Supplementary Information: Contrasting Computational Models of Mate Preference Integration Across 45 Countries

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Supplementary Note 1: Agent-Based Models Using an Alternative Mating Market Structure

Agents in six of the primary agent-based models paired based on a mutual attraction model of mate choice. In these models, the attraction matrices for each sex were multiplied together elementwise and pairing began with the most mutually attracted pair. This market structure produced strong correspondence between the agent-based models and the human data. However, to test the robustness of these results, we also ran a separate set of models with a different mating market structure.

In this alternative model, agents paired based on minimum, rather than mutual attraction. In these models, agents computed their attraction to all opposite-sex agents using their preference integration algorithms just as in the primary models. However, the model then identified the least attracted member of each possible couple rather than the mutual attraction of all possible couples. The model next paired the agents with the highest minimum in-pair attraction value, iterating this pairing until all possible couples were formed. These minimum attraction models were identical to the mutual attraction models in all other respects.

We compared the results of the minimum attraction models to the human cross-cultural 115 sample using the same model training and testing procedure as in the primary agent-based 116 models. Supplementary Fig. S2 shows the results of this model comparison process. Just as in the 117 primary models, the model in which agents integrate their preferences according to a Euclidean 118 algorithm provides the strongest fit to the cross-cultural human sample among the six alternative 119 120 models of mate preference integration. The results of the primary agent-based models, in which the Euclidean algorithm produces the best approximation of the cross-cultural human data, are 121 122 therefore not limited to the mutual attraction model of mate choice.

123 Supplementary Note 2: Agent-Based Models Incorporating Incomplete Mate Search

Agents in each of the primary models conduct a complete search of their local mating 124 market: each agent has information on and ultimately selects from the total set of 100 potential 125 126 mates that exist in their population. While this number is within estimated limits on human social group sizes, this simplified population structure constitutes a potentially unrealistic assumption 127 for at least three reasons. First, this implicitly supposes that all individuals in the population have 128 perfectly overlapping social networks. Second, this population structure assumes that there is no 129 randomness within and no limitations on the mate search process. Third, this is a large set of 130 potential mates to consider, which may be computationally implausible. To assess whether the 131 results reported in the primary agent-based models are dependent on this assumption, we created 132 an alternative model in which mate search is incomplete. 133

These incomplete search models are identical to the primary agent-based models except for just one change. When the models compute the mutual attraction matrix, a random subset of 50 potential mates are eliminated immediately for each agent. These agent couples are therefore incapable of pairing regardless of what their attraction values would have been otherwise. This elimination simulates an incomplete and partially random search of the mating market by each agent and makes it such that different agents have slightly different—albeit overlapping—social networks in that each agent functionally "knows" just a random subset of the total population.

We compared the populations produced by these incomplete search models to the human cross-cultural sample using the same training and testing procedure as used for the primary agent-based models. Supplementary Fig. S3 presents these results. Simulating incomplete search does not substantially change the relative model fits. Across all parameter settings, the Euclidean agent-based models still provide the best overall fit to the human cross-cultural sample relative to all of the other agent-based models of mate preference integration and still provide a fit relatively
similar to the regression model both trained and tested on the data itself. The relatively good
performance of this model in explaining the human cross-cultural data therefore does not appear
to emerge because of the assumption of complete mate search in the primary agent-based
models.

Supplementary Note 3: Comparing Agent-Based Models and Human Data Beyond Self Report

The primary agent-based models showed a strong correspondence between the Euclidean model and the human cross-cultural data. However, a limitation of the human sample is that all data is self-report: participants reported both their own traits and preferences as well as the traits of their partners, if applicable. It is possible that this led to biased reports of mates, yielding biased results.

We addressed this problem in two ways. First, the preference-updating model allowed us 158 to test the hypothesis that biased reports of preferences (or biased perception of partners) would 159 160 spuriously produce the pattern of results observed in the human cross-cultural data. Although this biased report model can produce comparable levels of mate preference fulfillment as observed 161 across cultures, it cannot produce the correlations between participant mate value and mate 162 preference fulfillment, ideal mate value, or partner mate value (Supplementary Figure S1; Figure 163 3). This suggests that rating bias alone cannot account for the correspondence between the 164 165 Euclidean agent-based model and the human cross-cultural sample.

Second and furthermore, we were able to leverage the design of this study to extract partner ratings for a subset of the sample, allowing us to conduct the same tests on data that did not rely exclusively on self-report. Although data collection in the cross-cultural sample was

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169 entirely self-report, and although participants were not specifically recruited in dyads, in some cases participants did complete the study along with their actual romantic partner. These dvadic 170 participations were not recorded; however, we can, through participant responses, infer which 171 participants were members of dyads rather than participating alone. We used two sets of criteria 172 for inferring dyads from the cross-cultural human sample: a "strict" criterion and a "less-strict" 173 criterion. For the strict criterion, we classified two participants as belonging to a dyad if they had 174 complimentary answers on the following questions: city of residence, own age and partner age, 175 relationship length, relationship status, whether they saw their partner in the last week, whether 176 they met their partner in the last week, number of children, and age of youngest child. This dyad 177 inference process additionally only searched for heterosexual couples. The less strict criterion 178 excluded information about number and age of children under the assumption that some mated 179 180 individuals could have different responses to these questions if they had children from prior relationships. 181

Pairing participants into dyads based on the strict criteria produced a sample of n = 394participants belonging to 197 inferred romantic dyads. Using the less-strict criteria resulted in n= 498 participants belonging to 249 dyads. To assess the risk of pairing participants into false dyads by chance, we ran the same dyad inference procedure on a sample in which we first randomly scrambled the responses used to pair participants into dyads within city. On this scrambled data, both dyad inference procedures produced zero inferred dyads.

With dyads, we can compare agent-based models to the human samples using responses beyond self-report. Rather than relying on self-reports for self and partner traits, we calculated composite trait scores for all participants by averaging self- and partner-reports. We then conducted the same analyses on these samples as in the full cross-cultural human sample.

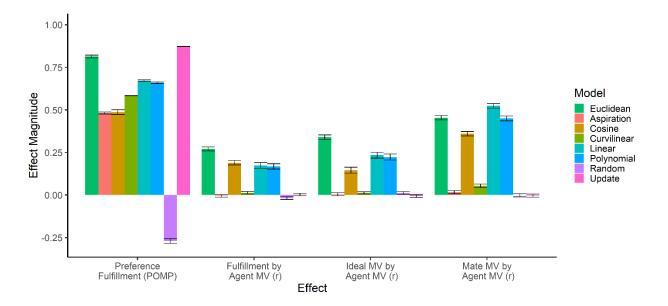
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192 Supplementary Figs. S4 and S5 show the results of these analyses for the strict and lessstrict dyads respectively. In both cases, most models produced substantially lower predicted-193 observed value correlations than the Euclidean model; the only exceptions were the linear and 194 polynomial models. For the less-strict dyads, the linear and polynomial models produced 195 observed-predicted value correlations comparable to or higher than the Euclidean model in most 196 parameter settings. For the strict dyads, the linear and polynomial models produced observed-197 predicted value correlations that approximated the Euclidean models in only one parameter 198 setting. However, the Euclidean model produced a lower RMSE than the linear and polynomial 199 200 models across all parameter settings; it was only matched by the preference-updating model on RMSE in 3 out of the 9 parameter settings. Overall, across all 9 parameter settings and across the 201 two model fit estimates, the Euclidean agent-based model still produced the best fit to the human 202 203 cross-cultural data in both the strict and less strict dyad inference criteria. This suggests the strong correspondence between the Euclidean agent-based model and the cross-cultural human 204 data is not an artifact of self-report data collection. 205

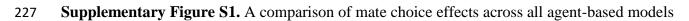
206 Supplementary Note 4: Institutional Review Boards and Ethics Committees that Approved

- 207 this Study
- 208 Ethical Committee of the Institute of Psychology, University of Wroclaw
- The Survey and Behavioural Research Ethics Committee at the Chinese University of HongKong
- 211 The ANU Human Research Ethics Committee at The Australian National University
- 212 The Ethical Review Board of Vrije Universiteit Amsterdam
- 213 Ethics committee of the Department of Psychology, Faculty of Humanities and Social Sciences,
- 214 University of Zagreb
- 215 University of Crete Psychology Department Research Ethics Committee
- 216 South-West University Neofit Rilski, Department of Psychology
- 217 Research Ethics Committee of the University of Tartu (UTREC)

- 218 Ethical Committee of the Technical University of Dresden
- 219 Ethical Commission in Research of the ENES, UNAM, Morelia
- 220 Ethics Review Board of CUFE Business School
- 221 Scientific Council of the Institute of Ethnology and Anthropology, RAS, Moscow, Russia
- 222 Ethics Council of the University of Setif 2, Algeria
- 223 Institutional Review Board of the University of Texas at Austin

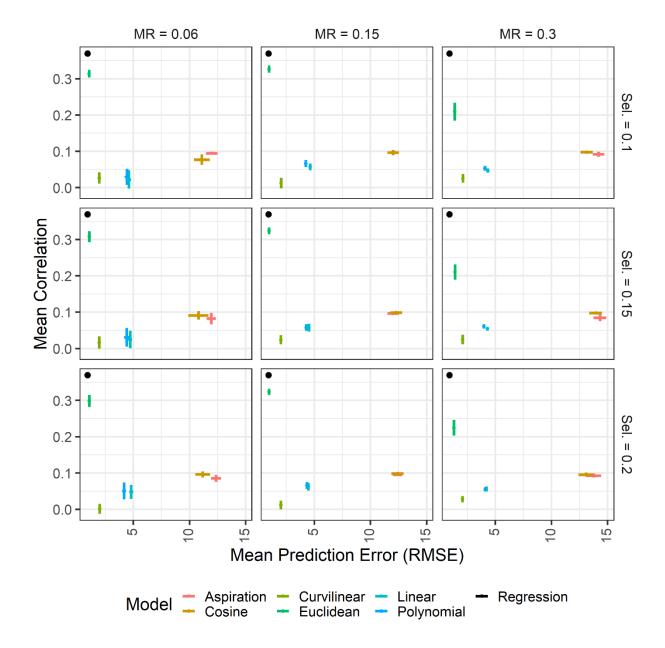






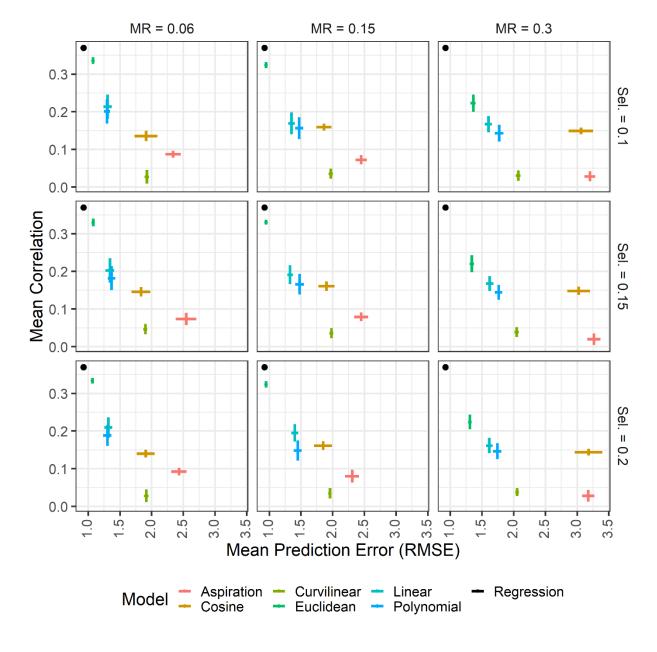
and across parameter settings. "POMP" = percentage of maximum possible; "r" = correlation.

229 Error bars represent 95% confidence intervals.



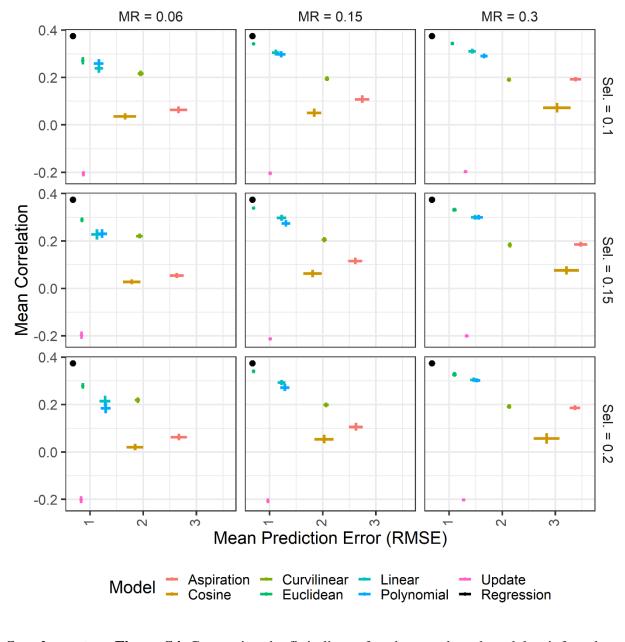


Supplementary Figure S2. Comparing the fit indices of each agent-based model to the crosscultural human data for models in which mate choice was based on minimum attraction. Error
bars represent 95% confidence intervals in both directions. "MR" = mutation rate; "Sel." =
selection strength.

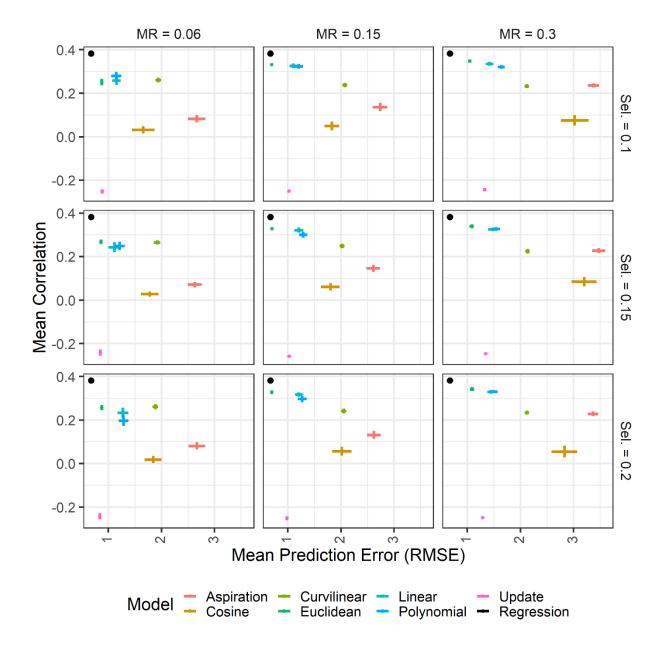




Supplementary Figure S3. Comparing the fit indices of each agent-based model to the crosscultural human data for models in which agents conduct an incomplete search of the mating
market. Error bars represent 95% confidence intervals in both directions. "MR" = mutation rate;
"Sel." = selection strength.



Supplementary Figure S4. Comparing the fit indices of each agent-based model to inferred
dyads from the cross-cultural human data using the strict dyad inference procedure. Error bars
represent 95% confidence intervals in both directions. "MR" = mutation rate; "Sel." = selection
strength.





Supplementary Figure S5. Comparing the fit indices of each agent-based model to inferred
dyads from the cross-cultural human data using the less-strict dyad inference procedure. Error
bars represent 95% confidence intervals in both directions. "MR" = mutation rate; "Sel." =
selection strength.

258 Supplementary Table S1

259 *Model fit statistics from out-of-sample prediction accuracy procedure across models and across*

260 *parameter settings*.

Model	Mutation Rate	Selection Strength	RMSE Mean	RMSE 95% CI	<i>r</i> Mean	<i>r</i> 95% CI
Euclidean	0.06	0.1	1.06	1.04 - 1.08	0.34	0.33 - 0.35
Euclidean	0.06	0.15	1.05	1.04 - 1.07	0.33	0.32 - 0.34
Euclidean	0.06	0.2	1.06	1.05 - 1.08	0.34	0.33 - 0.34
Euclidean	0.15	0.1	0.95	0.94 - 0.95	0.34	0.33 - 0.34
Euclidean	0.15	0.15	0.95	0.95 - 0.96	0.34	0.33 - 0.34
Euclidean	0.15	0.2	0.95	0.95 - 0.95	0.33	0.33 - 0.34
Euclidean	0.3	0.1	1.29	1.26 - 1.31	0.27	0.26 - 0.29
Euclidean	0.3	0.15	1.30	1.27 - 1.33	0.25	0.24 - 0.27
Euclidean	0.3	0.2	1.29	1.26 - 1.32	0.23	0.21 - 0.25
Aspiration	0.06	0.1	2.41	2.27 - 2.55	0.08	0.07 - 0.1
Aspiration	0.06	0.15	2.38	2.27 - 2.49	0.08	0.07 - 0.1
Aspiration	0.06	0.2	2.42	2.29 - 2.55	0.08	0.07 - 0.1
Aspiration	0.15	0.1	2.52	2.4 - 2.64	0.07	0.06 - 0.08
Aspiration	0.15	0.15	2.41	2.3 - 2.51	0.06	0.05 - 0.08
Aspiration	0.15	0.2	2.42	2.31 - 2.52	0.09	0.07 - 0.1
Aspiration	0.3	0.1	3.21	3.12 - 3.3	0.02	0 - 0.03
Aspiration	0.3	0.15	3.30	3.18 - 3.41	0.02	0 - 0.03
Aspiration	0.3	0.2	3.19	3.1 - 3.27	0.03	0.02 - 0.04
Cosine	0.06	0.1	1.68	1.49 - 1.86	0.17	0.15 - 0.18
Cosine	0.06	0.15	1.76	1.63 - 1.9	0.15	0.13 - 0.16
Cosine	0.06	0.2	1.80	1.68 - 1.93	0.15	0.14 - 0.16
Cosine	0.15	0.1	1.77	1.67 - 1.88	0.17	0.16 - 0.19
Cosine	0.15	0.15	1.75	1.61 - 1.89	0.19	0.17 - 0.2
Cosine	0.15	0.2	1.92	1.77 - 2.07	0.16	0.15 - 0.17
Cosine	0.3	0.1	2.84	2.62 - 3.06	0.17	0.16 - 0.18
Cosine	0.3	0.15	2.98	2.78 - 3.18	0.15	0.14 - 0.16
Cosine	0.3	0.2	2.68	2.47 - 2.89	0.18	0.16 - 0.19
Curvilinear	0.06	0.1	1.91	1.87 - 1.94	0.03	0.02 - 0.05
Curvilinear	0.06	0.15	1.89	1.85 - 1.93	0.03	0.02 - 0.05
Curvilinear	0.06	0.2	1.86	1.83 - 1.9	0.04	0.02 - 0.05
Curvilinear	0.15	0.1	1.99	1.97 - 2.02	0.03	0.02 - 0.04
Curvilinear	0.15	0.15	1.96	1.93 - 1.99	0.04	0.02 - 0.05
Curvilinear	0.15	0.2	1.98	1.95 - 2.01	0.03	0.01 - 0.04
Curvilinear	0.3	0.1	2.03	2 - 2.06	0.05	0.04 - 0.06
Curvilinear	0.3	0.15	2.04	2.01 - 2.06	0.04	0.03 - 0.05

Curvilinear	0.3	0.2	2.03	2.01 - 2.06	0.04	0.03 - 0.05
Linear	0.06	0.1	1.29	1.24 - 1.34	0.21	0.19 - 0.24
Linear	0.06	0.15	1.26	1.19 - 1.33	0.24	0.21 - 0.26
Linear	0.06	0.2	1.36	1.29 - 1.43	0.20	0.17 - 0.23
Linear	0.15	0.1	1.31	1.26 - 1.37	0.22	0.19 - 0.24
Linear	0.15	0.15	1.38	1.31 - 1.44	0.21	0.19 - 0.24
Linear	0.15	0.2	1.39	1.33 - 1.44	0.19	0.17 - 0.22
Linear	0.3	0.1	1.59	1.54 - 1.64	0.19	0.17 - 0.21
Linear	0.3	0.15	1.64	1.57 - 1.7	0.17	0.15 - 0.19
Linear	0.3	0.2	1.61	1.55 - 1.66	0.18	0.16 - 0.2
Polynomial	0.06	0.1	1.30	1.24 - 1.37	0.22	0.19 - 0.24
Polynomial	0.06	0.15	1.32	1.25 - 1.39	0.21	0.18 - 0.24
Polynomial	0.06	0.2	1.35	1.28 - 1.41	0.22	0.2 - 0.24
Polynomial	0.15	0.1	1.37	1.31 - 1.44	0.20	0.18 - 0.23
Polynomial	0.15	0.15	1.43	1.37 - 1.5	0.19	0.16 - 0.22
Polynomial	0.15	0.2	1.40	1.33 - 1.46	0.20	0.18 - 0.23
Polynomial	0.3	0.1	1.78	1.72 - 1.84	0.15	0.12 - 0.17
Polynomial	0.3	0.15	1.70	1.63 - 1.76	0.16	0.14 - 0.18
Polynomial	0.3	0.2	1.65	1.59 - 1.71	0.18	0.16 - 0.2
Random	0.06	0.1	8.07	7.67 - 8.47	0.08	0.07 - 0.09
Random	0.06	0.15	8.04	7.54 - 8.53	0.09	0.08 - 0.1
Random	0.06	0.2	8.62	8.04 - 9.2	0.09	0.07 - 0.1
Random	0.15	0.1	8.50	8.07 - 8.92	0.09	0.08 - 0.09
Random	0.15	0.15	8.33	8.01 - 8.65	0.08	0.07 - 0.09
Random	0.15	0.2	8.30	7.85 - 8.75	0.08	0.06 - 0.09
Random	0.3	0.1	9.07	8.65 - 9.49	0.09	0.08 - 0.09
Random	0.3	0.15		9.51 -		
			9.93	10.34	0.07	0.06 - 0.08
Random	0.3	0.2	9.38	8.97 - 9.79	0.08	0.07 - 0.09
Update	0.06	0.1	1.05	1.04 - 1.06	0.02	0 - 0.04
Update	0.06	0.15	1.05	1.04 - 1.06	0.03	0.01 - 0.06
Update	0.06	0.2	1.06	1.05 - 1.07	0.02	-0.01 - 0.05
Update	0.15	0.1	1.11	1.09 - 1.13	0.00	-0.02 - 0.01
Update	0.15	0.15	1.11	1.09 - 1.13	-0.01	-0.03 - 0
Update	0.15	0.2	1.09	1.08 - 1.1	-0.01	-0.02 - 0.01
Update	0.3	0.1	1.33	1.31 - 1.36	-0.01	-0.02 - 0
Update	0.3	0.15	1.35	1.32 - 1.37	-0.02	-0.030.01
Update	0.3	0.2	1.30	1.28 - 1.32	-0.02	-0.030.01