

1 **Inheritance of neural substrates for motivation and pleasure experience**

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31 **Abstract**

32 Despite advances in the understanding of the reward system and the role of
33 dopamine in recent decades, the heredity of the underlying neural mechanisms is
34 not known. In the present study, a Monetary Incentive Delay (MID) task was used to
35 examine the haemodynamic activation of the nucleus accumbens (*NAcc*), a key hub
36 of the reward system, in 86 healthy monozygotic twins and 88 dizygotic twins during
37 the anticipation of monetary incentives. The participants also completed self-report
38 measures of pleasure experience. Using a voxel-wise heritability mapping method,
39 activation of the bilateral *NAcc* during the anticipation of monetary gains was found
40 to have significant heritability ($h^2 = 0.20-0.49$). Moreover, significant shared genetic
41 covariance was observed between pleasure experience and *NAcc* activation when
42 anticipating monetary gain. These findings suggest that *NAcc* activation and self-
43 reported pleasure experience may both be heritable, and their phenotypic
44 correlation may be partially explained by shared genetic variation.

45

46 **Keywords:** Reward System, Nucleus Accumbens, Heritability, Motivation, Pleasure

47 **Introduction**

48 The reward system plays a key role in human behaviour and emotion (*Iversen, 2010*).
49 The nucleus accumbens (*NAcc*), situated in the ventral striatum, is regarded as the
50 hub of the mesolimbic and mesocortical reward systems (*Baldo & Kelley, 2007*;
51 *Berridge & Robinson, 1998; Haber & Knutson, 2010*). However, the contribution of
52 the *NAcc* to reward processing is not fully understood. Compelling evidence supports
53 the notion that the reward processing system can be parsed into anticipatory and
54 consummatory phases (*Baldo & Kelley, 2007; Craig, 1917*). Dopaminergic activity in
55 the *NAcc* is associated with salience attribution of motivation, which assigns
56 motivational significance to different incentives in the anticipatory period (*Berridge,*
57 *2003, 2007, 2012*). Despite these advances in understanding the reward system, the
58 heritability of reward processing and its component phenotypes are largely unknown.

59 Studies in the last decade have suggested a relationship between dopaminergic
60 gene variation and ventral striatal activation measured by functional MRI reward
61 tasks in anticipating, predicting, or receiving monetary incentives (*Aarts et al., 2010*;
62 *Dreher, Kohn, Kolachana, Weinberger, & Berman, 2009; Forbes et al., 2009; Hahn et*
63 *al., 2011; Nikolova, Ferrell, Manuck, & Hariri, 2011; Yacubian et al., 2007*). Although
64 single genetic polymorphisms have been associated with ventral striatal activation to
65 a modest extent, studies that examine single or few polymorphisms, are seldom
66 replicated and tend to be underpowered. Evidence from the Psychiatric Genomics
67 Consortium indicates that psychiatric phenotypes are polygenic, with any one gene
68 only contributing a small amount to the overall variance. Thus, to have meaningful
69 explanatory power, it is essential to either use genome-wide common variant data,

70 aggregating the effects of all polymorphisms, or to examine family-based genetic
71 variation. The prediction of ventral striatal activation using polygenic risk scores for
72 psychosis has already revealed the cumulative effect of genes (*Bossong & Kahn,*
73 *2016; Lancaster et al., 2016*), and it is expected that related component phenotypes
74 are similarly polygenic. However, the extent to which genetic factors influence *NAcc*
75 and ventral striatal brain activation, particularly in the anticipatory period for reward,
76 is not clearly understood.

77 In this study, we examined measures of shared genetic variance among
78 dimensional psychiatric phenotypes, using a voxel-wise topographical approach to
79 map striatal activation. While previous studies have mainly employed regions of
80 interest methodology, voxel-wise analysis affords much finer heritability mapping,
81 thereby reducing statistical noise in heritability estimation. Hypoactivation of the
82 *NAcc* and the ventral striatum in anticipating monetary rewards had been reported
83 both in patients with schizophrenia (*Radua et al., 2015*) and in their unaffected
84 biological relatives. Probands and biological relatives also exhibit increased
85 anhedonia that co-segregates in families (*Docherty, Sponheim, & Kerns, 2015;*
86 *Kendler, Thacker, & Walsh, 1996; Li et al., 2015*). These results suggest that impaired
87 motivation is associated with genetic factors underlying schizophrenia (*de Leeuw,*
88 *Kahn, & Vink, 2015; Grimm et al., 2014; Vink et al., 2016*). Thus, mapping the
89 heritability of brain activation in anticipating and approaching reward may help
90 clarify its potential role as an endophenotype for psychosis (*Braff, Freedman, Schork,*
91 *& Gottesman, 2007; Gottesman & Gould, 2003*).

92 Another important matter to consider is the similar ventral striatal dysfunction

93 reported in patients with major depressive disorder, addiction, and their family
94 members (*Beck et al., 2009; Knutson, Bhanji, Cooney, Atlas, & Gotlib, 2008; Pizzagalli*
95 *et al., 2009; Wrase et al., 2007*). Since anhedonia and motivational deficits are also
96 relevant to major depressive disorder, the problem of non-specificity needs to be
97 addressed. This study aims to examine the circuitry and behavioral manifestations of
98 dimensional clinical traits, in line with Research Domain Criteria (RDoC) (*Cuthbert,*
99 *2014; Cuthbert & Insel, 2010*).

100 Anhedonia, the diminished ability to experience pleasure, has long been regarded
101 as a core symptom of schizophrenia and major depression disorder (*Meehl, 1975;*
102 *Meehl, 1990; Pizzagalli, 2014*). Cumulative evidence has also demonstrated a
103 significant heritability estimate for anhedonia ranging from 0.3 to 0.7 (*Kendler &*
104 *Hewitt, 1992; Linney et al., 2003; MacDonald, Pogue-Geile, Debski, & Manuck, 2001*).
105 Although previous findings support an association between motivation-related *NAcc*
106 activation and anhedonia traits (*Vignapiano et al., 2016; Wacker, Dillon, & Pizzagalli,*
107 *2009*), their shared genetic covariance has not been examined. Investigating the
108 heritability of *NAcc* activation and anhedonia could facilitate the identification of
109 shared regions of the genome and the exploration of intervention for amotivation
110 and anhedonia, both of which indicate poor prognosis and are refractory to currently
111 available treatment (*Kring & Barch, 2014*).

112 In the present study, we adopted a healthy-twin design to examine the heritability
113 of pleasure experience and its shared genetic covariance with *NAcc* activation during
114 the anticipation of monetary rewards using the Monetary Incentive Delay Task (MID).
115 We hypothesized that both motivation-related *NAcc* activation and pleasure

116 experience would exhibit significant heritability. We further hypothesized that
117 motivation-related *NAcc* activation and pleasure experience would share significant
118 genetic covariance.

119

120 **Results**

121 **Demographics**

122 The sample included 43 pairs of same-sex monozygotic (MZ) twins and 44 pairs of
123 same-sex dizygotic (DZ) twins, who were matched in gender ratio, age, and years of
124 education. In addition, their head motion parameters were also comparable (Table
125 1). The MZ and DZ twins demonstrated comparable scores on the Temporal
126 Experience Pleasure Scale (TEPS), whereas DZ twins scored lower than MZ twins on
127 the revised Chinese versions of Chapman Social Anhedonia Scale (RCSAS) and
128 Chapman Physical Anhedonia Scale (RCPAS). The ICC of RCPAS and TEPS scores
129 among the MZ twins were twice that of the DZ twins. However, the ICC of RCSAS
130 scores among MZ and DZ twins did not significantly vary from 0 (Table 1). These
131 findings suggest that in this healthy sample, there was insufficient power to detect
132 significant genetic or phenotypic variation in RCSAS scores.

133

134 **Brain activation in contrast [Gain vs. No-incentive] of MID task**

135 For this contrast, during the anticipatory phase, there was significant activation of
136 the bilateral *NAcc* and the thalamus in all participants. Activation of the bilateral

137 *NAcc* was also observed in MZ and DZ twins respectively. Furthermore, activation of
138 the left insula was observed in MZ twins, whereas activation of the right insula was
139 observed in DZ twins (Table 2 & Figure 1B).

140

141 **Brain activation in contrast [Loss vs. No-incentive] of MID task**

142 Significant activation of the bilateral *NAcc* and the thalamus were observed in the
143 contrast [Loss vs. No-incentive] during the anticipatory phase in all participants.

144 Significant activation of the bilateral *NAcc* was observed in both MZ and DZ twins,
145 while activation of the left globus pallidus and the right thalamus was observed in
146 MZ twins and DZ twins respectively (Table 2 & Figure 1B).

147

148 **Heritability brain mapping**

149 In the voxel-by-voxel heritability brain mapping, two clusters were detected with
150 significant heritability in the contrast [Gain vs. No-incentive]. The right one contained
151 33 voxels, while the left one contained 15 voxels. The coordinates of the peak point
152 of the two clusters were [9,15,-3] and [-9,18,-6], which were located at the right
153 *NAcc* and the left *NAcc* respectively (Figure 3). The h^2 of each voxel within both
154 clusters ranged from 0.2 to 0.49, and the average h^2 was 0.34 (Figure 3). However,
155 we did not find any significant heritability for the contrast [Loss vs. No-incentive].

156

157 **Genetic model fitting**

158 As shown in Table 3, the Cholesky trivariate model (AIC = 382.4) was not worse than
159 the saturated model (AIC = 406.45) ($\Delta-2LL = 41.94$, $\Delta df = 33$, $p = 0.14$). The nested
160 sub-models were compared with the trivariate model. A marginally significant
161 deterioration emerged when all the additive genetic paths (a11, a12, a13, a22, a23,
162 a33) were deleted ($\Delta-2LL = 12.59$, $\Delta df = 6$, $p = 0.05$), whereas the model did not
163 worsen when we discarded all the common environmental paths (c11, c12, c13, c22,
164 c23, c33) ($\Delta-2LL = 0.25$, $\Delta df = 6$, $p = 1$). Results of model comparison indicated that
165 additive genetic factors, rather than common environmental factors, significantly
166 contributed to the full model. The trivariate AE model (AIC = 370.65) was adopted
167 for the subsequent parameter dropping and model comparison. After dropping one
168 path, Model X (with path e21 dropped) was found to have the smallest AIC (368.66)
169 in its class and was hence adopted ($\Delta-2LL = 0.01$, $\Delta df = 1$, $p = 0.94$). Based on Model
170 X, a second path was further discarded. Finally, Model XV (with paths e21 and e31
171 dropped) had the smallest AIC (367.35) among all the tested models and was
172 selected as the best model ($\Delta-2LL = 0.69$, $\Delta df = 1$, $p = 0.4$). A third path was further
173 dropped based on Model XV, but all the sub-models significantly deteriorated
174 compared with Model XV.

175 In the best-fitting Model XV (Figure 4), the h^2 of bilateral *NAcc* activation during
176 the anticipation of monetary gain was 0.43 [95% Confidential Interval (CI): 0.19-0.62],
177 the h^2 of RCPAS scores was 0.61 (95%CI: 0.39-0.75), and the h^2 of TEPS scores was
178 0.29 (95%CI: 0.01-0.54). *NAcc* activation shared the same genes with RCPAS ($r_g = -$
179 0.45) and TEPS ($r_g = 0.59$) scores. In addition, scores on the RCPAS and the TEPS were
180 also influenced by some of the same genes ($r_g = -0.72$). Addictive genetic factors

181 contributed almost 100% to the phenotypic correlation between *N*Acc activation and
182 RCPAS scores ($r_{ph} = -0.23$, $r_{ph(g)} = -0.23$) and between *N*Acc activation and TEPS scores
183 ($r_{ph} = 0.21$, $r_{ph(g)} = 0.21$). Sixty-four percent of the phenotypic correlation between
184 RCPAS and TEPS scores ($r_{ph} = -0.47$) was attributed to additive genetic factors ($r_{ph(g)} =$
185 -0.3), while 36% of the correlation was attributed to environmental factors ($r_{ph(e)} =$
186 0.17).

187

188 Discussion

189 This is the first biometrical study to examine the heritability of neural substrates
190 underlying reward processing and the shared genetic covariance of motivation-
191 related *N*Acc activation and pleasure experience. Consistent with our hypothesis,
192 activation in the bilateral *N*Acc during the anticipation of monetary gain was
193 significantly heritable. The heritability estimate of each voxel within the bilateral
194 *N*Acc, while low-to moderate, was significant and ranged from 0.2 to 0.49, whilst the
195 heritability estimate of *N*Acc activation as a whole was 0.43. RCPAS and the TEPS also
196 exhibited significant heritability in healthy twins, at 0.61 and 0.29 respectively. Even
197 with a modest sample size for ACE modeling, motivation-related *N*Acc activation
198 evidenced significant shared genetic covariation with both self-reported measures of
199 pleasure experience. This suggests that the significant phenotypic correlation
200 between *N*Acc activation and pleasure experience is partially accounted for by
201 shared genetic variation.

202 Bilateral *N*Acc activation during the anticipatory phase for monetary incentives,

203 found in our whole brain analysis, is consistent with previous findings (*Knutson, Fong,*
204 *Adams, Varner, & Hommer, 2001; Knutson & Greer, 2008; Knutson, Westdorp, Kaiser,*
205 *& Hommer, 2000*), which supports the validity of the MID task in correlating with
206 *NAcc* activation *in vivo*. Evidence from animal studies supports the role of dopamine
207 within the *NAcc* in salience attribution, an essential component of motivation and
208 goal-directed behaviour formulation (*Berridge, 2007, 2012; Berridge & Robinson,*
209 *1998*). Although fMRI measures brain haemodynamics rather than neurotransmitter
210 chemistry, previous studies have linked activation at the *NAcc* and the ventral
211 striatum in rewarding tasks to local dopaminergic activity. Amphetamine-induced
212 dopamine release at the *NAcc* has been associated with local haemodynamic
213 activation in reward processing (*Knutson & Gibbs, 2007; Oswald et al., 2007*). These
214 data suggest that *NAcc* activation measured through fMRI could indirectly reflect
215 local dopaminergic activity. In addition, polymorphisms of dopamine have been
216 associated with ventral striatal activation in reward processing, suggesting that
217 facets of the mesolimbic reward system may be heritable (*Dreher et al., 2009; Forbes*
218 *et al., 2009; Yacubian et al., 2007*). Indeed, significant MZ twin correlation in *NAcc*
219 activation has previously been reported (*Silverman et al., 2014*). In the present study,
220 we corroborated previous findings through quantifying the genetic and
221 environmental effects on the motivation-related *NAcc* activation. Stokes and
222 colleagues (2013) reported a significant heritability estimate of 0.21 for
223 dopaminergic activities of the right ventral striatum in the resting state. In this study,
224 we found a heritability estimate of 0.4 for bilateral *NAcc* activation in anticipating
225 monetary gains. The considerably larger sample size in this study, relative to

226 previous research, lends further support to this finding.

227 Quantifying the heritability of *NAcc* activation in anticipating monetary incentives
228 could facilitate our understanding of the genetic effect on reward processing and
229 detection of associated genetic loci. Voxel-wise heritability estimation is an
230 alternative methodology that may be more sensitive in detecting genetic effects, and
231 as such may supplement findings from previous regions of interest analysis often
232 limited by small sample sizes. Across single-gene polymorphism studies (*Dreher et al.,*
233 *2009; Forbes et al., 2009; Yacubian et al., 2007*), twin studies (*Silverman et al., 2014*)
234 or studies estimating the heritability of striatal dopaminergic activity (*Stokes et al.,*
235 *2013*), all of which adopted the mean value within a region of interest (ROI), a
236 lateralization bias toward the right *NAcc* or ventral striatal activation has been
237 reported. However, such lateralization pattern was not observed in the present
238 voxel-wise analysis. This is consistent with a voxel-wise heritability approach being
239 more sensitive in detecting the heredity of brain activation compared with
240 traditional ROI analysis.

241 It should be noted that only the *NAcc* activation in anticipating monetary gain,
242 rather than loss, showed significant heritability. This result is consistent with
243 previous findings reporting significant correlation between *NAcc* activation in older
244 and younger MZ twins in anticipating monetary gain but not loss (*Silverman et al.,*
245 *2014*). One possible explanation is that there exists less individual difference in
246 anticipating monetary gain than loss, even though the *NAcc* activation appears to be
247 sensitive to both incentive conditions. The small or non-significant heritability could
248 be attributed to the high phenotypic variance within both MZ and DZ twins due to

249 limited sample size. It is notable that the studies mentioned above only linked
250 dopaminergic gene polymorphism to ventral striatal activation in processing
251 monetary gain but not loss, which deserves further investigation.

252 We also investigated the heritability of pleasure experience. In this study, physical
253 anhedonia traits measured by the RPCAS also demonstrated significant heritability,
254 whilst experiential pleasure measured by the TEPS was characterized by moderate
255 but significant heritability. These findings are consistent with previous studies (*Hay*
256 *et al., 2001; Kendler & Hewitt, 1992; Linney et al., 2003*). In these studies, however,
257 significant heritability has also been detected in social anhedonia which was not
258 found in our study. Cultural factors may be a possible influence accounting for this
259 difference, but this requires further investigation.

260 In the best-fitting genetic model, *NAcc* activation during the anticipation of
261 monetary gain exhibited significant genetic share with scores on the RPCAS and the
262 TEPS. In addition, the phenotypic correlation between *NAcc* activation and pleasure
263 experience was almost entirely attributed to genetic factors. These data suggest that
264 motivation-related *NAcc* activation during the anticipation of monetary rewards may
265 share common additive genes with pleasure experience, and these genes contribute
266 significantly to the phenotypic expression. Locating the shared genes of these two
267 phenotypes could facilitate clarification of the underlying neurobiological
268 mechanisms of amotivation and anhedonia in schizophrenia and major depressive
269 disorder.

270 The main limitation of this study is the modest sample size, which was relatively

271 small for statistical methods applying ACE models. While 196 participants with 174
272 valid data sets could be regarded as a medium to large sample in task-based fMRI
273 research, these preliminary results must be replicated in a larger cohort. Importantly,
274 adopting voxel-wise analysis with correction for multiple comparisons could partially
275 compensate for the relatively small sample size. One primary problem in genetic
276 modeling lies in within-group variation, which is sensitive to the presence of outliers;
277 however, in this study we detected none. Furthermore, demographic variables and
278 head movements were carefully matched among subgroups with an aim to enhance
279 the validity of our findings.

280 In conclusion, our findings suggest that motivation-related *NAcc* activation in
281 anticipating monetary gain and pleasure experience are at least partially heritable.
282 Importantly, motivation-related *NAcc* activation and pleasure experience exhibit
283 significant shared genetic covariance. Future molecular studies examining shared
284 polygenicity of these traits would further inform this research. Locating and refining
285 areas of the genome associated with expression of these traits will ultimately aid in
286 the understanding of the underlying neurobiological mechanisms of treatment-
287 refractory symptoms.

288

289 **Materials and methods**

290 **Participants**

291 Forty-seven pairs of same-sex dizygotic (DZ) twins and 51 pairs of same-sex
292 monozygotic (MZ) twins were recruited from the Twin Registry of the Institute of

293 Psychology, the Chinese Academy Sciences (*Chen et al., 2010; Chen et al., 2013*). The
294 zygosity of each twin was jointly determined by DNA analysis based on saliva, and
295 two zygosity questionnaires (*Chen et al., 2010*). Potential participants were excluded
296 from the study if they: 1) had a personal or family history of diagnosable mental
297 disorders; b) had a history of head trauma or encephalopathy; 3) had a history of
298 substance abuse, including tobacco and alcohol; 4) had an Intelligence Quotient (IQ)
299 lower than 70; 5) had severe hearing or visual impairment; or 6) were ambidextrous
300 or left-handed. This information was verified by the Twin Registry, the participants
301 themselves, and their guardians. Detailed experimental procedures conformed to
302 the Declaration of Helsinki and all participants gave written informed consent. All
303 participants completed checklists capturing experiential pleasure and hedonic traits
304 before the brain scans. They then undertook the Monetary Incentive Delay (MID)
305 task inside the scanner. Each participant received 450 RMB as compensation. The
306 study was approved by the Ethics Committee of the Institute of Psychology, the
307 Chinese Academy of Sciences.

308

309 **Self-report measures of pleasure experience**

310 The revised Chinese versions of the Chapman Physical Anhedonia Scale (RCPAS) and
311 the Chapman Social Anhedonia Scale (RCSAS) were administered to measure
312 physical and social anhedonic traits, respectively (*Chan, Wang, et al., 2012*). The
313 RCPAS consists of 61 true-false items, whereas the RCSAS consists of 40 true-false
314 items. These two scales have been stable and valid in measuring anhedonic traits

315 across time and along the schizophrenia spectrum (*Chan, Gooding, et al., 2016*). The
316 Chinese version of the Temporal Experience Pleasure Scale (TEPS) is a 19-item
317 checklist that was used to measure anticipatory and consummatory pleasure in each
318 participant (*Chan, Shi, et al., 2012*). The Chinese version has good psychometric
319 properties for measuring anhedonia across the different stages of schizophrenia
320 (*Chan et al., 2010; Chan, Shi, et al., 2012; Li et al., 2015*).

321

322 **Monetary Incentive Delay (MID) task**

323 We adopted the original version of the MID task developed by Knutson and
324 colleagues (*Knutson et al., 2000*) to the abridged imaging version (*Chan, Li, et al.,*
325 *2016*). In each trial of the task, a 250-millisecond cue indicating three different
326 conditions was first presented at the centre of the screen, followed by a blank
327 interval that jittered between 2000 and 2500 milliseconds. Then a blue target with
328 adjusted duration was displayed, followed by an interval that jittered between 500
329 and 3500 milliseconds. Finally, a 1650-millisecond feedback was presented followed
330 by an inter-trial interval that jittered between 4000 and 7000 milliseconds. Each trial
331 lasted 12000 milliseconds (Figure 1A).

332 Participants were asked to hit the target as quickly as possible by pressing the
333 right button on a panel with their right thumb. The initial duration of the target was
334 set at 300 milliseconds and changed according to the subsequent performance of
335 each participant. If a target was successfully hit twice, the target duration was
336 reduced by 20 milliseconds. Alternatively, if a target was missed twice, 20

337 milliseconds were added to the target duration. Using this strategy, the hit rate of
338 each participant was controlled at around 66.7%. The three cues indicated three
339 different conditions: a triangle indicated a monetary gain condition, a square
340 indicated a monetary loss condition, and a circle indicated a no-incentive condition.
341 Participants gained five monetary points if they hit the target in the monetary gain
342 condition, or lost five monetary points if they missed the target in the monetary loss
343 condition. In the no-incentive condition, participants did not gain or lose any points
344 whether the target was hit or not. Two runs containing 10 gain, 10 loss and 10 no-
345 incentive conditions in each run were applied. The trials in each run were presented
346 in a pseudo-random order. Participants practiced with an independent 30-trial run
347 before entering the scanner and were informed that their final monetary points
348 gained in the scanner could be converted into cash and added to their compensation.
349 This abridged version has been shown to activate the *N*Acc effectively in healthy,
350 subclinical and clinical samples (*Chan, Li, et al., 2016; Smoski, Rittenberg, & Dichter,*
351 *2011*).

352

353 **Brain image acquisition**

354 Brain imaging data were collected with 32-channel head coil in a 3 T Siemens Trio
355 MRI Scanner. An experienced radiologist who was blind to this study was responsible
356 for data acquisition. A T2-weighted FLAIRE sequence (TR = 4000ms; TE = 90ms; FOV =
357 200mm²; slices = 19; flip angle = 120°; image matrix = 256 x 512; voxel dimensions =
358 0.9 x 0.4 x 5mm³) was first used to ascertain that each participant had no organic

359 brain disorders. Then a gradient-echo echo-planner sequence (TR = 2000ms; TE =
360 30ms; FOV = 210mm²; slices = 32; flip angle = 90°; image matrix = 64x64; voxel
361 dimensions = 3.3 x 3.3 x 4mm³; Number of TR = 184 for each run) was applied to
362 acquire the functional brain activation imaging data of each participant while
363 performing the MID task. Finally, a high resolution structural brain image was
364 acquired for anatomical registration (TR = 2300ms; TE = 3ms; FOV = 256mm²; flip
365 angle = 9°; image matrix = 256x256; voxel dimensions = 1 x 1 x 1mm³). Each
366 participant wore earplugs during scanning. Their heads were fixed with a vacuum
367 pillow and sponge pads to minimize head motion.

368

369 **Imaging data processing**

370 The latest version of the SPM 12 (Wellcome Trust Centre for Neuroimaging) was
371 used for imaging data processing. The functional images were first realigned into the
372 first volume of each scanning sequence for movement correction, followed by slice
373 timing correction. The observed head motion parameters, three translations and
374 three rotations, were calculated into the framewise displacement (FD), a
375 comprehensive and reliable index for head movement (*Power, Barnes, Snyder,*
376 *Schlaggar, & Petersen, 2012*). Participants with maximum head motion higher than 2
377 mm and 2 degrees, and mean FD larger than 0.25 mm were excluded from the final
378 analysis, along with their twin. Individual high-resolution brain structure image was
379 non-linearly registered to the Montreal Neurological Institute (MNI) template that
380 produced a transformation matrix. Using this matrix, all functional brain images were

381 normalized into a common standard atlas. Functional images were resampled into 3
382 $3 \times 3 \times 3 \text{ mm}^3$ and spatially smoothed with a 6mm full-width-at-half-maximum (FWHM)
383 Gaussian isotropic kernel. A 128 Hz high-pass filter was applied to the time series of
384 each voxel to remove low-frequency noise.

385 The preprocessed functional imaging data were included in a first-level general
386 linear model (GLM) with three predictors of interest during the anticipatory phase
387 for monetary incentives: gain, loss, and no-incentive. First, the data for each
388 participant was analyzed to provide a voxel-wise t-statistic map for each contrast,
389 [gain vs. no-incentive] and [loss vs. no-incentive], during the anticipatory phase. The
390 time points of target hitting and feedback period were included as parametric
391 modulation to minimize their influence on the anticipation for incentives. Six raw
392 head movement parameters were also included as covariates to remove motion
393 effect. For each contrast, the t-statistics map of all the participants were included
394 into a GLM with the t-statistics as the dependent variable and the FD as covariate to
395 further minimize head motion effect. To clarify whether the bilateral *NAcc* were
396 activated in both MZ and DZ twins, one-sample t-tests were also applied to the t-
397 statistics of the MZ and DZ groups. The statistical significance threshold of the whole
398 brain analysis was set as $p < 0.001$ with FWE correction and cluster voxel size > 100 .
399 Since 11 pairs of twins were excluded due to excessive head movements, 44 pairs of
400 DZ twins and 43 pairs of MZ twins were included in the final analysis.

401

402 **Statistical analysis**

403 Pearson chi-square test was used to test if the gender ratio of MZ and DZ twins were
404 different from each other. The matching of age and years of education between MZ
405 and DZ twins was tested with independent t-test. Univariate general linear model
406 with gender, age, and years of education as covariates was used to compare FD,
407 scores on the RCSAS, the RCPAS, the TEPS and their various subscales between MZ
408 and DZ twins. The intraclass correlation coefficients (ICC) of behavioral phenotypes
409 among the MZ and DZ twins were calculated respectively. If the ICC of a phenotype
410 among MZ twins was significantly twice larger than that for DZ twins, the phenotype
411 in question may be influenced by familial factors.

412

413 **Heritability brain mapping**

414 Voxel-by-voxel heritability brain mapping was carried out with the latest version of
415 the OpenMx (*Neale et al., 2016*), FSL (*Jenkinson, Beckmann, Behrens, Woolrich, &*
416 *Smith, 2012*) and in-house MATLAB (The MathWorks, Inc., Natick, Massachusetts,
417 United States) scripts. Since mapping the heritability of all voxels in the whole brain
418 may increase the possibility of type II error, we adopted the Oxford-GSK-Imanova
419 structural striatal atlas which contained the core brain regions sensitive to
420 dopaminergic activity and reward tasks (*Tziortzi et al., 2011*). The structural striatal
421 template was first resampled into a 3 x 3 x 3 mm³ mask containing 765 voxels. The T
422 values of voxels in the striatal mask were extracted from the two contrast files, [gain
423 vs. no-incentive] and [loss vs. no-incentive] of each participant. There were no
424 outliers more than three standard deviations from the mean T value. Age, gender,

425 years of education, and FD were regressed out from the extracted t values to remove
426 their possible influences on heritability estimation (*Bergen, Gardner, & Kendler, 2007*;
427 *Lenroot et al., 2009*). Finally, the standardized residuals were submitted to the
428 genetic model. A conventional univariate ACE model was used, in which A denotes
429 additive genetic effects, C denotes common environmental effects, and E denotes
430 unique environmental effects. MZ twins are assumed to share 100 percent of the
431 additive genetic variance and common environmental variance, whereas the DZ
432 twins are assumed to share 50 percent of the additive genetic variance and 100
433 percent of common environmental variance. The part accounted for by A in the total
434 variance was defined as the heritability estimate h^2 of this phenotype (*Neale & Maes,*
435 *2004*). To clarify the significance of components A, C and E, sub-models AE and CE
436 were compared to the full ACE model, and model E was compared to AE and CE
437 models respectively. If model fit significantly decreased, then the dropped factor was
438 considered essential in the model. In model selection, the model with the smallest
439 Akaike's Information Criterion (AIC) value was selected as the best-fit model. We
440 adopted the p value of model comparison between the AE and the E model to test
441 the significance of h^2 if the AE model was detected as the best-fit model the full ACE
442 model failed to surpass its sub-models in any voxel from the Oxford-GSK-Imanova
443 structural striatal atlas) (*Neale & Maes, 2004*). Finally, FDR correction with adjusted p
444 < 0.05 was applied to the acquired p-maps to adjust for multiple comparisons.
445 Comparing to the full ACE model in brain functional or structural studies, the method
446 in the present study allowed us to quantify the heritability of brain activation and
447 relevant significance in the best-fit genetic model, and to correct for multiple tests

448 (*Li et al., 2018*). The cluster tool of FSL was used to identify clusters in which h^2 was
449 significant. Masks with voxels in which the 95% confidence interval of h^2 did not
450 contain zero were also added onto the brain heritability map.

451

452 **Multivariate Model fitting**

453 A trivariate Cholesky ACE model was fitted to examine the genetic sharing between
454 *NAcc* activation and pleasure experience (RCPAS and TEPS scores) (Figure 2). T values
455 of the contrast [gain vs. no-incentive] were extracted from bilateral *NAcc* mask with
456 significant heritability from the heritability brain mapping step. Gender, age, and
457 years of education were then regressed from the extracted mean T value, RCPAS,
458 and TEPS scores. The FD value was additionally regressed from the extracted mean T
459 value for head motion correction. The *NAcc* activation during the anticipation of
460 monetary loss failed to show significant heritability. In addition, MZ twin correlation
461 in social anhedonia was not higher than DZ twin correlation and both correlation
462 coefficients were not significant. Hence, The *NAcc* activation in contrast [loss vs. no-
463 incentive] and RCSAS were not included in the multivariate genetic model presented
464 in Figure 2. The trivariate ACE model was first compared with the saturated model in
465 which all the constraints were set as free. Then the nested sub-models were
466 compared with the full trivariate ACE model in a stepwise manner. We first
467 discarded all the model paths containing A, C or E effect in a stepwise manner
468 (Figure 2 & Table 3). After that we discarded one path from the best fitted model
469 observed from the above step, and then two paths until the model significantly

470 deteriorated (indicated by $p < 0.05$). The model with the smallest AIC was selected as
471 the best-fit model, and the likelihood ratio chi-squared statistic, minus two times log
472 likelihood difference ($-2LL$) were applied for model comparison. The contribution of
473 A, C, and E to the phenotype correlation between two phenotypes were estimated
474 using the following formulae: $r_{ph(g)} = \sqrt{a_{11}^2} * r_g * \sqrt{a_{22}^2}$; $r_{ph(c)} = \sqrt{c_{11}^2} * r_c * \sqrt{c_{22}^2}$;
475 $r_{ph(e)} = \sqrt{e_{11}^2} * r_e * \sqrt{e_{22}^2}$ (Toulopoulou et al., 2015).

476

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489

490 **Author contributions**

491 Zhi Li designed the study, collected and analyzed the data, and wrote up the

492 manuscript. Yi Wang, Chao Yan, Ke Li and Ya-wei Zeng collected all the data and
493 commented on the first draft of the manuscript. Eric F. C. Cheung, Anna R. Docherty,
494 Pak C. Sham, Raquel E. Gur and Ruben C. Gur provided significant comments to the
495 manuscript. Raymond C. K. Chan conceptualized the idea, designed the study,
496 interpreted the findings and commented the manuscript critically.

497

498 **Additional files**

499 Figure 1 & Table 2 –Source Data 1_[loss vs. no-incentive]

500 Figure 1 & Table 2 –Source Data 2_[gain vs. no-incentive]

501 Figure 3-Source Data

502 Figure 4 & Table 3 -Source Data 1

503 Figure 4-& Table 3 Source Data 2

504 Raw data 1_Activation in each voxel of stritaum_[loss vs. no-incentive]

505 Raw data 2_Activation in each voxel of stritaum_[gain vs. no-incentive]

506 Source Code_Heritability Brain Mapping 1

507 Source Code_Heritability Brain Mapping 2

508 Source Code_Multivariate Model fitting

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743

744 Table1. Demographics of participants

	MZ (N = 86)	ICC	DZ (N = 88)	ICC	$\chi^2/t/F$	p	ALL (N = 174)
Gender (Male/Female)	46/40	/	46/42	/	0.026	0.872	92/82
Age	19.98(1.89)	/	19.8(1.76)	/	-0.66	0.513	19.89(1.82)
Education	12.33(1.75)	0.671**	12.44(1.63)	0.591**	0.46	0.647	12.39(1.69)
FD	0.13(0.04)	0.204	0.13(0.04)	-0.059	0.156	0.694	0.13(0.04)
RCSAS	11.38(5.96)	0.087	7.57(4.48)	0.281	22.38	< 0.001**	9.45(5.59)
RCPAS	22.12(8.03)	0.490**	18.97(7.66)	0.201	6.29	0.013*	20.52(7.98)
TEPS	4.06(0.59)	0.352*	4.08(0.59)	-0.02	0.004	0.947	4.07(0.59)
TEPS_Anticipation	4.11(0.67)	0.396**	4.13(0.7)	-0.021	0.19	0.662	4.12(0.68)
TEPS_Consummation	4.11(0.77)	0.346*	4.12(0.75)	0	0.19	0.667	4.14(0.76)

745 Note: *, p < 0.01; **, p < 0.05; MZ = Monozygotic twins; DZ = Dizygotic twins; ICC = Interclass correlation coefficient; FD = Frame Displacement; RCSAS =
 746 Revised Chapman Social Anhedonia Scale; RCPAS = Revised Chapman Physical Anhedonia Scale; TEPS = Temporal Experience Pleasure Scale.

747

748 Table2. Whole brain activation in anticipating monetary incentive

Region(L/R)	MZ (N = 86)		DZ (N = 88)		ALL (N = 174)	
	T	Peak Coord.	T	Peak Coord.	T	Peak Coord.
Gain vs. No-incentive						
NAcc (R)	12.1	[6,9,3]	13.41	[-12,6,-6]	16.73	[6,9,0]
NAcc (L)	11.27	[-6,6,0]	12.38	[9,9,-3]	16.63	[-9,6,-3]
Thalamus					14.16	[0,-9,3]
Insula (L)	10.52	[-27,27,3]				
Insula (R)			10.26	[33,24,3]		
Loss vs. No-incentive						
NAcc (R)	10.7	[0,-6,0]	12.22	[-12,6,-9]	15.18	[9,3,-3]
NAcc (L)	10.4	[6,6,0]	11.73	[9,3,-3]	15.01	[-9,3,0]
Thalamus					13.99	[0,-6,0]
Thalamus (R)			11.32	[12,-3,6]		
Globus pallidus (L)	10.36	[-9,3,0]				

749 Note: All the results were corrected with FEW method, $p < 0.001$, cluster voxel size > 100 ;
750 MZ = Monozygotic twins; DZ = Dizygotic twins; L = Left; R = Right; Coord. = Coordinate; NAcc
751 = Nucleus Accumbens.

752

753 Table3. Model fitting and selection

No.	Model	ep	-2LL	df	AIC	diffLL	diffdf	<i>p</i>
I	Saturated Model	54	1342.45	468	406.45	/	/	/
	Cholesky Trivariate Model	21	1384.4	501	382.4	41.94	33	0.14
II	Drop a or c matrix							
III	Drop c matrix	15	1384.65	507	370.65	0.25	6	1
IV	Drop a matrix	15	1396.98	507	382.98	12.59	6	0.05
	Drop one path based on the model III							
V	Drop a31	14	1387.21	508	371.21	2.56	1	0.11
VI	Drop a32	14	1387.68	508	371.68	3.03	1	0.08
VII	Drop a21	14	1390.61	508	374.61	5.95	1	0.01
VIII	Drop e32	14	1390.07	508	374.07	5.42	1	0.02
IX	Drop e31	14	1385.22	508	369.22	0.57	1	0.45
X	Drop e21	14	1384.66	508	368.66	0.01	1	0.94
	Drop two paths based on the model X							
XI	Drop e21 and a31	13	1387.37	509	369.37	2.71	1	0.1
XII	Drop e21 and a32	13	1388.4	509	370.4	3.75	1	0.05
XIII	Drop e21 and a21	13	1393.18	509	375.18	8.53	1	0
XIV	Drop e21 and e32	13	1390.07	509	372.07	5.42	1	0.02
XV	Drop e21 and e31	13	1385.35	509	367.35	0.69	1	0.4
	Drop three paths based on the model XV							
XVI	Drop e21 and e31 and a31	12	1393.29	510	373.29	7.94	1	0
XVII	Drop e21 and e31 and a21	12	1394.03	510	374.03	8.68	1	0
XVIII	Drop e21 and e31 and a32	12	1388.44	510	368.44	3.09	1	0.08
XIX	Drop e21 and e31 and e32	12	1390.56	510	370.56	5.21	1	0.02

754 Note: No. = Model number; Model = Parameters drop by this model; ep = estimate parameter; -2LL = minus 2 log
755 likelihood; df = degree of freedom; AIC = Akaike information criterion; diffLL = the difference of minus 2 log
756 likelihood between two models; diffdf = the difference of the degree of freedom between two models; *p* indicates
757 the significance of model deterioration between two models. The trivariate genetic model was compared with the
758 saturated model first, then the sub-models II – IV were compared with the full genetic model from which the model
759 III was selected as the best-fitted model for the next step parameter dropping. One parameter was first drop from
760 the model III in which the model X was selected. Then two parameters were drop based on the model X. Finally, the
761 model XV with the smallest AIC among all tested sub-models was chosen as the best fitted model, which model did
762 not deteriorate by compared with the model X (*p* > 0.05).

763

764 **Legends**

765 **Figure1. Monetary incentive delay (MID) task and brain activation in anticipating**

766 **monetary gain and loss.** A: The Workflow of one trial in the MID task; B: The

767 activation of bilateral nucleus accumbens (*NAcc*) was found in contrast [Gain vs. no-

768 incentive] during the anticipatory phase, the white-red color bar indicates the

769 statistical t value; C: The activation of bilateral *NAcc* was found in contrast [Loss vs.

770 no-incentive] during the anticipatory phase, the white-blue color bar indicates the

771 statistical t value.

772

773 **Figure2. Full trivariate genetic model with Cholesky decomposition.** The *NAcc*

774 indicates the extracted t value from the contrast file of [Gain vs. No-incentive], with

775 the mask from the voxel-wise heritability mapping of brain activation. The RPCAS

776 indicates the physical anhedonia trait, whilst the TEPS indicates the experiential

777 pleasure. The A indicates the additive genetic effect, the C indicates the common

778 environmental effect, and the E indicates the unique environmental effect. The

779 lowercase with number indicates the path of model, such as 'a21' indicates the

780 influence from the additive gene effect of *NAcc* to RPCAS.

781

782 **Figure3. Voxel-wise heritability mapping on brain activation.** In the standard

783 striatum atlas on the right, two clusters with significant heritability in bilateral *NAcc*

784 are detected, which ranges from 0.2 to 0.49 in each voxel (reflected by the white-red

785 color bar). The five pie charts on the left indicate the heritability and unique

786 environmental effect of AE model on the two clusters, in which the golden color
787 indicates the heritability whilst the blue color indicates the unique environmental
788 effect.

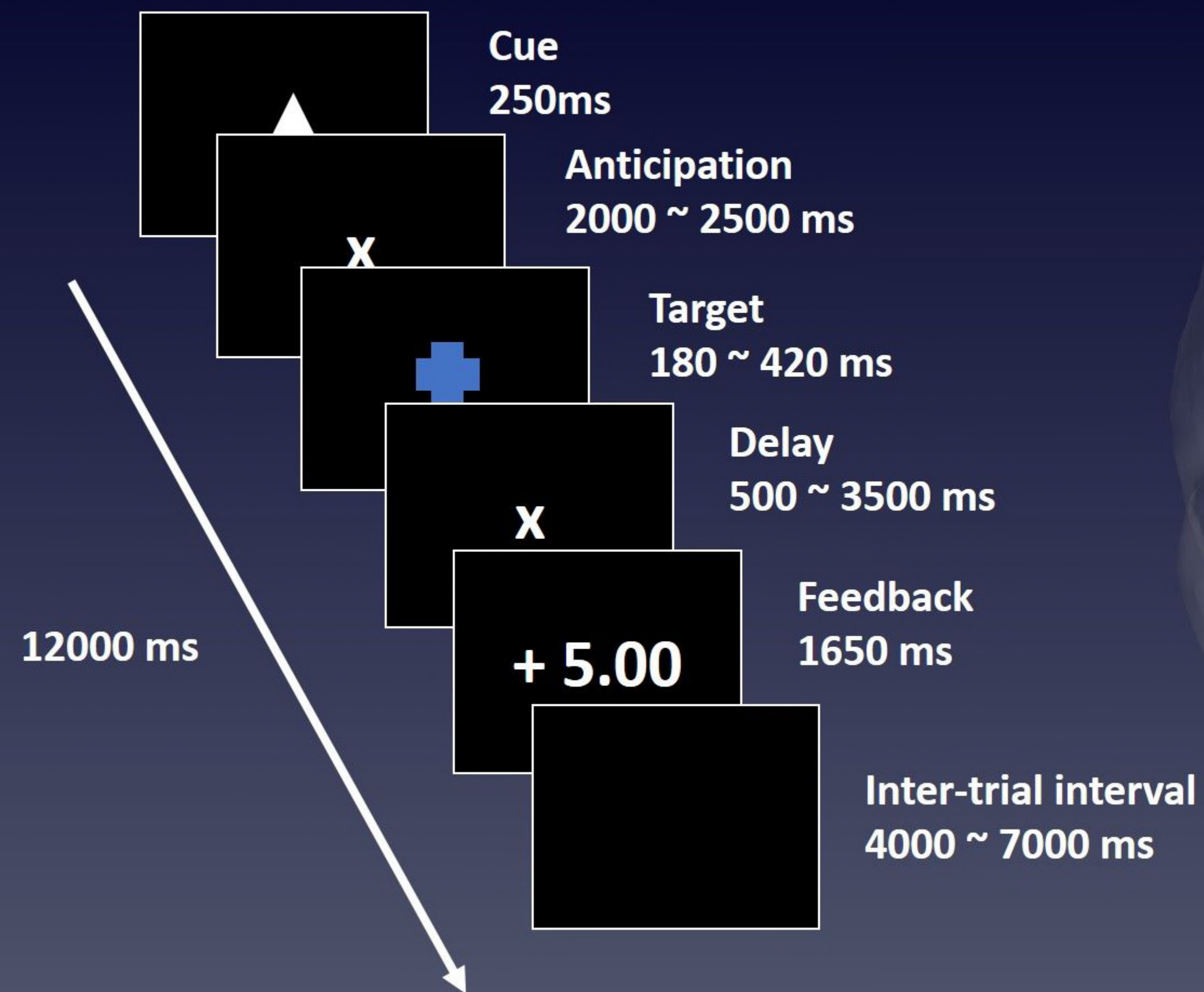
789

790 **Figure4. The best-fitted trivariate genetic model.** Only the additive genetic and
791 unique environmental effects contribute to this model. The h^2 indicates the
792 heritability with 95% confidence interval of each single phenotype, the r_{ph} indicates
793 the phenotypic correlation between phenotypes, the r_g indicates the genetic
794 correlation, and the r_e indicates the unique environmental correlation. The $r_{ph(g)}$ and
795 $r_{ph(e)}$ indicates the contributions to phenotypic correlation, from the additive gene
796 and unique environment respectively. The standard path coefficients with 95%
797 confidence interval were also supplied in this figure.

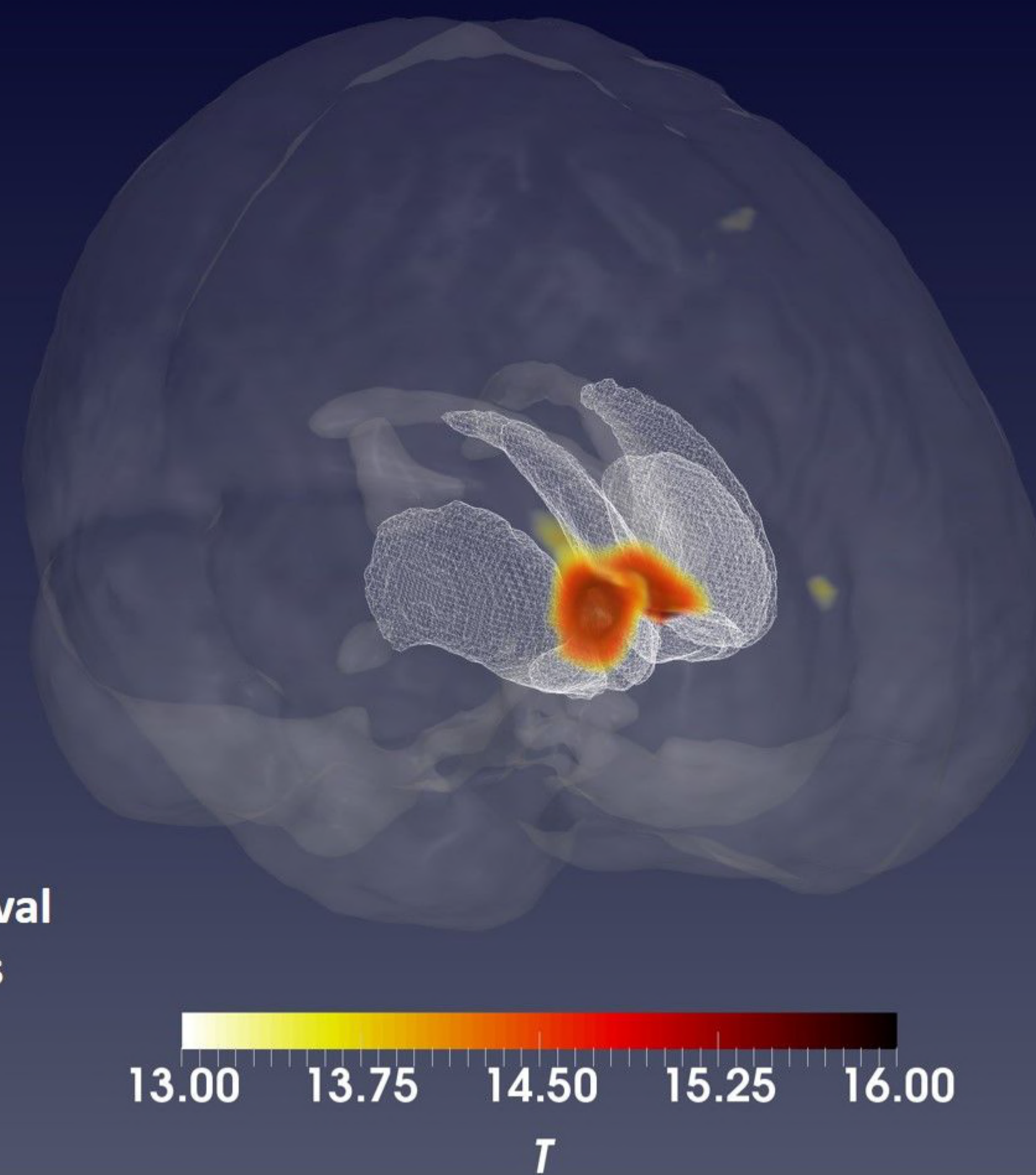
798

799

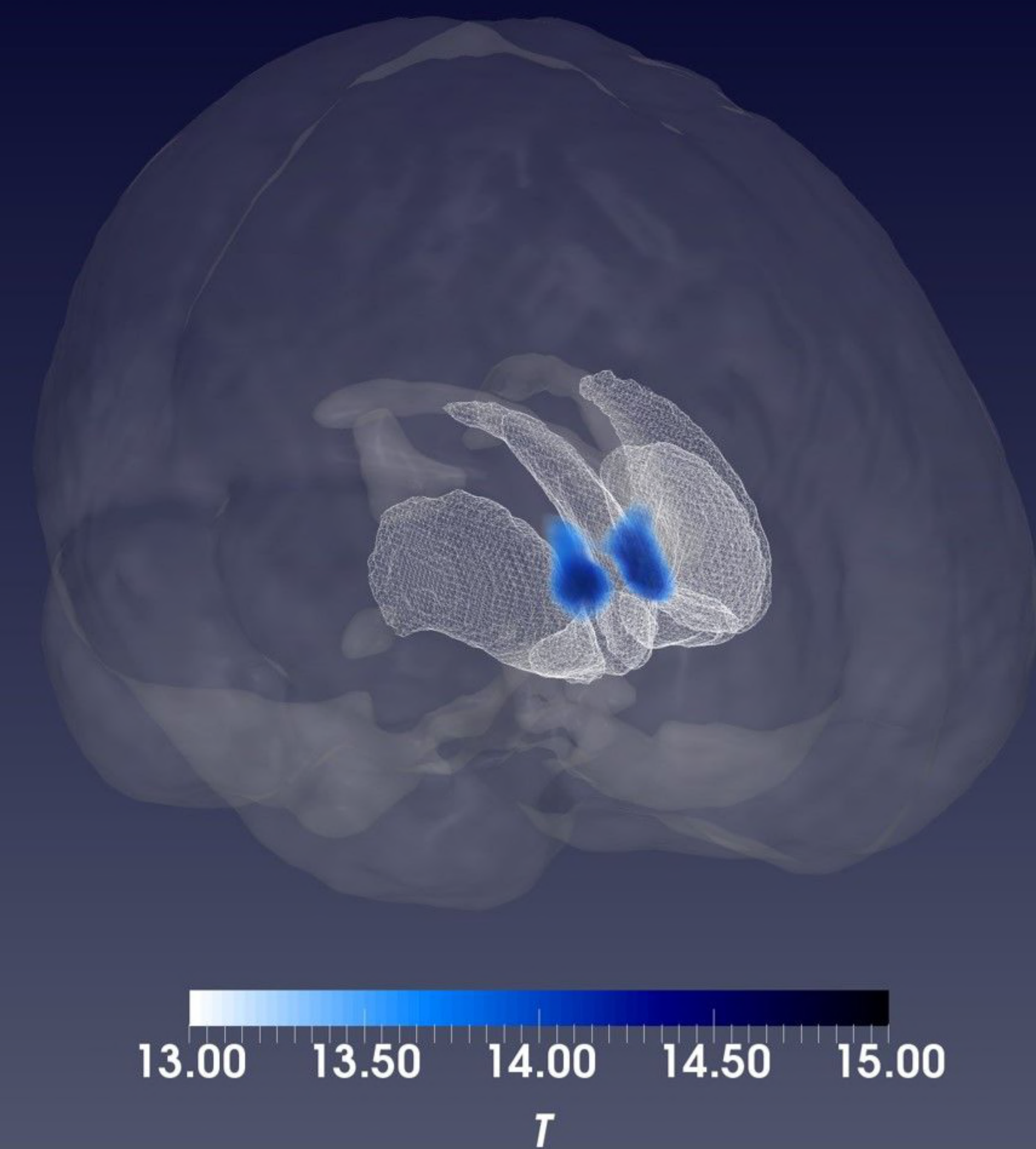
A. Procedure of One trial

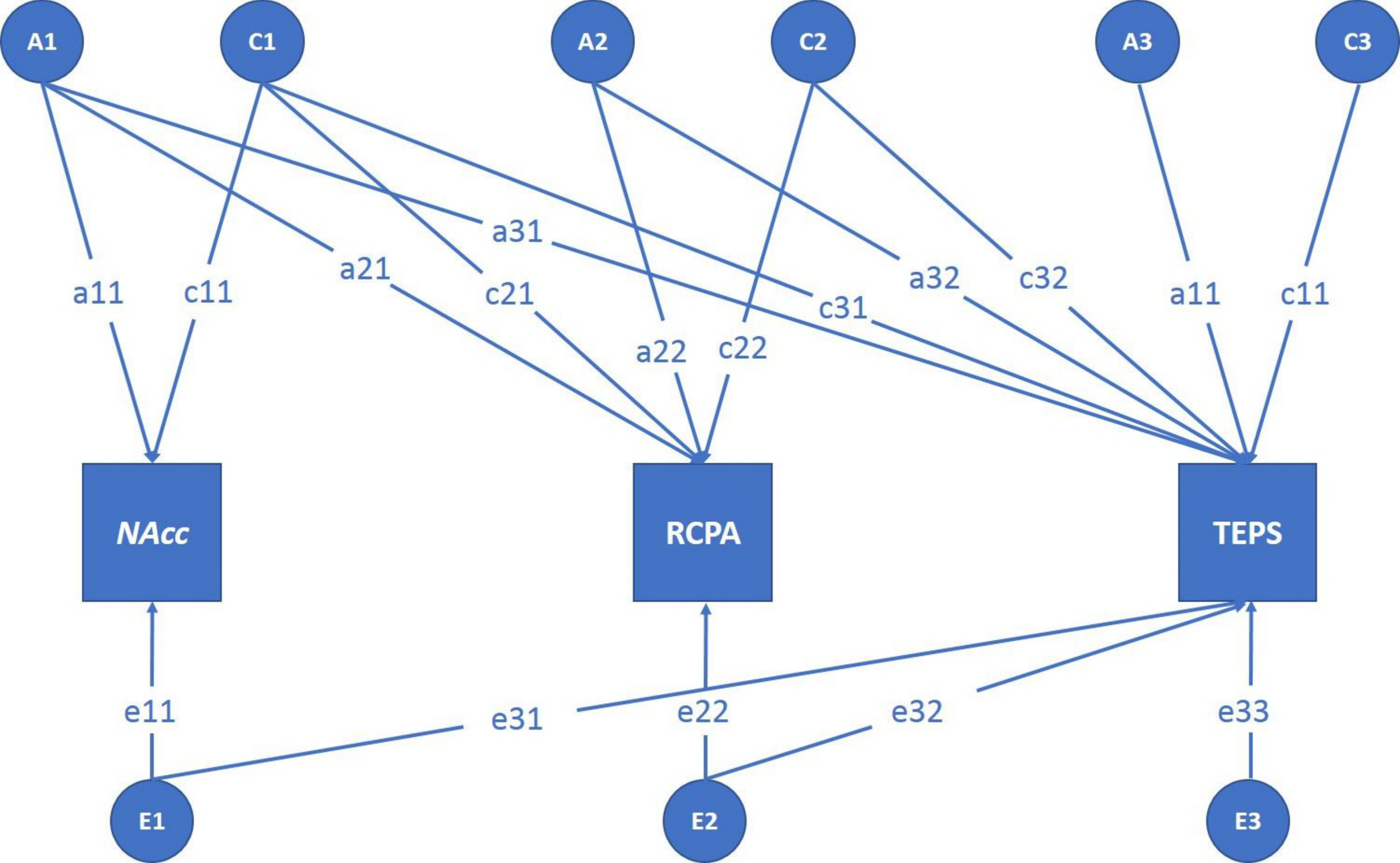


B. Gain vs. No-incentive

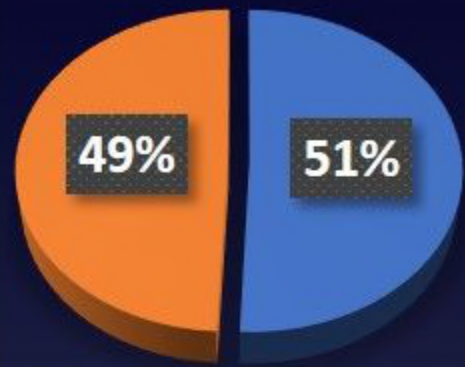


C. Loss vs. No-incentive

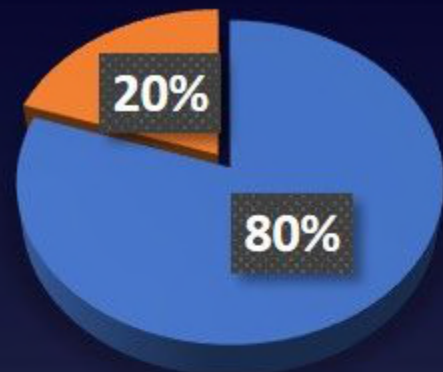




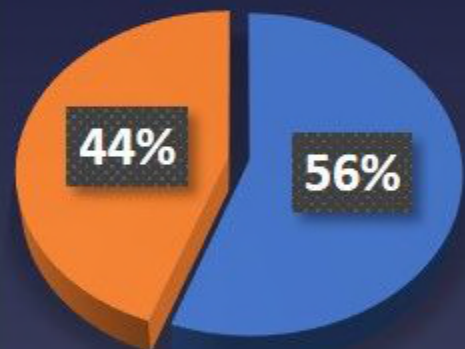
A. Max h^2 vs. Min e^2



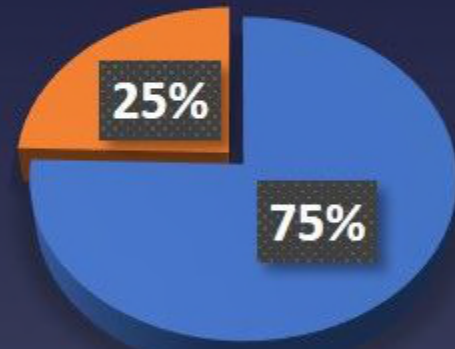
B. Min h^2 vs. Max e^2



C. Left peak point



D. Right peak point



E. Mean h^2 vs. e^2

