main

July 9, 2021

1 Examining the overlap between antipsychotics analysis with main DE analysis

```
[1]: import pandas as pd
```

1.1 Load DE genes results

```
[2]: ap = pd.read_csv("../../_m/genes/diffExpr_sz_APVctl_full.txt", sep='\t',␣
     ↪index_col=0)
     noap = pd.read_csv("../../_m/genes/diffExpr_sz_noAPVctl_full.txt", sep='\t',␣
     ↪index_col=0)
     degs = pd.read_csv("../../../_m/genes/diffExpr_szVctl_full.txt", sep='\t',␣
     ↪index_col=0)
```

1.1.1 FDR 5% comparison

```
[3]: def get_degs(df, fdr):
         return df[(df["adj.P.Val"] < fdr)]
```

```
[4]: len(set(get_degs(ap, 0.05).index) & set(get_degs(noap, 0.05).index))
```

```
[4]: 331
```

```
[5]: len(set(get_degs(ap, 0.05).index) & set(get_degs(noap, 0.05).index)) /␣
     ↪len(set(get_degs(noap, 0.05).index))
```

```
[5]: 0.4962518740629685
```

```
[6]: len(set(get_degs(ap, 0.05).index) & set(get_degs(degs, 0.05).index))
```

```
[6]: 1929
```

```
[7]: len(set(get_degs(ap, 0.05).index) & set(get_degs(degs, 0.05).index)) /␣
     ↪len(set(get_degs(ap, 0.05).index))
```

```
[7]: 0.7165676077265973
```

```
[8]: len(set(get_degs(noap, 0.05).index) & set(get_degs(degs, 0.05).index))
```

[8]: 520

```
[9]: len(set(get_degs(noap, 0.05).index) & set(get_degs(degs, 0.05).index)) /␣
     ↪len(set(get_degs(noap, 0.05).index))
```

[9]: 0.7796101949025487

[ ]: