Code ▾

MRS_analysis_code_NN

Analysis of INS.CRE is provided as the template. the same scripts were run in all four metabolites of interest

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First sets of analyses: The effects of age on concentrations and how it interacts with bilingualism

Model 1:First GAM looking at the smoothed effect of age. Subj and sex treated as random effects

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```
m.age <- bam(INS.CRE ~ s(subject, bs="re") + s(sex, bs="re") +
            s(Age), data=dat.placement, method="REML")
summary(m.age)
plot(m.age)
plot_smooth(m.age, view="Age",ylab = "Concentration", main = "INS/CRE", hide.label = TRUE, co
l = "green")
plot_data(m.age, view="Age", cex=1, col = "green")
```

Model 2: Second GAM with nativeness as ordered factor, looking at ageXbilingualism interactions, examined for each level of nativeness separately. This will only produce p values for the interaction, and will need to be followed up with Model 3 for the interaction to be unpacked. Subject and sex treated as random effects.

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```
# Ordered factor for nativeness, and set contrasts. Ref= MOnolingual
dat.placement$nativeness <- relevel(dat.placement$nativeness, ref="Monolingual")
dat.placement$OFnativeness <- as.ordered(as.factor(dat.placement$nativeness))
contrasts(dat.placement$OFnativeness) <- 'contr.treatment'
contrasts(dat.placement$OFnativeness)

## ORDERED FACTOR MODEL: REFERENCE + DIFFERENCE SMOOTH
## For the model specification, note that we include both s(Age), nativeness, and interaction
m.native <- bam(INS.CRE ~ s(subject, bs="re") + OFnativeness + s(sex, bs="re") +
            s(Age) + s(Age, by=OFnativeness),
          data=dat.placement, method="REML")
summary(m.native)
# This one will show the difference smooths
plot(m.native)
# Plot of separate smooths (from difference smooth model)
plot_smooth(m.native, view="Age", plot_all="OFnativeness", ylab = "Concentration", hide.label = TRUE, main = "INS/CRE", col = c("blue", "red2"))

####################################################################

# Ordered factor for nativeness, and set contrasts. Ref= Bilingual
dat.placement$nativeness <- relevel(dat.placement$nativeness, ref="Bilingual")
dat.placement$OFnativeness <- as.ordered(as.factor(dat.placement$nativeness))
contrasts(dat.placement$OFnativeness) <- 'contr.treatment'
contrasts(dat.placement$OFnativeness)

## ORDERED FACTOR MODEL: REFERENCE + DIFFERENCE SMOOTH
## For the model specification, note that we include both s(Age), nativeness, and interaction
m.nonnative <- bam(INS.CRE ~ s(subject, bs="re") + OFnativeness + s(sex, bs="re") +
            s(Age) + s(Age, by=OFnativeness),
          data=dat.placement, method="REML")
summary(m.nonnative)
# This one will show the difference smooths
plot(m.nonnative)
# Plot of separate smooths (from difference smooth model)
plot_smooth(m.nonnative, view="Age", plot_all="OFnativeness", ylab = "Concentration", hide.label = TRUE, main = "INS/CRE", col = c("blue", "red2"))
```

Model 3: Third GAM, looking at each level of Nativeness separately and producing separate smooths per group. Only useful if the agexbilingualism interaction is significant above. Subject and sex treated as random effects

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```
## FACTOR MODEL: SEPARATE SMOOTHS
## For the model specification, note that we do *not* include s(Age) separately

m.all <- bam(INS.CRE ~ s(subject, bs="re") + nativeness + s(sex, bs="re") + s(Age, by=nativeness),
          data=dat.placement, method="REML")
summary(m.all)

# Plot of separate smooths (from difference smooth model)
plot_smooth(m.all, view="Age", plot_all="nativeness", ylab = "Concentration", hide.label = TRUE, main = "INS/CRE", col = c("blue", "red2"))
plot_data(m.all, view="Age", split_by="nativeness", ylab = "Concentration", cex=1, main = "INS/CRE", col = c("blue", "red2"))
```

Second sets of analyses: The effects of bilingual experiences on metabolite concentrations.

L2 home

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```
m.home <- bam(INS.CRE ~ s(subject, bs="re") + s(sex, bs="re") +
            s(Age) + s(L2_home), data=dat.placement, method="REML")
summary(m.home)
plot(m.home)
plot_smooth(m.home, view="L2_home", col = "purple", hide.label = TRUE, main = "INS/CRE", xlab = "L2 home", ylab = "Concentration")
```

L2 social

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```
m.social <- bam(INS.CRE ~ s(subject, bs="re") + s(sex, bs="re") +
            s(Age) + s(L2_social), data=dat.placement, method="REML")
summary(m.social)
plot(m.social)
plot_smooth(m.social, view="L2_social", col = "purple", hide.label = TRUE, main = "INS/CRE", xlab = "L2 social", ylab = "Concentration")
```

LSBQ composite score

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```
m.LSBQ_composite <- bam(INS.CRE ~ s(subject, bs="re") + s(sex, bs="re") +
            s(Age) + s(LSBQ_composite), data=dat.placement, method="REML")
summary(m.LSBQ_composite)
plot(m.LSBQ_composite)
plot_smooth(m.LSBQ_composite, view="LSBQ_composite", col = "purple", hide.label = TRUE, main = "INS/CRE", xlab = "LSBQ composite score", ylab = "Concentration")
```