

Cwiek, A., Rajtmajer, S. M., Wyble, B., Honavar, V., Grossner, E. & Hillary, F. G. (2022). Supporting information for “Feeding the machine: Challenges to reproducible predictive modeling in resting-state connectomics.” *Network Neuroscience*, 6(1), 29–48. [https://doi.org/10.1162/netn\\_a\\_00212](https://doi.org/10.1162/netn_a_00212)

## Supplemental Materials

**Table S1: Frequency of the neurological disorders/syndromes included in this review**

	Frequency	Percent
Alzheimer’s disease (MCI, FTD)	66	26.4%
Mood and psychiatric (depression/ptsd)	40	16.0%
Schizophrenia	34	13.6%
Autism spectrum	33	13.2%
Brain Injury/stroke	15	6.0%
Motor disease (PD, HD)	15	6.0%
ADHD	14	5.6%
Epilepsy	13	5.2%
Health/Medical	10	4.0%
Multiple sclerosis	7	2.8%
Substance Abuse	4	1.6%
Infants/Children	4	1.6%
Other	9	3.6%
Multiple	15	6.0%

**Table S2: Demographic information collected from the systematic review**

	Percentage of Studies:	Count:
<b>Participants:</b>	100%	250
<b>Sex:</b>	86.8%	217
<b>Age:</b>	88.8%	222
<b>Left/Right Handed</b>	<b>27.2%</b>	<b>68</b>
<b>Education:</b>	<b>35.6%</b>	<b>89</b>
<b>Times Since Diagnosis:</b>	<b>25.6%</b>	<b>64</b>
<b>Age of Diagnosis:</b>	<b>10.8%</b>	<b>27</b>
<b>Race / Ethnicity:</b>	<b>5.6%</b>	<b>14</b>
<b>Socioeconomic Status:</b>	<b>0.8%</b>	<b>2</b>

**Formula S1: Accuracy derived from sensitivity and specificity scores based upon sample size**

$$Accuracy = \frac{(Sn * CG) + (Sp * HC)}{(CG + HC)}$$

Where *Sn* = sensitivity, *CG* = condition group sample size, *Sp* = Specificity, and *HC* = healthy control sample size.