

Set specific weights were then used to assess the outcome. For both discussed and triaged applications, optimal full matching was implemented using Mahalanobis distance. For discussed applications, we used exact matching for the pre- vs post-2009 period since NIH rescaled their priority scores in 2009.¹⁶ For triaged applications, we also used exact matching within fiscal year. We defined match quality using standardized mean differences (SMDs), with $\text{abs}(\text{SMD}) < 0.20$ judged as acceptable balance and $\text{abs}(\text{SMD}) < 0.10$ being excellent balance,^{17,18} and then compared the match quality for alternative matching protocols including propensity score-based distances. The best match quality (the smallest SMDs for the most important covariates) was achieved with optimal full matching and was performed using the “Optmatch” package in R.¹⁹