = FALSE)
fit_pbo_est_4 = lmer(y ~ tt + I(tt^2) + W4 + W4 * tt + W4 * I(tt^2) +
                       (tt + I(tt^2) |subj),
                     data = dat_pbo, REML = FALSE)
fit_drg_est_4 = lmer(y ~ tt + I(tt^2) + W4 + W4 * tt + W4 * I(tt^2) +
                       (tt + I(tt^2)|subj),
                     data = dat_drg, REML = FALSE)
fit_pbo_est_5 = lmer(y ~ tt + I(tt^2) + W5 + W5 * tt + W5 * I(tt^2) +
                       (tt + I(tt^2) |subj),
                     data = dat_pbo, REML = FALSE)
fit_drg_est_5 = lmer(y ~ tt + I(tt^2) + W5 + W5 * tt + W5 * I(tt^2) +
                       (tt + I(tt^2)|subj),
                     data = dat_drg, REML = FALSE)
```

```
## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## unable to evaluate scaled gradient

## Warning in checkConv(attr(opt, "derivs"), opt$par, ctrl = control$checkConv, :
## Model failed to converge: degenerate Hessian with 1 negative eigenvalues
```

```r
fit_pbo_est_6 = lmer(y ~ tt + I(tt^2) + W6 + W6 * tt + W6 * I(tt^2) +
                       (tt + I(tt^2) |subj),
                     data = dat_pbo, REML = FALSE)
fit_drg_est_6 = lmer(y ~ tt + I(tt^2) + W6 + W6 * tt + W6 * I(tt^2) +
                       (tt + I(tt^2)|subj),
                     data = dat_drg, REML = FALSE)
```

```r
l1 = summary(fit_pbo_est_1)$logLik + summary(fit_drg_est_1)$logLik
l2 = summary(fit_pbo_est_2)$logLik + summary(fit_drg_est_2)$logLik
l3 = summary(fit_pbo_est_3)$logLik + summary(fit_drg_est_3)$logLik
l4 = summary(fit_pbo_est_4)$logLik + summary(fit_drg_est_4)$logLik
l5 = summary(fit_pbo_est_5)$logLik + summary(fit_drg_est_5)$logLik
l6 = summary(fit_pbo_est_6)$logLik + summary(fit_drg_est_6)$logLik
```

```r
likes = c(l0,l1,l2,l3,l4,l5, l6)
```

| Method | Purity (coefficient) | Purity (outcome) | loglikelihood (condition) | loglikelihood (outcome) | loglikelihood (mean) | Random |
|---|---|---|---|---|---|---|
| loglikelihood | -6094.255 | -6097.163 | -6094.360 | -6131.375 | -6132.756 | -6109.696 |
| p-value | | 0.121 | 0.975 | 0.991 | 5.55e-16 | 1.11e-16 |