

# **Final Presentation**

**CS631**

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# The Data

**Data was collected by me to examine c-Fos levels in the fear circuit after contextual fear conditioning**

## **4 variables**

- 2 numeric - animal IDs and average c-fos counts
- 2 categorical - behavioral group and brain region
  - Behavioral group - comparing initial learning ( **COND** ) to relearning ( **REC EXT** and **REC EXT** ) and no-learning controls ( **HAND** )
  - Brain Regions of Interest-
    - **Hippocampus** and Dentate Gyrus ( **DG** )
    - Bed nucleus of the stria terminalis ( **d/vBNST** )

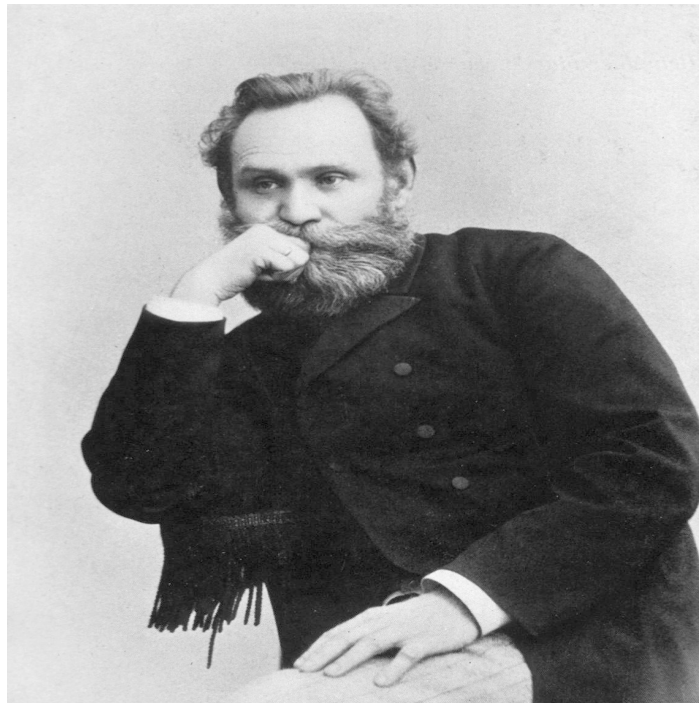
# The Data Cont'd

```
# A tibble: 6 x 4
  id count group region
<int> <dbl> <chr> <chr>
1    21   34   COND Hippocampus
2    22   26   COND Hippocampus
3    41  38.9   COND Hippocampus
4    42  24.6   COND Hippocampus
5    61  19.6   COND Hippocampus
6    62   37   COND Hippocampus
```

# The Audience

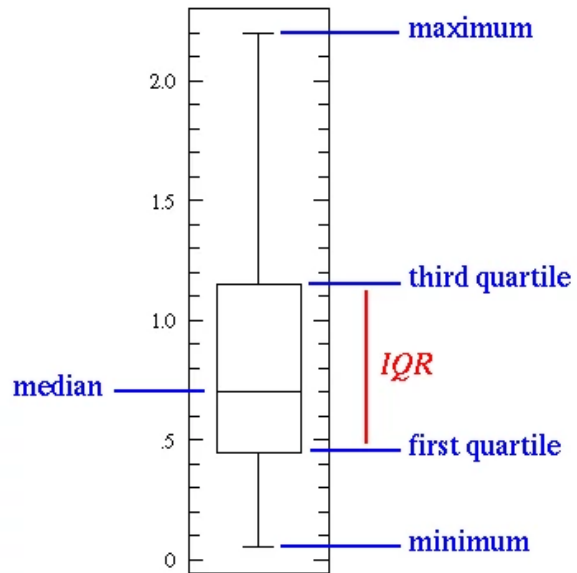
**Learning and memory researchers and YOU!**

**Ivan Pavlov**



# Graph Type

## The Box-plot



# **What am I attempting to show?**

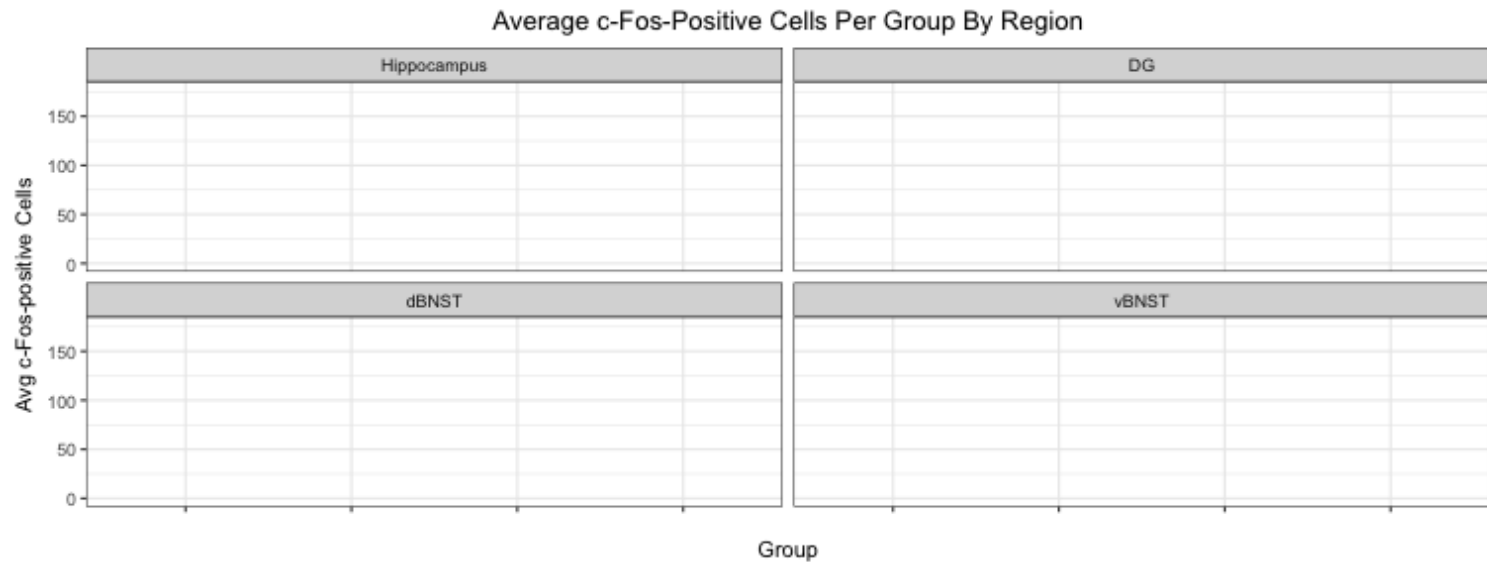
**The importance of activity in different brain regions to learning and relearning a contextual fear memory**

**Why?**

Learning and re-learning likely involve similar circuits, but re-learning may recruit a remote memory that is distributed throughout the cortex

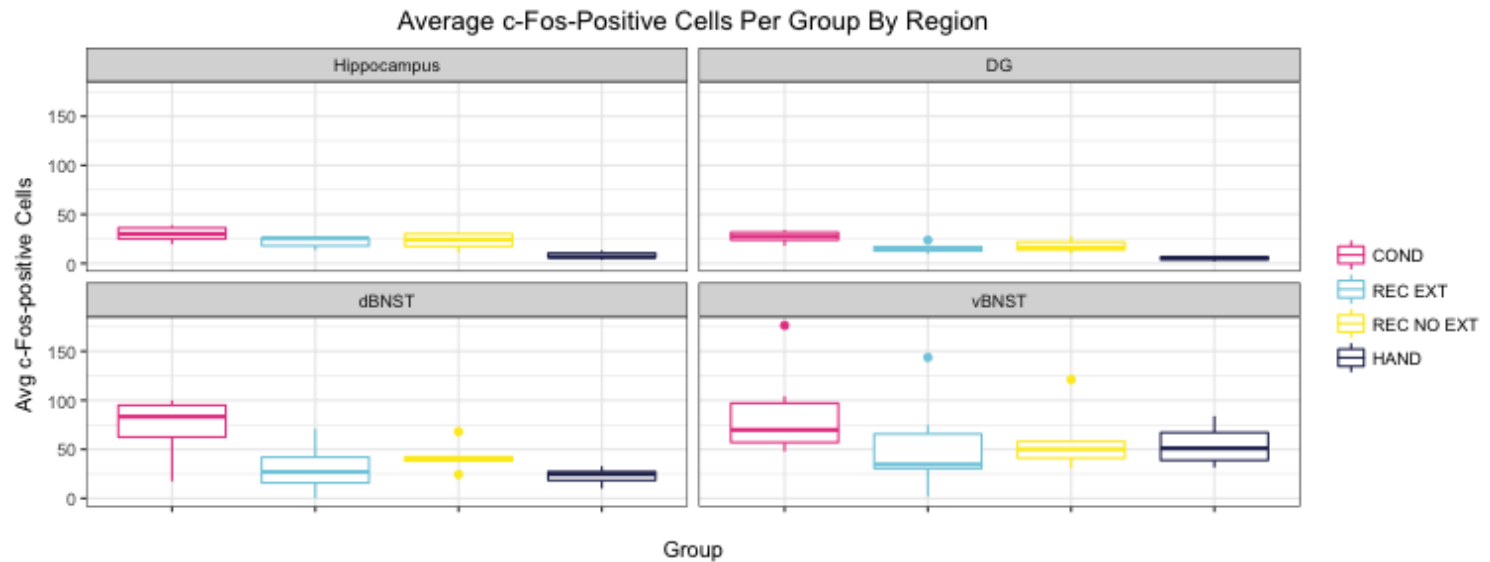
**And now, the box plot!**

# Graph Orientation

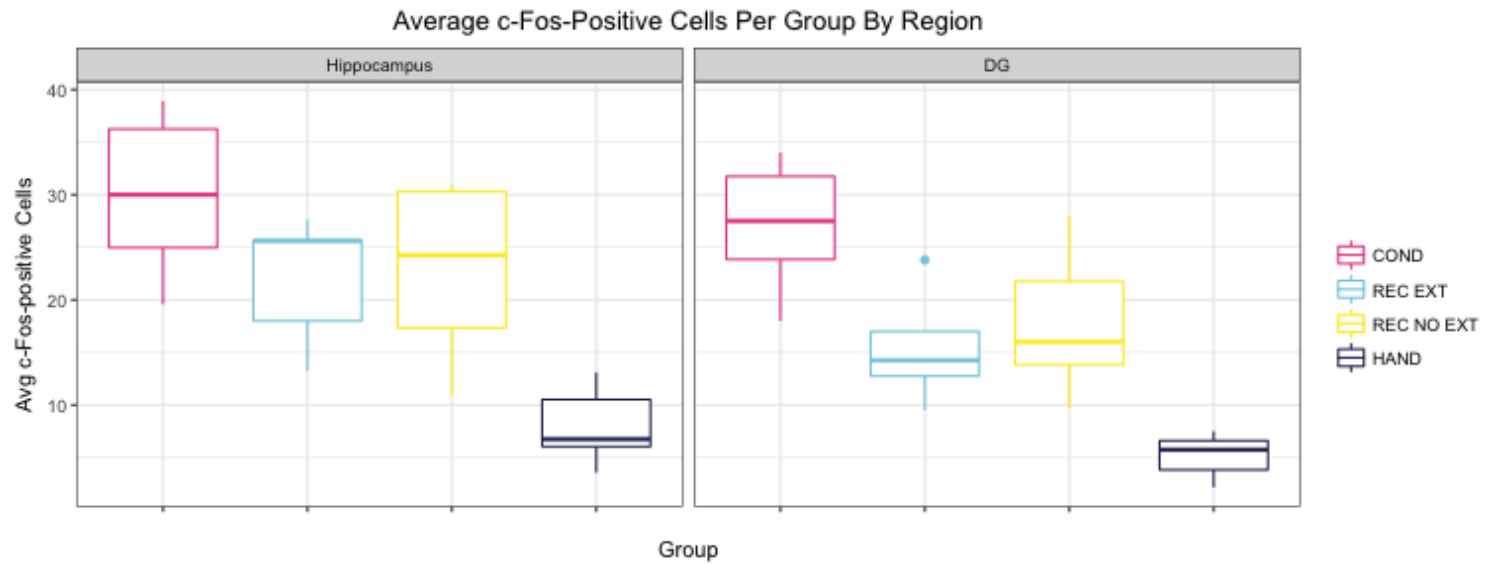




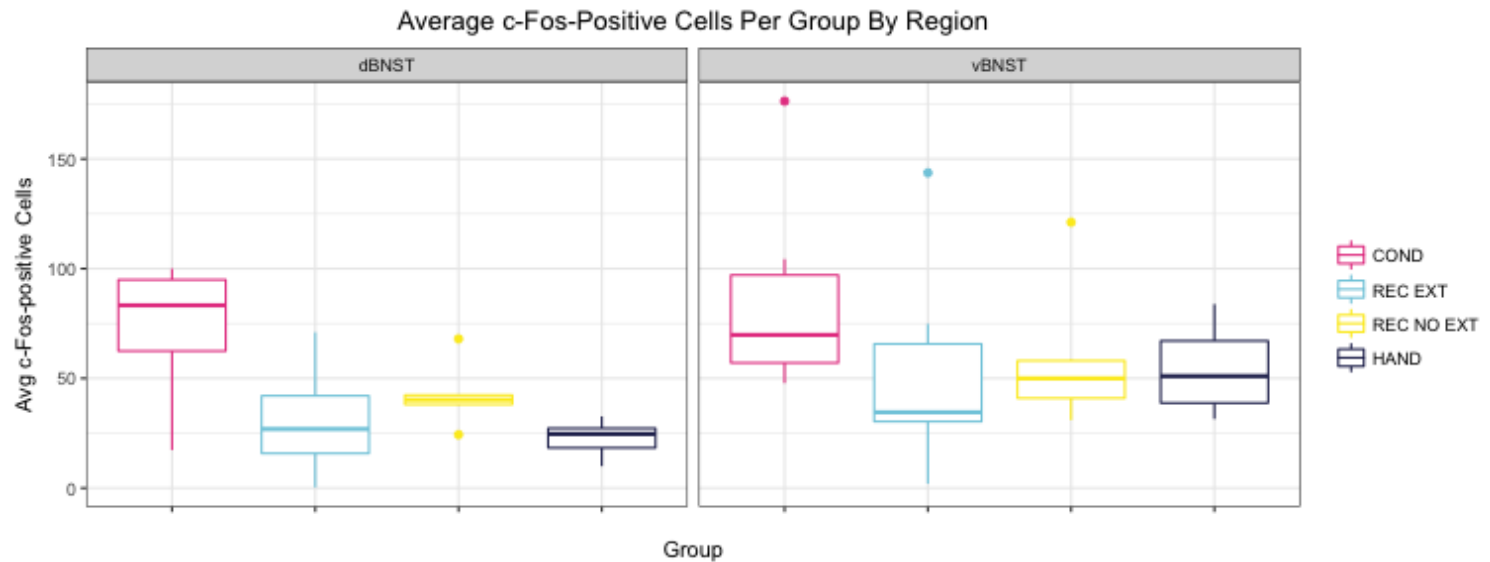
# The Graph



# Hippocampus



# BNST



# The Code: Mapping

```
plot <- data2 %>% ggplot(aes(fct_relevel(group, group_rl), count, color = fct_
geom_boxplot() +
facet_wrap(~fct_relevel(region, c("Hippocampus", "DG", "dBNST", "vBNST")))) +
theme_bw() +
labs(x = "Group", y = "Avg c-Fos-positive Cells") +
scale_color_manual(name="", values= beyonce_palette(66) [c(11,5,7,1)]) +
ggtitle("Average c-Fos-Positive Cells Per Group By Region") +
theme(plot.title = element_text(hjust = 0.5)) +
scale_x_discrete(labels = c("", "", "", ""))
```

# The Code: Geom Boxplot + Facet Wrap

```
plot ← data2 %>% ggplot(aes(fct_relevel(group, group_rl), count, color = fct_
geom_boxplot() +
facet_wrap(~fct_relevel(region, c("Hippocampus", "DG", "dBNST", "vBNST")))) +
theme_bw() +
labs(x = "Group", y = "Avg c-Fos-positive Cells") +
scale_color_manual(name="", values= beyonce_palette(66) [c(11,5,7,1)]) +
ggtitle("Average c-Fos-Positive Cells Per Group By Region") +
theme(plot.title = element_text(hjust = 0.5)) +
scale_x_discrete(labels = c("", "", "", ""))
```

# The Code: Graph Formatting

```
plot ← data2 %>% ggplot(aes(fct_relevel(group, group_rl), count, color = fct_
geom_boxplot() +
facet_wrap(~fct_relevel(region, c("Hippocampus", "DG", "dBNST", "vBNST")))) +
theme_bw() +
labs(x = "Group", y = "Avg c-Fos-positive Cells") +
scale_color_manual(name="", values= beyonce_palette(66) [c(11,5,7,1)]) +
ggtitle("Average c-Fos-Positive Cells Per Group By Region") +
theme(plot.title = element_text(hjust = 0.5)) +
scale_x_discrete(labels = c("", "", "", ""))
```

# The Code: Color

```
plot ← data2 %>% ggplot(aes(fct_relevel(group, group_rl), count, color = fct_
geom_boxplot() +
facet_wrap(~fct_relevel(region, c("Hippocampus", "DG", "dBNST", "vBNST")))) +
theme_bw() +
labs(x = "Group", y = "Avg c-Fos-positive Cells") +
scale_color_manual(name="", values= beyonce_palette(66) [c(11,5,7,1)]) +
ggtitle("Average c-Fos-Positive Cells Per Group By Region") +
theme(plot.title = element_text(hjust = 0.5)) +
scale_x_discrete(labels = c("", "", "", ""))
```

