





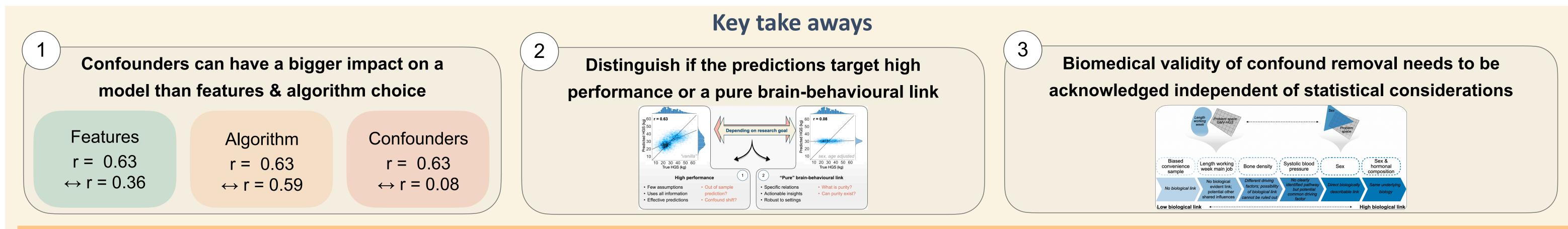


6,137

# The Confound Continuum -

# A 2D confounder assessment for Al in precision medicine

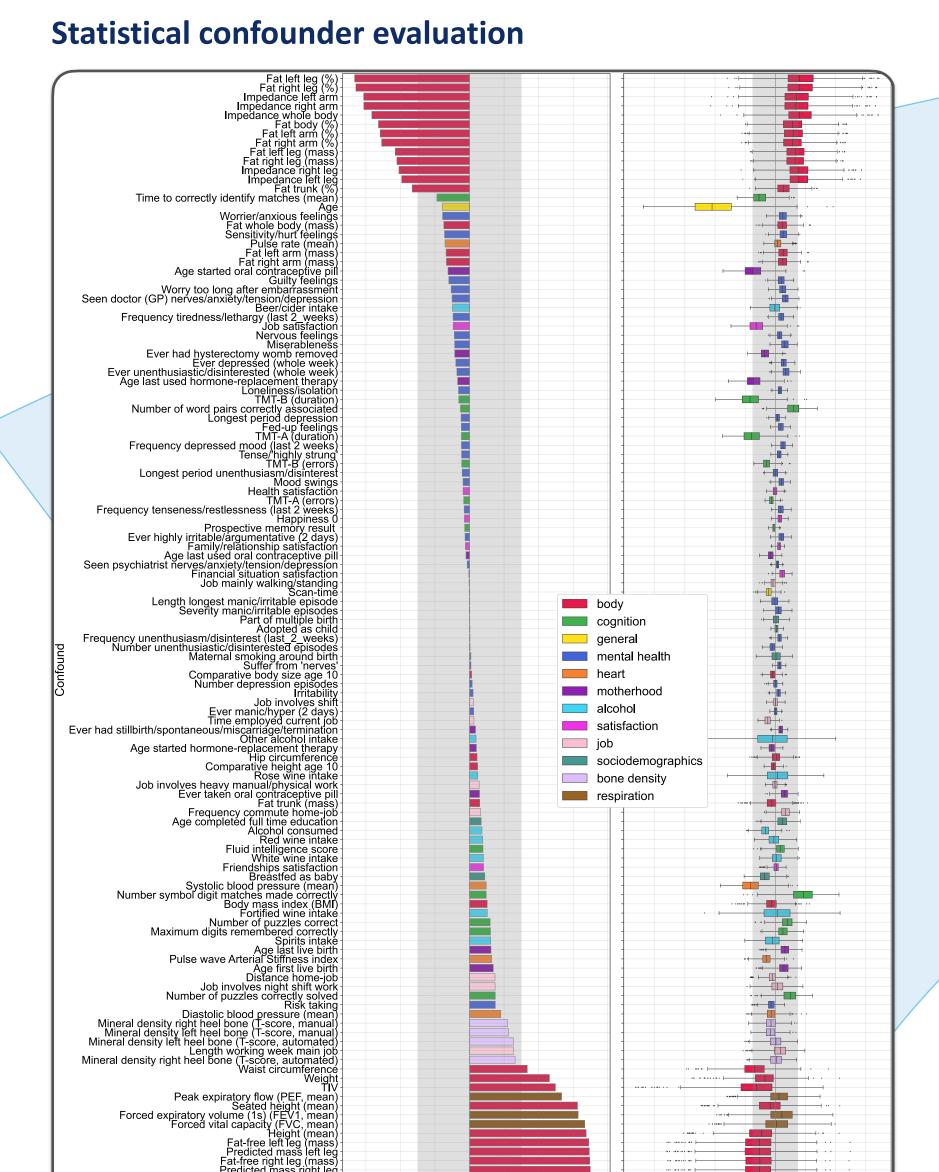
Vera A. Komeyer<sup>1,2</sup>, Simon B. Eickhoff<sup>1,2</sup>, Christian Grefkes<sup>3,4,5</sup>, Kaustubh R. Patil<sup>1,2</sup>, Federico Raimondo<sup>1,2</sup>



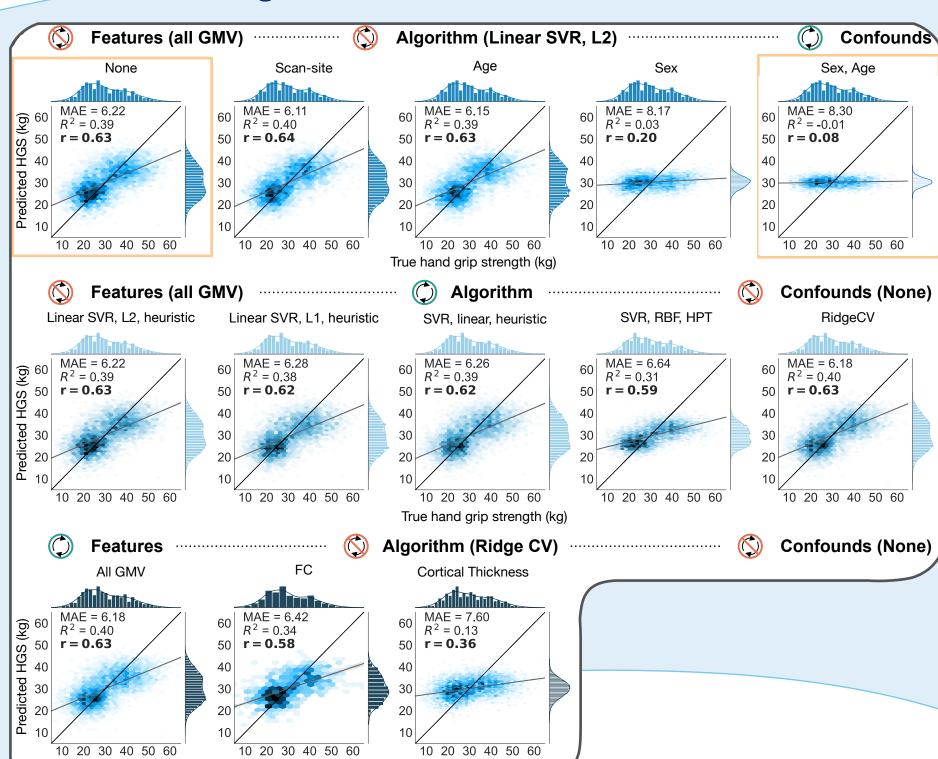
## Think about statistical AND conceptual implications of confound removal → interpret respectively

#### Methods Introduction Goal Individual-level behavioural predictions from neuroimaging-derived features **Learning Algorithms Features** Setups Gray matter volume (GMV): ❖ Linear SVR<sup>5,6</sup> (heuristic C<sup>7</sup>, L1 /L2 loss) Brain features only Confounding can influence brain-derived features and phenotypical targets **Problem** Cortex<sup>2</sup>, Subcortex<sup>3</sup>, Cerebellum<sup>4</sup> \* RBF SVR Confound features only \* Removing confounders changes the feature-target relationship Functional Connectivity (FC) \* Ridge regression Brain & confounder features → affected model interpretation Cortical Thickness (CT) Feature / Algorithm / Confounder setup Ntrain N<sub>test</sub> (hold-out) \* Statistical confounder evaluations cannot account for biomedical validity of confound removal GMV / LinearSVR (L2) / 21,169 to 21,782 5,293 to 5,446 **Changing confound removal** Confounders **GMV / Changing learning algorithm / No** ❖ Develop a use-case dependent conceptual dimension → Confound Continuum 21,782 5,446 confound removal Scan-site \* Age \* Sex & Age \* Exemplify confounder impact by predicting the robust, reliable and clinically relevant target **Changing features / Ridge CV / No** Sex Scan-time hand grip strength (HGS)<sup>1</sup> confound removal

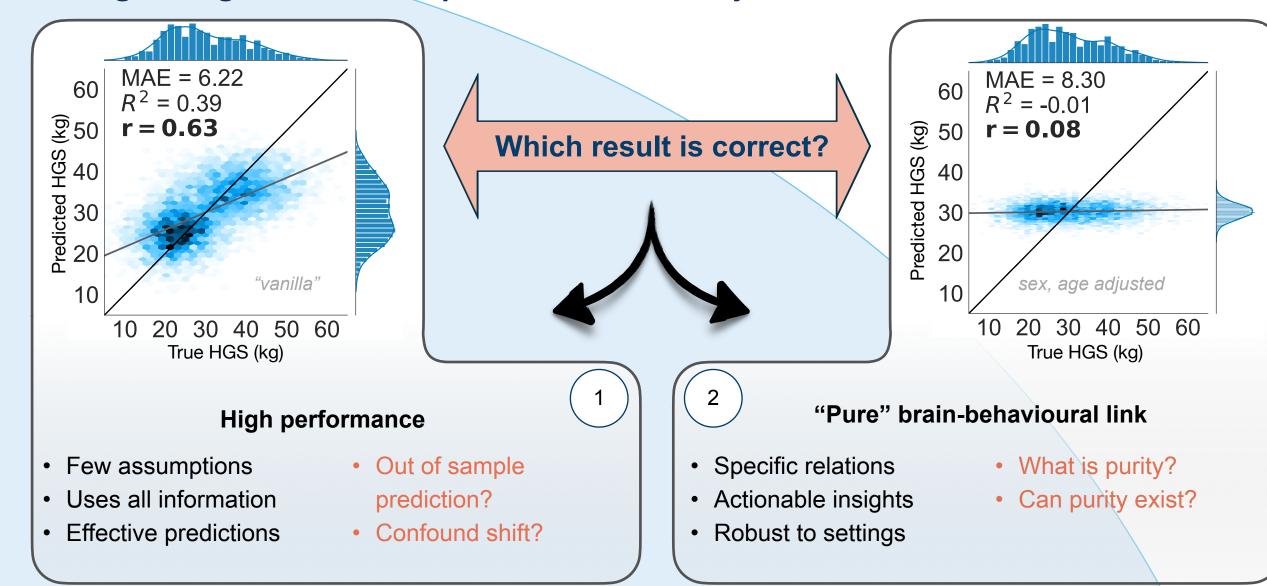
## Results



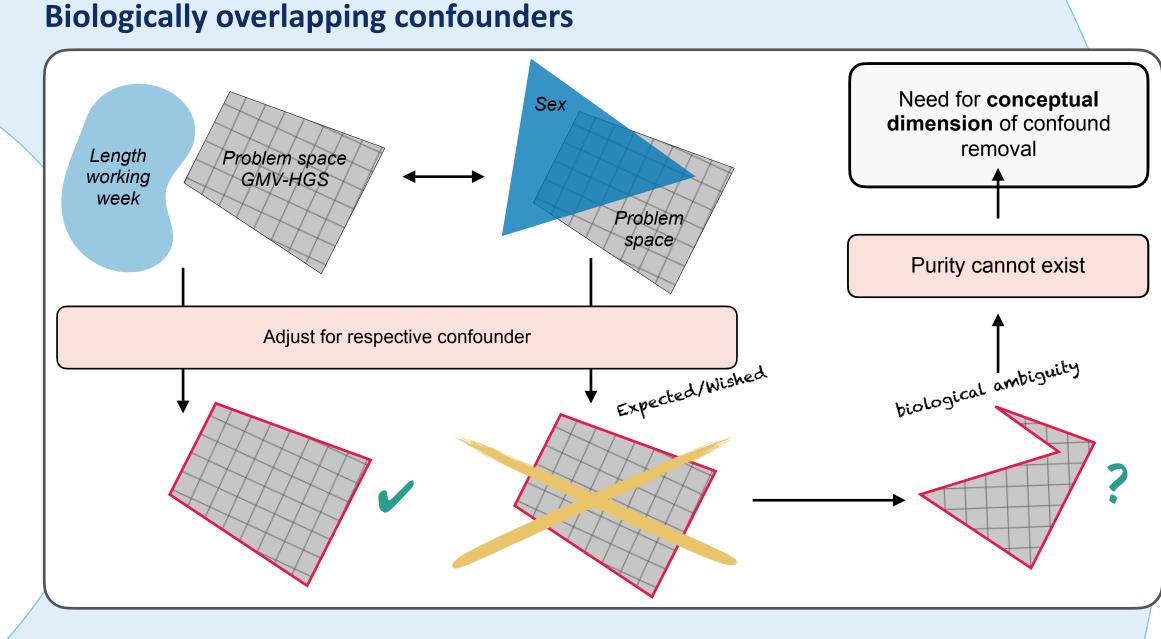
#### Confound removal impacts predictive performance more than feature or algorithm choice



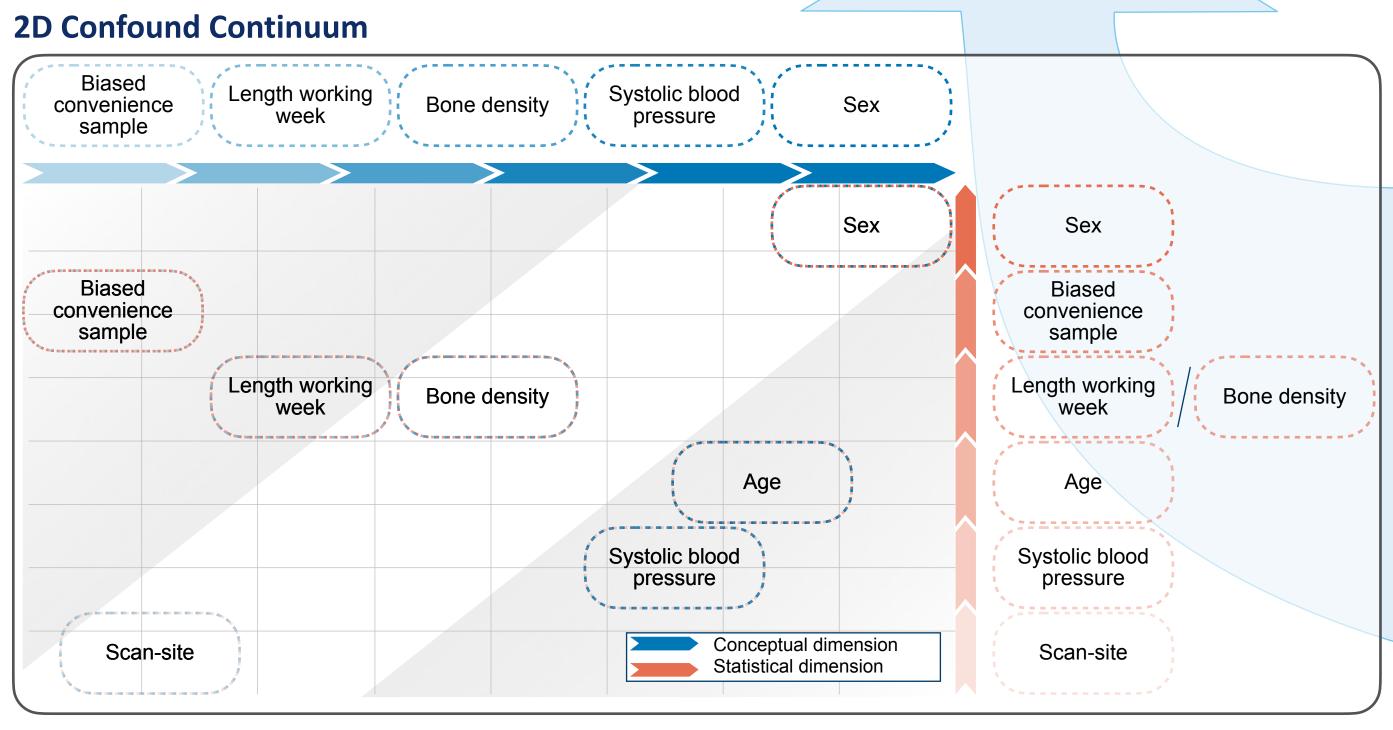
# Distinguishing between two possible research objectives



**Conceptual Confound Continuum** 



#### **Interpretation matters** "Sex and age encodings in GMV drive "We can decently predict HGS" → no claims on neural encodings linear HGS predictions" 10 20 30 40 50 60 10 20 30 40 50 60 e.g. individualised medicine e.g. enhanced understanding of brain function



-0.6 -0.4 -0.2 0.0 0.2 0.4 0.6 0.80.5 -0.4 -0.3 -0.2 -0.1 0.0 0.1 0.2 0.3

# Length Problem space GMV-HGS **4**-----**>** Biased convenience sample composition

No biological evident Negligible biological link link; potential other shared influences Low biological link

Different driving factors; possibility of biological link cannot be ruled out

No clearly identified pathway but potential common driving factor

Direct biologically describable link

Same underlying biolog High biological link 

### References

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