

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 comparative cell-cell communication between the diagnosis groups.
- Implementation: It first run the cell-chat pipeline on the subset of samples from each diagnosis separately (stored), and then use `mergeCellChat` function to merge the two cellchat object and identify the differential pattern and measure the strength of the evidence.
- Nuances noted: despite cell chat V2 have spatially aware cell-cell communication analysis, we didn't use it. That's because that 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 the without accounting 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
```

