Analysis of the efficiency of MC-MoCo

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This document contains the statistical analysis described in *A Motion Correction Strategy for Multi-Contrast based 3D parametric imaging: Application to Inhomogeneous Magnetization Transfer (ihMT)*, by L. Soustelle et al., to appear in *Magnetic Resonance in Medicine*. The source code of this document, and its related data, is available at https://github.com/lamyj/mcmoco-data/.

The data contains in each row contains the position in physical space of one marker of one ihMT-weighted image of one subject, placed either before motion-correction (*Pre-MoCo*) or after application of a motion-correction algorithm (*MC-MoCo* or *MCFLIRT*).

```
positions = read.csv("positions.csv", colClasses=c(Volume="factor"))
kable(head(positions))
```

Subject	Volume	Marker	Method	x	y	z
Control_01	1	L-MFG	MC-MoCo	120.041	184.933	92.992
Control_01	1	L-MFG	MCFLIRT	121.001	185.953	93.086
Control_01	1	L-MFG	Pre-MoCo	120.008	185.274	92.848
Control_01	1	LR-SCCG	MC-MoCo	99.040	132.002	71.108
Control_01	1	LR-SCCG	MCFLIRT	98.944	131.918	70.902
Control_01	1	LR-SCCG	Pre-MoCo	98.890	131.567	70.633

## Quantification of the residual motion

For each subject and each set of images (uncorrected, MCFLIRT- and MC-MoCo-corrected), a reference point of each landmark is defined as the centroid of the landmark locations across the images of the set.

```
references = aggregate(
    cbind(x, y, z) ~ Subject + Marker + Method, positions, mean)
```

The reference points are used to quantify the amount of native motion (uncorrected images) and residual motion (MCFLIRT- and MC-MoCo-corrected images) by averaging the distances between the reference points and their corresponding landmarks across all the subjects.

```
df = merge(
    positions, references, by=c("Subject", "Marker", "Method"),
    suffixes=c("", "_c"))
df$Distance = sapply(
    1:nrow(df),
    function(i) { with(df[i,], norm(c(x, y, z) - c(x_c, y_c, z_c), "2")) })
distances = aggregate(Distance ~ Subject + Marker + Method, df, mean)
```

A boxplot of the native motion evaluated on the images before motion correction and of residual motion evaluated after application of MCFLIRT and MC-MoCo show a lower residual motion for MC-MoCo compared to that of MCFLIRT for all landmarks. The residual motion value is additionally rather constant across all markers for MC-MoCo.
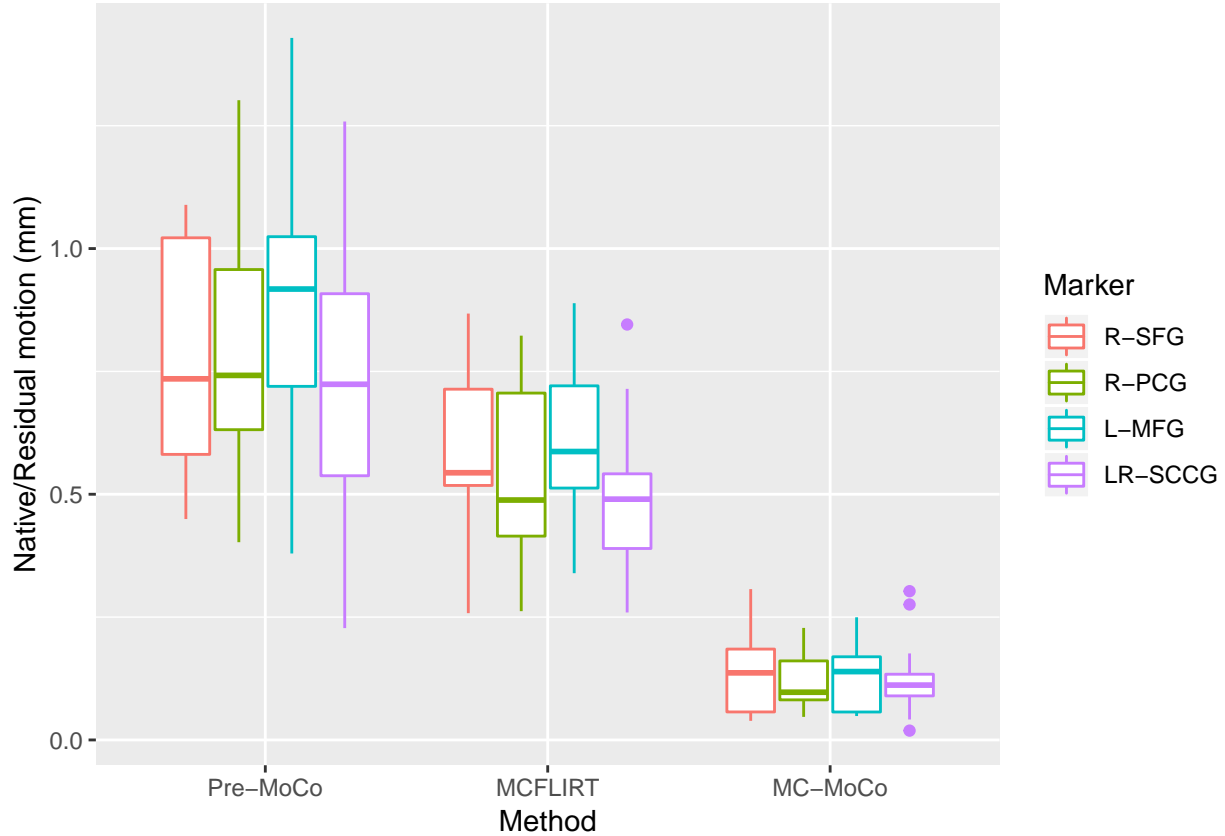
Statistical analysis

To evaluate the performance of MC-MoCo and MCFLIRT, and to verify that the behavior of both methods is constant across landmarks and between the two groups of subjects, we use a mixed-effect linear model with fixed effects for the motion correction method, the landmark, and the subject group (deduced from the subject ID), and with a random effect for the subject to account for the non-independence of the observations within a subject.

```
# Deduce Group factor from subject ID
distances$Group = as.factor(
    sapply(distances$Subject, sub, pattern="(.*)_.*", replacement="\\1"))
# Re-order to improve readability of hypothesis testing.
distances$Method = factor(distances$Method, c("MC-MoCo", "MCFLIRT", "Pre-MoCo"))
model = lme(Distance ~ Method + Marker + Group, random=~1|Subject, distances)
```

The residuals of the mixed-effects linear model show neither deviation from a normal distribution (Shapiro-Wilk test, p=0.574) nor apparent structure in the variance of the residuals, thus validating the model.
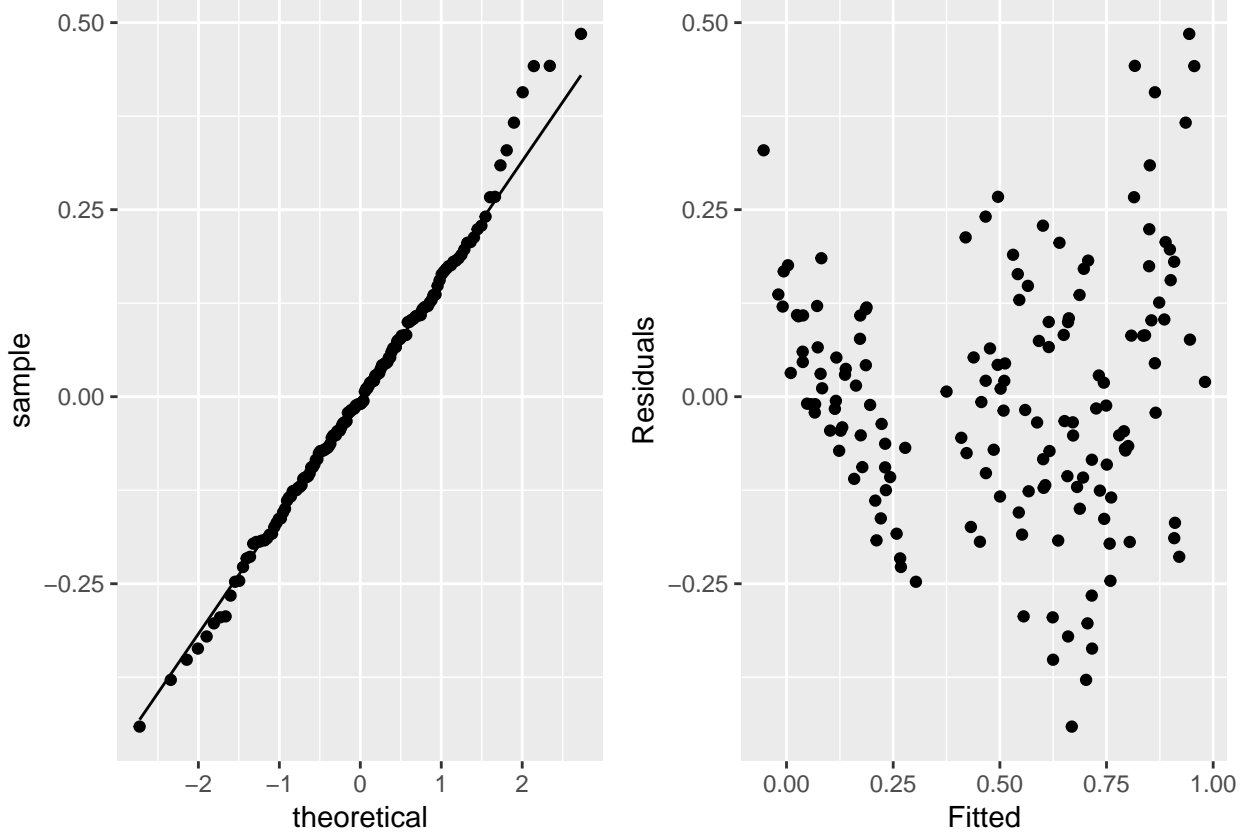
The analysis of the individual factors shows a significant effect of the motion-correction methods, indicating a difference between the non-corrected images and the motion-corrected images, but no difference either across the landmarks or between the two groups of subjects, thereby indicating that differences in residual motions depends only on the algorithm.

	numDF	denDF	F-value	p-value
(Intercept)	1	138	329.596	<1e-10
Method	2	138	200.971	<1e-10
Marker	3	138	1.859	0.140
Group	1	11	2.928	0.115

Further linear hypotheses tests comparing the native motion from residual motions derived from MCFLIRT and MC-MoCo show statistically significant reductions for MCFLIRT and for MC-MoCo as well as signficant reduction of MC-MoCo compared to MCFLIRT.

```
hypotheses = glht(model, linfct=mcp(Method="Tukey"))
```

	Estimate	Std. Error	z value	Pr(>|z|)
MCFLIRT - MC-MoCo == 0	0.429	0.034	12.540	< 1e-10
Pre-MoCo - MC-MoCo == 0	0.678	0.034	19.817	< 1e-10
Pre-MoCo - MCFLIRT == 0	0.249	0.034	7.277	< 1e-10