S3: FSL output to tables and plots

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## Regions of interest

We created two masks containing regions of interest, one only containing the bilateral fusiform gyrus, the other additionally containing the following regions: ACC\_pre\_L, ACC\_pre\_R, ACC\_sub\_L, ACC\_sub\_R, ACC\_sup\_L, ACC\_sup\_R, Amygdala\_L, Amygdala\_R, Insula\_L, Insula\_R, Precuneus\_L, Precuneus\_R, SupraMarginal\_R and Temporal\_Rup\_R. All regions were extracted from the AAL3 atlas.

The ROI mask only containing the fusiform gyri was used to assess the colour prediction errors in the comparison group, as well as group differences in neural correlates of colour prediction errors. The other ROI mask was used to evaluate all other hypotheses, including emotion prediction error and prediction strength in the comparison group as well as the pooled sample and group differences in neural correlates of emotion prediction errors.

## Combine FSL output

# get one type of input from each contrast  
ls.files = dir(pattern = '.\*MNI-AAL.csv', path = "./results\_sig")  
  
for (file in ls.files) {  
 contrast = gsub("\_MNI-AAL.csv", "", file)  
 type = substr(contrast, nchar(contrast)-5, nchar(contrast)-5)  
 maxima = read\_csv(file.path("results\_sig", file), show\_col\_types = F)  
 if (nrow(maxima) == 0) next  
 summary = read\_delim(file.path("results\_sig",   
 paste0(contrast, '\_cluster-summary.txt')),   
 show\_col\_types = F)  
 output = read\_delim(file.path("results\_sig",   
 paste0(contrast, '\_randomise\_output\_all.txt')),   
 show\_col\_types = F)  
   
 relinfo =   
 merge(  
 output %>% select(`Cluster Index`, Voxels),   
 maxima %>% select(`Cluster Index`, `Value`, MNIx, MNIy, MNIz, AALname)  
 ) %>%  
 mutate(  
 H = if\_else(MNIx >= 0, "R", "L")  
 ) %>%  
 rename(  
 `Cluster size` = "Voxels",   
 "Region" = "AALname",  
 "x" = "MNIx",  
 "y" = "MNIy",  
 "z" = "MNIz"  
 ) %>%  
 arrange(desc(`Cluster Index`), desc(Value)) %>%  
 relocate(`Cluster Index`, Region, `Cluster size`, H)  
 colnames(relinfo)[colnames(relinfo) == "Value"] = paste0(type, "-value")  
   
 write\_csv(relinfo, file = file.path("results\_sig", paste0(contrast, '.csv')))  
   
}

## Hypothesis-guided ROI analysis

# COMP: same areas as Stefanics et al. (2019), Neuroimage  
  
read\_csv(file.path("results\_sig", 'hgf\_ctr\_eps\_c\_ROI\_fstat1.csv'), show\_col\_types = F) %>%  
 kable(., caption = 'COMP: colour prediction error')

COMP: colour prediction error

| Cluster Index | Region | Cluster size | H | f-value | x | y | z |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 1 | Fusiform gyrus | 241 | R | 24.3 | 30 | -70 | -10 |
| 1 | Fusiform gyrus | 241 | R | 23.1 | 32 | -60 | -14 |
| 1 | Fusiform gyrus | 241 | R | 22.9 | 28 | -60 | -16 |
| 1 | Fusiform gyrus | 241 | R | 20.8 | 30 | -64 | -16 |
| 1 | Fusiform gyrus | 241 | R | 17.8 | 28 | -52 | -18 |
| 1 | Fusiform gyrus | 241 | R | 14.2 | 32 | -78 | -6 |

read\_csv(file.path("results\_sig", 'hgf\_ctr\_mu\_e\_ROI\_fstat1.csv'), show\_col\_types = F) %>%  
 kable(., caption = 'COMP: emotion prediction strength')

COMP: emotion prediction strength

| Cluster Index | Region | Cluster size | H | f-value | x | y | z |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 1 | Precuneus | 3 | R | 26 | 6 | -76 | 52 |

# pooled: same areas as Stefanics et al. (2019), Neuroimage  
  
read\_csv(file.path("results\_sig", 'hgf\_all\_eps\_c\_ROI\_fstat1.csv'), show\_col\_types = F) %>%  
 kable(., caption = 'Pooled: colour prediction error')

Pooled: colour prediction error

| Cluster Index | Region | Cluster size | H | f-value | x | y | z |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 7 | Fusiform gyrus | 230 | R | 39.8 | 32 | -60 | -16 |
| 7 | Fusiform gyrus | 230 | R | 35.9 | 28 | -70 | -12 |
| 7 | Fusiform gyrus | 230 | R | 24.5 | 34 | -74 | -14 |
| 6 | Superior temporal gyrus | 58 | R | 19.2 | 50 | -40 | 22 |
| 5 | Insula | 57 | R | 23.3 | 32 | 24 | -4 |
| 5 | Insula | 57 | R | 22.3 | 42 | 26 | -4 |
| 5 | Insula | 57 | R | 16.1 | 42 | 22 | -10 |
| 4 | Anterior cingulate cortex, supracallosal | 47 | R | 22.0 | 8 | 34 | 24 |
| 3 | Fusiform gyrus | 28 | L | 32.1 | -28 | -56 | -16 |
| 2 | Superior temporal gyrus | 15 | R | 17.9 | 52 | -6 | -14 |
| 1 | Superior temporal gyrus | 2 | R | 13.9 | 50 | -18 | -8 |

read\_csv(file.path("results\_sig", 'hgf\_all\_mu\_c\_ROI\_fstat1.csv'), show\_col\_types = F) %>%  
 kable(., caption = 'Pooled: colour prediction strength')

Pooled: colour prediction strength

| Cluster Index | Region | Cluster size | H | f-value | x | y | z |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 7 | Precuneus | 2401 | L | 30.5 | -8 | -70 | 40 |
| 7 | Precuneus | 2401 | R | 28.0 | 12 | -46 | 42 |
| 7 | Precuneus | 2401 | R | 27.7 | 8 | -50 | 42 |
| 7 | Precuneus | 2401 | R | 26.8 | 4 | -56 | 50 |
| 7 | Precuneus | 2401 | R | 25.2 | 10 | -50 | 46 |
| 7 | Precuneus | 2401 | R | 24.1 | 2 | -62 | 48 |
| 6 | SupraMarginal gyrus | 553 | R | 25.5 | 58 | -44 | 36 |
| 6 | SupraMarginal gyrus | 553 | R | 24.4 | 58 | -46 | 44 |
| 6 | Superior temporal gyrus | 553 | R | 22.9 | 48 | -40 | 10 |
| 6 | SupraMarginal gyrus | 553 | R | 21.9 | 52 | -44 | 38 |
| 6 | SupraMarginal gyrus | 553 | R | 21.2 | 52 | -40 | 44 |
| 6 | Superior temporal gyrus | 553 | R | 20.4 | 58 | -50 | 18 |
| 5 | Anterior cingulate cortex, supracallosal | 254 | R | 22.4 | 10 | 24 | 26 |
| 5 | Anterior cingulate cortex, pregenual | 254 | R | 20.9 | 8 | 40 | 16 |
| 5 | Anterior cingulate cortex, pregenual | 254 | R | 15.1 | 8 | 46 | 14 |
| 4 | Insula | 171 | L | 23.3 | -28 | 22 | 4 |
| 4 | Insula | 171 | L | 22.4 | -32 | 20 | -8 |
| 4 | Insula | 171 | L | 21.2 | -28 | 26 | -4 |
| 4 | Insula | 171 | L | 16.8 | -36 | 16 | -2 |
| 3 | Insula | 119 | R | 26.9 | 32 | 24 | -4 |
| 3 | Insula | 119 | R | 24.2 | 38 | 26 | -4 |
| 3 | Insula | 119 | R | 22.1 | 42 | 20 | -8 |
| 3 | Insula | 119 | R | 14.6 | 44 | 22 | 0 |
| 2 | Precuneus | 63 | R | 13.1 | 20 | -54 | 20 |
| 2 | Precuneus | 63 | R | 11.9 | 14 | -54 | 18 |
| 1 | Precuneus | 3 | R | 12.5 | 4 | -46 | 14 |

read\_csv(file.path("results\_sig", 'hgf\_all\_mu\_e\_ROI\_fstat1.csv'), show\_col\_types = F) %>%  
 kable(., caption = 'Pooled: emotion prediction strength')

Pooled: emotion prediction strength

| Cluster Index | Region | Cluster size | H | f-value | x | y | z |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 4 | Precuneus | 124 | R | 23.9 | 8 | -78 | 56 |
| 4 | Precuneus | 124 | R | 23.6 | 6 | -74 | 52 |
| 4 | Precuneus | 124 | R | 18.2 | 16 | -70 | 48 |
| 3 | Fusiform gyrus | 86 | R | 30.1 | 32 | -52 | -20 |
| 3 | Fusiform gyrus | 86 | R | 21.5 | 28 | -52 | -14 |
| 3 | Fusiform gyrus | 86 | R | 20.4 | 32 | -62 | -18 |
| 3 | Fusiform gyrus | 86 | R | 17.9 | 30 | -62 | -14 |
| 2 | Fusiform gyrus | 62 | L | 24.7 | -30 | -64 | -16 |
| 2 | Fusiform gyrus | 62 | L | 22.8 | -34 | -60 | -18 |
| 2 | Fusiform gyrus | 62 | L | 20.4 | -34 | -54 | -18 |
| 2 | Fusiform gyrus | 62 | L | 17.9 | -34 | -54 | -22 |
| 1 | Precuneus | 2 | R | 13.2 | 14 | -74 | 48 |

# Neural adaptation  
  
read\_csv(file.path("results\_sig", 'smp\_adapt\_neg\_ROI\_tstat1.csv'), show\_col\_types = F) %>%  
 kable(., caption = 'ALL: repetition suppression')

ALL: repetition suppression

| Cluster Index | Region | Cluster size | H | t-value | x | y | z |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 3 | Fusiform gyrus | 55 | R | 4.36 | 28 | -80 | -16 |
| 3 | Fusiform gyrus | 55 | R | 4.24 | 36 | -76 | -16 |
| 2 | Fusiform gyrus | 27 | R | 4.62 | 38 | -56 | -22 |
| 1 | Fusiform gyrus | 12 | R | 4.16 | 32 | -56 | -14 |

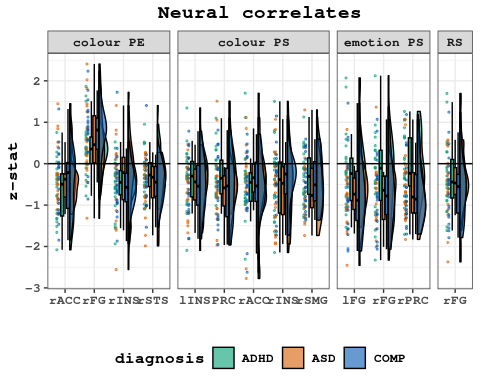
## Plotting

Plot the participants’ activation in clusters larger than 100 voxels to visualise the effects.

# custom colour palette  
custom.col = c("#009E73", "#D55E00", "#0058b2", "#CC79A7")  
  
# load in the extracted activation  
df.act = read\_csv(file.path("fMRI\_data", "grp\_use-sorted.csv"),   
 show\_col\_types = F) %>%  
 mutate(  
 diagnosis = fct\_recode(diagnosis,   
 "COMP" = "CTR")  
 ) %>%  
 select(diagnosis) %>%  
 mutate(  
 # load zstats for eps-c  
 `colour PE-rFG` = scan(file.path("fMRI\_data", "eps\_c\_C7\_meants.txt")),  
 `colour PE-rSTS` = scan(file.path("fMRI\_data", "eps\_c\_C6\_meants.txt")),  
 `colour PE-rINS` = scan(file.path("fMRI\_data", "eps\_c\_C5\_meants.txt")),  
 `colour PE-rACC` = scan(file.path("fMRI\_data", "eps\_c\_C4\_meants.txt")),  
 # load zstats for mu-z  
 `colour PS-rINS` = scan(file.path("fMRI\_data", "mu\_c\_C3\_meants.txt")),  
 `colour PS-lINS` = scan(file.path("fMRI\_data", "mu\_c\_C4\_meants.txt")),  
 `colour PS-rACC` = scan(file.path("fMRI\_data", "mu\_c\_C5\_meants.txt")),  
 `colour PS-rSMG` = scan(file.path("fMRI\_data", "mu\_c\_C6\_meants.txt")),  
 `colour PS-PRC` = scan(file.path("fMRI\_data", "mu\_c\_C7\_meants.txt")),  
 # load zstats for mu-e  
 `emotion PS-rPRC` = scan(file.path("fMRI\_data", "mu\_e\_C4\_meants.txt")),  
 `emotion PS-rFG` = scan(file.path("fMRI\_data", "mu\_e\_C3\_meants.txt")),  
 `emotion PS-lFG` = scan(file.path("fMRI\_data", "mu\_e\_C2\_meants.txt")),  
 # load zstat for neural adaptation  
 `RS-rFG` = scan(file.path("fMRI\_data", "adapt\_meants.txt"))  
 ) %>%  
 pivot\_longer(cols = -diagnosis, names\_to = c("parameter", "region"),   
 names\_sep = "-", values\_to = "activation")  
  
# plot   
df.act %>%  
 ggplot(aes(region, activation, fill = diagnosis, colour = diagnosis)) + #  
 geom\_rain(rain.side = 'r',  
boxplot.args = list(color = "black", outlier.shape = NA, show.legend = FALSE, alpha = .8),  
violin.args = list(color = "black", outlier.shape = NA, alpha = .6),  
boxplot.args.pos = list(  
 position = ggpp::position\_dodgenudge(x = 0, width = 0.3), width = 0.3  
),  
point.args = list(show\_guide = FALSE, alpha = .5, size = 0.5),  
violin.args.pos = list(  
 width = 0.6, position = position\_nudge(x = 0.16)),  
point.args.pos = list(position = ggpp::position\_dodgenudge(x = -0.25, width = 0.1))) +  
 scale\_fill\_manual(values = custom.col) +  
 scale\_color\_manual(values = custom.col) +  
 labs(title = "Neural correlates", x = "", y = "z-stat") +   
 facet\_grid(. ~ parameter, scales = "free", space = "free") +  
 geom\_hline(yintercept = 0) +  
 theme\_bw() +   
 theme(legend.position = "bottom",   
 plot.title = element\_text(hjust = 0.5),   
 legend.direction = "horizontal",   
 text = element\_text(size = 12, family = "mono", face = "bold")  
 )

## Warning: The `show\_guide` argument of `layer()` is deprecated as of ggplot2 2.0.0.  
## ℹ Please use the `show.legend` argument instead.  
## ℹ The deprecated feature was likely used in the ggrain package.  
## Please report the issue at <https://github.com/njudd/ggrain/issues>.  
## This warning is displayed once every 8 hours.  
## Call `lifecycle::last\_lifecycle\_warnings()` to see where this warning was  
## generated.

## Warning in (function (mapping = NULL, data = NULL, stat = "half\_ydensity", :  
## Ignoring unknown parameters: `outlier.shape`



ggsave("neural\_zstat.pdf",  
 units = "mm", width = 270, height = 100, dpi = 300)