

Differential cell-cell communication between SCZ and NTC using cellchat V2

Method

- A rough summary of cell chat V2.
- Rational of using cell chat V2: enabling the comparative cell-cell communication between the diagnosis groups.
- Implementation: It first runs the cell-chat pipeline on the subset of samples from each diagnosis separately (stored), and then uses `mergeCellChat` function to merge the two cellchat objects and identify the differential pattern and measure the strength of the evidence.
- Nuanced note: despite cell chat V2 having spatially aware cell-cell communication analysis, we didn't use it. That's because our objective is to identify the communication pattern, or the differential communication pattern, at the cortical layer level instead of at the spot level, and hence. We decided to use it without accounting for more nuanced spatial coordinate information.

Code

Results

the total number of interactions and interaction strength for SCZ and NTC respectively

- # of interaction: There's more interaction among NTC group compared to SCZ group.

```
gg1 <- compareInteractions(cellchat, show.legend = F, group = c(1, 2))  
gg2 <- compareInteractions(cellchat, show.legend = F, group = c(1, 2), measure = "weight")  
gg1 + gg2
```

