

SUPPLEMENTARY MATERIAL FOR THE PAPER “MODELING ANGLE-SPECIFIC ISOKINETIC HAMSTRING TO QUADRICEPS RATIO USING MULTILEVEL GENERALIZED ADDITIVE MODELS”

R code for the models of isokinetic strength curves using generalized additive multilevel models

```
#concentric knee extension
```

```
ke1<-brm(bf(kn_ext_cc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0|id)),
  data = ke,
  family = gaussian(),
  chains = 4,
  control = list(adapt_delta = 0.95,max_treedepth = 15))
```

```
summary(ke1)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: kn_ext_cc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0 | id)
Data: ke (Number of observations: 2319)
Samples: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 2000
```

```
Smooth Terms:
          Estimate Est.Error 1-95% CI u-95% CI Eff.Sample Rhat
sds(sangle_ext_ref0_1) 162.54   39.70  103.59  258.84     500 1.01
```

```
Group-Level Effects:
~id (Number of levels: 30)
          Estimate Est.Error 1-95% CI u-95% CI Eff.Sample Rhat
sd(Intercept)          39.25   5.58   30.22   52.20     441 1.01
sd(angle_ext_ref0)      0.81   0.11    0.63    1.06     450 1.00
cor(Intercept,angle_ext_ref0) -0.35  0.16  -0.64  -0.02     403 1.00
```

```
Population-Level Effects:
          Estimate Est.Error 1-95% CI u-95% CI Eff.Sample Rhat
Intercept    138.24    7.81  123.40  153.25     296 1.01
sangle_ext_ref0_1 -83.71    9.22 -101.85  -66.16    1025 1.00
```

```
Family Specific Parameters:
          Estimate Est.Error 1-95% CI u-95% CI Eff.Sample Rhat
sigma     10.73    0.16   10.43   11.04    1693 1.00
```

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

```
#eccentric knee extension
```

```
ke2<-brm(bf(kn_ext_ecc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0|id)),  
  data = ke,  
  family = gaussian(),  
  chains = 4,  
  control = list(adapt_delta = 0.95,max_treedepth = 15))
```

```
summary(ke2)
```

```
Family: gaussian
```

```
Links: mu = identity; sigma = identity
```

```
Formula: kn_ext_ecc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0 | id)
```

```
Data: ke (Number of observations: 2310)
```

```
Samples: 2 chains, each with iter = 4000; warmup = 1000; thin = 1;  
total post-warmup samples = 6000
```

```
Smooth Terms:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sds(sangle_ext_ref0_1)	45.05	14.37	24.56	79.68	2287	1.00

```
Group-Level Effects:
```

```
~id (Number of levels: 30)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sd(Intercept)	57.21	7.66	44.08	74.27	1397	1.00
sd(angle_ext_ref0)	0.66	0.09	0.51	0.87	1562	1.00
cor(Intercept,angle_ext_ref0)	-0.76	0.08	-0.88	-0.57	2095	1.00

```
Population-Level Effects:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
Intercept	134.01	7.27	119.69	148.32	1208	1.00
sangle_ext_ref0_1	-14.01	6.50	-26.48	-1.21	3017	1.00

```
Family Specific Parameters:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sigma	12.25	0.18	11.90	12.62	6000	1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

```
#hamstrings by quadriceps at each angular position as dependent variable"
```

```
ke3<-brm(bf(H_Q~ s(angle_ext_ref0) + (angle_ext_ref0|id)),  
  data = ke,  
  family = gaussian(),  
  chains = 4,  
  control = list(adapt_delta = 0.99,max_treedepth = 15))
```

```
summary(ke3)
```

```
Family: gaussian
```

```
Links: mu = identity; sigma = identity
```

```
Formula: H_Q ~ s(angle_ext_ref0) + (angle_ext_ref0 | id)
```

```
Data: ke (Number of observations: 2319)
```

```
Samples: 2 chains, each with iter = 4000; warmup = 1000; thin = 1;
```

```
total post-warmup samples = 6000
```

```
Smooth Terms:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sds(sangle_ext_ref0_1)	2.76	0.94	1.53	5.08	1387	1.00

```
Group-Level Effects:
```

```
~id (Number of levels: 30)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sd(Intercept)	0.94	0.13	0.73	1.24	654	1.00
sd(angle_ext_ref0)	0.02	0.00	0.01	0.02	682	1.00
cor(Intercept,angle_ext_ref0)	-0.98	0.01	-0.99	-0.96	809	1.00

```
Population-Level Effects:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
Intercept	1.23	0.06	1.12	1.34	473	1.00
sangle_ext_ref0_1	-2.40	0.29	-2.99	-1.85	1859	1.00

```
Family Specific Parameters:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sigma	0.39	0.01	0.38	0.40	6000	1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

```
#knee flexion#
```

```
kf1<-brm(bf(kn_flex_cc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0|id)),  
  data = kf,  
  family = gaussian(),  
  chains = 4,  
  control = list(adapt_delta = 0.95,max_treedepth = 15))
```

```
summary(kf1)
```

```
Family: gaussian  
Links: mu = identity; sigma = identity  
Formula: kn_flex_cc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0 | id)  
Data: kf (Number of observations: 844)  
Samples: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;  
total post-warmup samples = 2000
```

```
Smooth Terms:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sds(sangle_ext_ref0_1)	114.17	28.09	72.93	181.78	634	1.01

```
Group-Level Effects:
```

```
~id (Number of levels: 11)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sd(Intercept)	25.61	6.48	16.39	40.52	967	1.00
sd(angle_ext_ref0)	0.44	0.12	0.28	0.72	636	1.00
cor(Intercept,angle_ext_ref0)	-0.30	0.27	-0.74	0.28	913	1.00

```
Population-Level Effects:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
Intercept	102.20	8.23	85.83	118.71	596	1.01
sangle_ext_ref0_1	-52.89	7.70	-67.51	-37.92	2000	1.00

```
Family Specific Parameters:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sigma	6.79	0.17	6.47	7.13	2000	1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

```

kf2<-brm(bf(kn_flex_ecc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0|id)),
  data = kf,
  family = gaussian(),
  chains = 4,
  control = list(adapt_delta = 0.95,max_treedepth = 15))

```

```
summary(kf2)
```

```

Family: gaussian
Links: mu = identity; sigma = identity
Formula: kn_flex_ecc_Nm ~ s(angle_ext_ref0) + (angle_ext_ref0 | id)
Data: kf (Number of observations: 844)
Samples: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
         total post-warmup samples = 2000

```

```
Smooth Terms:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sds(sangle_ext_ref0_1)	136.76	39.02	78.85	230.52	881	1.00

```
Group-Level Effects:
```

```
~id (Number of levels: 11)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sd(Intercept)	85.89	19.19	57.10	134.61	695	1.01
sd(angle_ext_ref0)	1.16	0.27	0.77	1.81	683	1.01
cor(Intercept,angle_ext_ref0)	-0.80	0.13	-0.95	-0.45	830	1.01

```
Population-Level Effects:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
Intercept	198.38	16.26	165.50	231.46	621	1.00
sangle_ext_ref0_1	68.10	21.78	26.49	112.56	1155	1.00

```
Family Specific Parameters:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sigma	24.49	0.59	23.40	25.61	2000	1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

```
#hamstrings by quadriceps at each angular position as dependent variable"
kf3<-brm(bf(H_Q~ s(angle_ext_ref0) + (1|id)),
  data = kf, family = gaussian(),
  chains = 4, control = list(adapt_delta = 0.99,max_treedepth = 15))
```

```
summary(kf3)
```

```
Family: gaussian
Links: mu = identity; sigma = identity
Formula: H_Q ~ s(angle_ext_ref0) + (1 | id)
Data: kf (Number of observations: 844)
Samples: 2 chains, each with iter = 2000; warmup = 1000; thin = 1;
total post-warmup samples = 2000
```

```
Smooth Terms:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sds(sangle_ext_ref0_1)	0.41	0.27	0.12	1.16	414	1.01

```
Group-Level Effects:
```

```
~id (Number of levels: 11)
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sd(Intercept)	0.21	0.05	0.13	0.33	340	1.00

```
Population-Level Effects:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
Intercept	0.58	0.07	0.44	0.72	295	1.00
sangle_ext_ref0_1	-0.06	0.11	-0.35	0.11	499	1.00

```
Family Specific Parameters:
```

	Estimate	Est.Error	l-95% CI	u-95% CI	Eff.Sample	Rhat
sigma	0.17	0.00	0.16	0.18	2000	1.00

Samples were drawn using sampling(NUTS). For each parameter, Eff.Sample is a crude measure of effective sample size, and Rhat is the potential scale reduction factor on split chains (at convergence, Rhat = 1).

```
#Figures codes
```

```
plot.ke1<-marginal_effects(ke1)
```

```
plot(plot.ke1)[[1]] +xlab("knee angular position,  
degrees")+ylab("Concentric knee extension moment of force,  
N.m")+scale_x_continuous(breaks=c(0,10,20,30,40,50,60,70,80,90))+scale_y_c  
ontinuous(breaks=c(50,100,150,200,250,300))
```

```
plot.ke2<-marginal_effects(ke2)
```

```
plot(plot.ke2)[[1]] +xlab("knee angular position,  
degrees")+ylab("Eccentric knee extension moment of force,  
N.m")+scale_x_continuous(breaks=c(0,10,20,30,40,50,60,70,80,90))+scale_y_c  
ontinuous(breaks=c(50,100,150,200,250,300))
```

```
plot.ke3<-marginal_effects(ke3)
```

```
plot(plot.ke3)[[1]] +xlab("knee angular position,  
degrees")+ylab("Functional hamstring by quadriceps ratio for knee  
extension")+scale_x_continuous(breaks=c(0,10,20,30,40,50,60,70,80,90))+sca  
le_y_continuous(breaks=c(0.5,1.0,1.5,2.0,2.5,3.0))
```

```
plot.kf1<-marginal_effects(kf1)
```

```
plot(plot.kf1)[[1]] +xlab("knee angular position,  
degrees")+ylab("Concentric knee flexion moment of force,  
N.m")+scale_x_continuous(breaks=c(0,10,20,30,40,50,60,70,80,90))+scale_y_c  
ontinuous(breaks=c(50,75,100,125,150,175))
```

```
plot.kf2<-marginal_effects(kf2)
```

```
plot(plot.kf2)[[1]] +xlab("knee angular position,  
degrees")+ylab("Eccentric knee flexion moment of force,  
N.m")+scale_x_continuous(breaks=c(0,10,20,30,40,50,60,70,80,90))+scale_y_c  
ontinuous(breaks=c(50,100,150,200,250,300))
```

```
plot.kf3<-marginal_effects(kf3)
```

```
plot(plot.kf3)[[1]] +xlab("knee angular position,  
degrees")+ylab("Functional hamstring by quadriceps ratio for knee  
flexion")+scale_x_continuous(breaks=c(0,10,20,30,40,50,60,70,80,90))+scale  
_y_continuous(breaks=c(0.2,0.3,0.4,0.5,0.6,0.7,0.8,0.9,1.0))
```