

1 **Appendix S1: Wind conditions across the winter range**

2

3 To analyse the effects of wind speed and direction on foraging time, we obtained hourly wind
4 data from Leuchars weather station (56° 23'N, 02° 52'W, 26km to the north of the breeding
5 colony; www.badc.nerc.ac.uk). The population is partially migratory with a winter
6 distribution spanning 486 km linear coastal distance to the north and 136 km linear coastal
7 distance to the south of the Isle of May (Grist *et al.* 2014). The locational data recorded by
8 the geolocation loggers are not sufficiently precise to provide accurate locations for study
9 individuals (Phillips *et al.* 2004). Thus, individuals may have been distributed across the
10 winter range, so we tested whether the wind conditions at Leuchars weather station were
11 representative of the winter range as a whole.

12 We calculated the correlation between daily mean wind direction (sine-transformed to
13 remove circularity) at Leuchars with daily mean wind direction recorded at three other
14 coastal weather stations distributed approximately evenly across the wintering range, two to
15 the north (Lossiemouth, 57° 42'N, 03° 18'W, 386 km linear coastline distance from the Isle
16 of May; Peterhead, 57° 30'N, 01° 46'W, 247 km linear coastline distance from the Isle of
17 May) and one to the south (Boulmer, 55° 25'N, 01° 35'W, 108 km linear coastline distance
18 from the Isle of May; Fig S1.1; wind data from www.badc.ac.uk; shags do not typically cross
19 land or long stretches of open sea so coastline distance is more biologically relevant than
20 Euclidean distance, Grist *et al.* 2014). We also correlated daily mean daily wind speed at
21 Leuchars with daily mean wind speed from the other three weather stations. The correlations
22 were calculated for 01/10/09-31/03/10 and 01/10/10-31/03/11, which incorporate the two
23 migratory periods in the study (Grist *et al.* 2014).

24 The Pearson correlation coefficients between sine wind direction at Leuchars and
25 Lossiemouth, Peterhead and Boulmer were, respectively 0.85, 0.85 and 0.85 (Fig S1.2 a, c

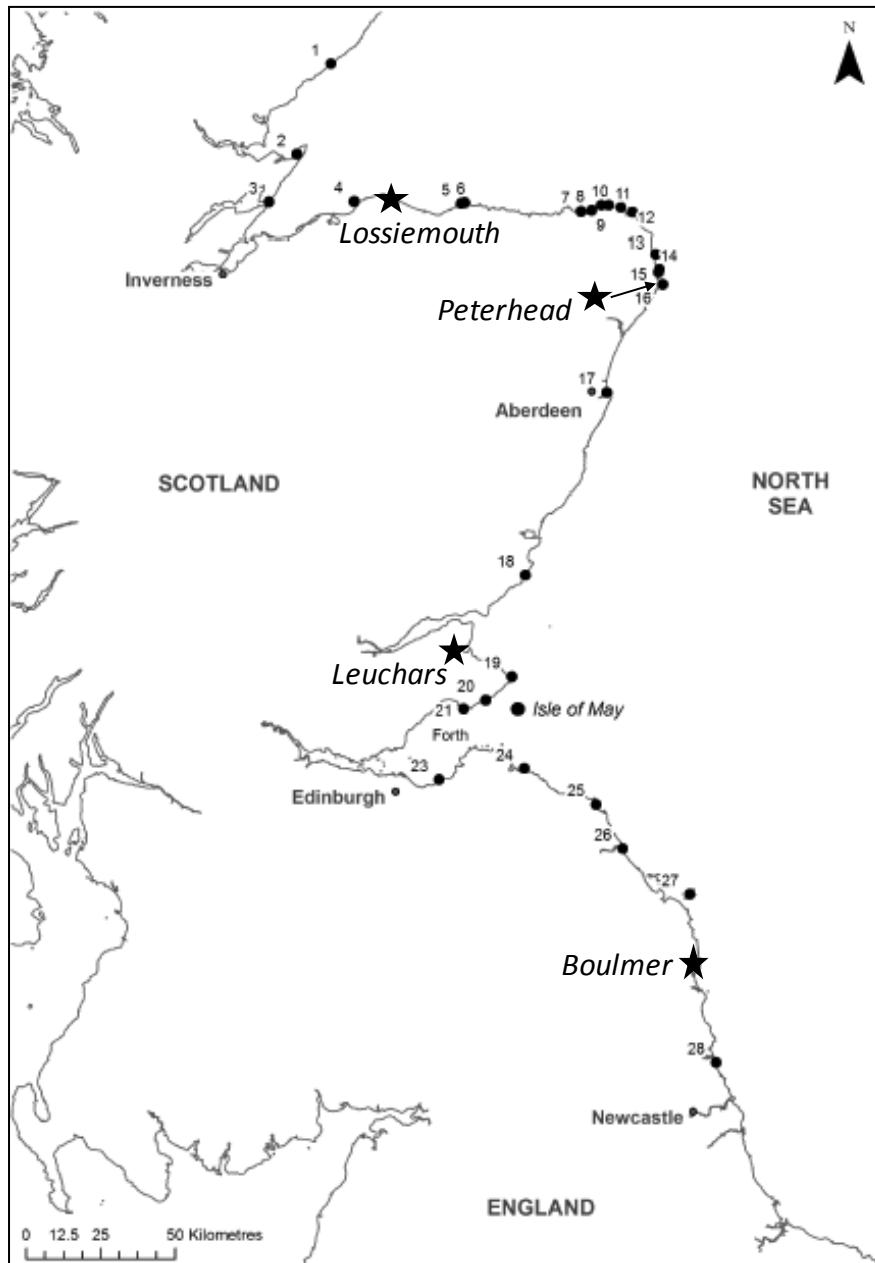
26 and e). The Pearson correlation coefficients between wind speed at Leuchars and
27 Lossiemouth, Peterhead and Boulmer were, respectively 0.66, 0.64 and 0.78 (Fig S1.2b, d
28 and f).

29

30 **References**

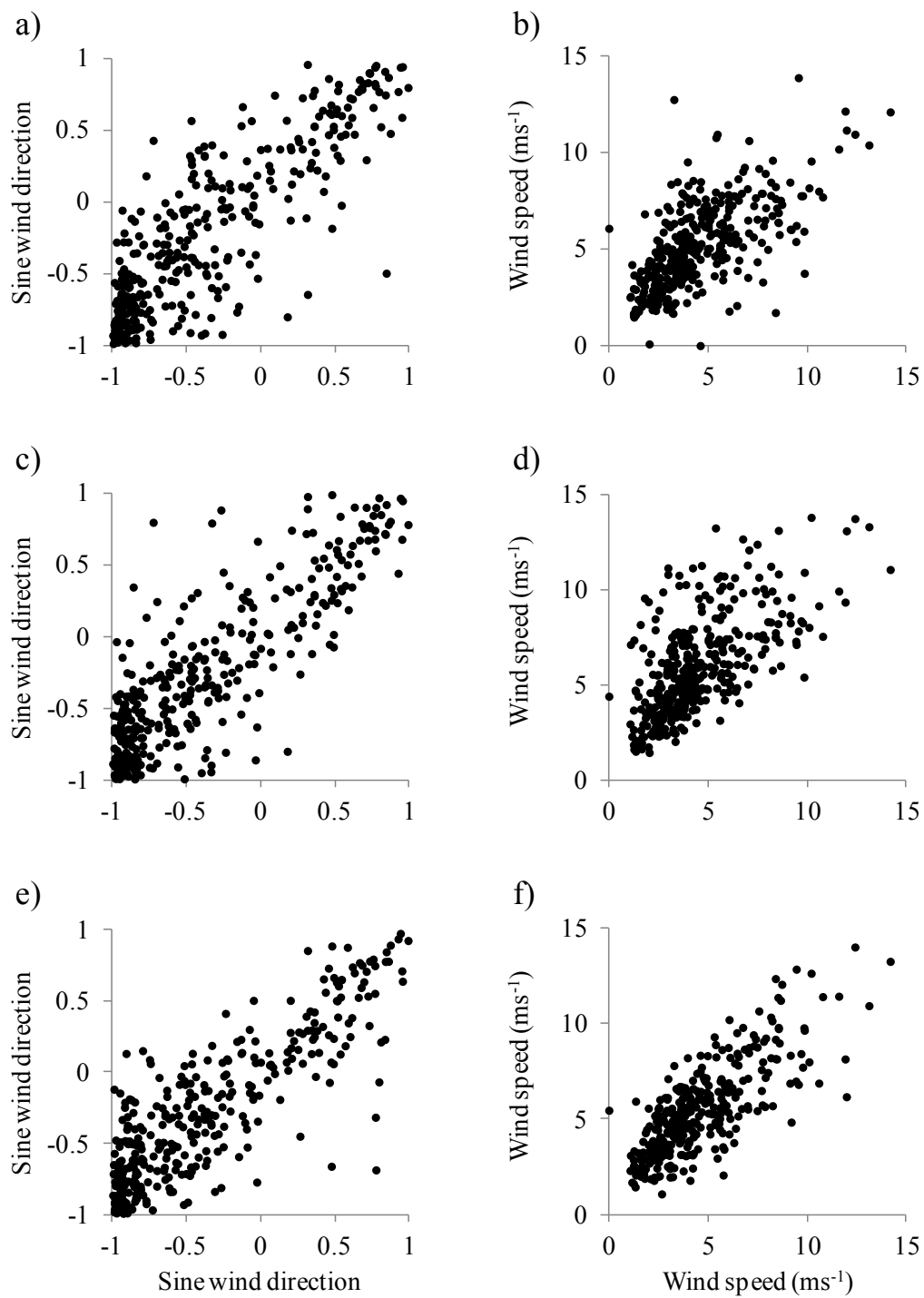
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32 J.M. (2014) Site fidelity and individual variation in winter location in partially migratory
33 European shags. *Plos One*, **9**, e98562.

34 Phillips, R.A., Silk, J.R.D., Croxall, J.P., Afanasyev, V. & Briggs, D.R. (2004) Accuracy of
35 geolocation estimates for flying seabirds. *Marine Ecology Progress Series*, **266**, 265-272.



36

37 Fig S1.1 Map showing the Isle of May (large circle), sites where shags were observed in
 38 winters 2009-2012 (numbered small circles; Grist et al. 2014) and four coastal weather
 39 stations (stars).



40

41 Fig S1.2. Relationship between daily mean sine wind direction at Leuchars weather station
 42 and at a) Lossiemouth weather station; c) Peterhead weather station; e) Boulmer weather
 43 station; relationship between daily mean wind speed at Leuchars weather station and at b)
 44 Lossiemouth weather station; d) Peterhead weather station; f) Boulmer weather station.

45 **Appendix S2: Model selection**

46

47 The full fixed effects model was as follows:

48

49 daily foraging time (h) = sex+wind speed+wind direction+year+date+date²+breeding status+

50 brood size+days since laying+days since laying²+days since laying³+age+age²+sex*(wind

51 speed+wind direction+date+date²+breeding status+brood size); random model = individual

52

53 All covariates were standardised by subtracting the mean and dividing by one standard

54 deviation (Zuur *et al.* 2009; Schielzeth 2010). We fitted all fixed effects to every model, and

55 tested all possible combinations of two-way interaction terms (n=48; Appendix S2). Model

56 selection was performed using Akaike Information Criterion (AICc), where the best model

57 had the lowest AICc value. Models within two AICc ($\Delta\text{AICc} < 2$) were considered to have

58 equal support (Burnham & Anderson 2002), unless they contained one or more parameters

59 and had a higher AICc than the best supported model, where this rule of thumb is not

60 considered appropriate (Burnham & Anderson 2002). Model selection was performed using

61 the *nlme* and *MuMIn* statistical packages in the program R (version 3.0.1).

62

63 The best supported model included all fixed effects and interaction terms between sex and

64 wind speed, wind direction, breeding status and brood size (Table S2.1). Two other models

65 were within two AICc ($\Delta\text{AICc} < 2$) of this model, containing the same effects plus sex by date,

66 and the same effects plus sex by date and sex by date², respectively. However, both models

67 were not considered to have equal support as the top model because they contained one or

68 more parameters and had a higher AICc (Burnham & Anderson 2002). These model outputs

69 therefore suggest limited support for a sex by date or sex by date² interaction.

70

71 **References**

72 Burnham, K.P. & Anderson, D.R. (2002) *Model Selection and Multimodel Inference: A*
73 *Practical Information-Theoretic Approach*, 2nd edn. edn. Springer, New York.

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75 *Methods in Ecology and Evolution*, **1**, 103-113.

76 Zuur, A.F., Ieno, E.N., Walker, N., Saveliev, A.A. & Smith, G.M. (2009) *Mixed Effects*
77 *Models and Extensions in Ecology with R*. Springer, New York.

78

79 Table S2.1. Model selection tables (n=48), ordered by AICc. The models within two AICc
 80 ($\Delta AICc < 2$) of the model with the lowest AIC are shown in bold

81

| model | sex interactions added to the main effects model | AICc | $\Delta AICc$ |
|-----------|---|---------------|---------------|
| 41 | sex*wind speed+sex*wind direction+sex*breeding status+sex*brood size | 207919 | 0.0 |
| 46 | sex*wind speed+sex*wind direction+sex*date+sex*breeding status+sex*brood size | 207920 | 0.6 |
| 47 | sex*wind speed+sex*wind direction+sex*date+sex*date²+sex*breeding status+sex*brood size | 207920 | 0.6 |
| 27 | sex*wind speed+sex*breeding status+sex*brood size | 207928 | 9.2 |
| 37 | sex*wind speed+sex*date+sex*breeding status+sex*brood size | 207928 | 9.3 |
| 42 | sex*wind speed+sex*date+sex*date ² +sex*breeding status+sex*brood size | 207930 | 11.2 |
| 28 | sex*wind direction+sex*breeding status+sex*brood size | 207943 | 23.9 |
| 38 | sex*wind direction+sex*date+sex*breeding status+sex*brood size | 207944 | 25.2 |
| 43 | sex*wind direction+sex*date+sex*date ² +sex*breeding status+sex*brood size+sex*brood size | 207946 | 27.5 |
| 44 | sex*wind speed+sex*wind direction+sex*date+sex*date ² +sex*breeding status | 207948 | 29.0 |
| 39 | sex*wind speed+sex*wind directionsex*date+sex*breeding status | 207949 | 29.9 |
| 11 | sex*breeding status+sex*brood size | 207949 | 30.3 |
| 29 | sex*wind speed+sex*wind directionsex*breeding status | 207949 | 30.5 |
| 21 | sex*date+sex*breeding status+sex*brood size | 207950 | 31.2 |
| 31 | sex*date+sex*date ² +sex*breeding status+sex*brood size | 207954 | 34.7 |
| 22 | sex*wind speed+sex*date+sex*breeding status | 207957 | 38.5 |
| 12 | sex*wind speed+sex*breeding status | 207959 | 39.6 |
| 32 | sex*wind speed+sex*date+sex*date ² +sex*breeding status | 207959 | 39.6 |
| 36 | sex*wind speed+sex*wind direction+sex*date+sex*date ² | 207973 | 54.1 |
| 13 | sex*wind direction+sex*breeding status | 207974 | 54.6 |
| 23 | sex*wind directionsex*date+sex*breeding status | 207974 | 54.8 |
| 45 | sex*wind speed+sex*wind direction+sex*date+sex*date ² +sex*brood size | 207974 | 54.8 |
| 33 | sex*wind direction+sex*date+sex*date ² +sex*breeding status | 207975 | 56.4 |
| 7 | sex*date+sex*breeding status | 207980 | 60.6 |
| 26 | sex*wind speed+sex*wind direction+sex*date | 207980 | 60.7 |
| 2 | sex*breeding status | 207980 | 60.9 |
| 17 | sex*date+sex*date ² +sex*breeding status | 207983 | 63.6 |
| 19 | sex*wind speed+sex*date+sex*date ² | 207983 | 63.8 |
| 34 | sex*wind speed+sex*date+sex*date ² +sex*brood size | 207983 | 64.3 |
| 16 | sex*wind speed+sex*wind direction | 207986 | 67.4 |
| 40 | sex*wind speed+sex*wind direction+sex*date+sex*brood size | 207987 | 68.1 |
| 30 | sex*wind speed+sex*wind direction+sex*brood size | 207993 | 74.3 |
| 9 | sex*wind speed+sex*date | 207995 | 75.7 |
| 35 | sex*wind direction+sex*date+sex*date ² +sex*brood size | 207995 | 76.1 |
| 20 | sex*wind direction+sex*date+sex*date ² | 207996 | 76.7 |
| 24 | sex*wind speed+sex*date+sex*brood size | 208001 | 82.5 |
| 18 | sex*date+sex*date ² +sex*brood size | 208002 | 82.7 |
| 6 | sex*date+sex*date ² | 208002 | 83.4 |
| 4 | sex*wind speed | 208003 | 83.8 |
| 10 | sex*wind direction+sex*date | 208004 | 84.6 |
| 14 | sex*wind speed+sex*brood size | 208009 | 89.8 |
| 5 | sex*wind direction | 208009 | 90.2 |
| 25 | sex*wind direction+sex*date+sex*brood size | 208011 | 92.1 |
| 1 | sex*date | 208015 | 96.2 |
| 15 | sex*wind direction+sex*brood size | 208016 | 97.3 |
| 0 | | 208022 | 103.1 |
| 8 | sex*date+sex*brood size | 208022 | 103.2 |
| 3 | sex*brood size | 208028 | 109.4 |

82

83

84 **Appendix S3: Within-individual and population correlations**

85

86 **Methods**

87

88 We fitted a series of alternative random effects structures to test the importance of individual
89 and population level auto-correlation between consecutive days and sex-specific
90 repeatability. This analysis was undertaken in the *asreml* statistical package in the program R
91 (version 3.0.1).

92 The first model (model 1) contained individual identity to account for consistent effects of
93 an individual in average daily foraging time. This term was equivalent to the random term
94 fitted in the first modelling step using AIC (Appendix S2). We also fitted the correlation
95 with an individual's foraging time on the previous day (see 'individual correlation' in Table 1
96 in main text and in Table S3.1), because the foraging behaviour of an individual on
97 consecutive days may be expected to be more similar than on non-consecutive days (because
98 of temporal autocorrelation in environmental conditions) and the residual variance. The
99 covariance of foraging time between successive days within individuals was calculated by
100 multiplying the correlation by the residual variance. We also fitted the correlation between
101 days (see 'population correlation' in Table 1 in main text and in Table S3.1) to measure the
102 correlation between the average daily foraging time of all individuals between successive
103 days (to examine whether all individuals were responding in the same way to between-day
104 effects due to e.g. shared environmental conditions) and the variance of the population's daily
105 foraging time (see 'population variance' in Table 1 in main text and in Table S3.1). The
106 covariance of the average daily foraging time across the population between successive days
107 was calculated by multiplying the correlation and the population variance. The total
108 correlation between successive foraging times (sometimes referred to as the temporal

109 correlation) was then calculated from the sum of the within and between individual
 110 covariances, divided by the total variance.

111 To assess the importance of the individual correlation, we carried out a second model
 112 (model 2) excluding this term from model 1. Similarly, to assess the importance of the
 113 population correlation we carried out a third model (model 3) excluding this term from model
 114 1. To test whether individual consistency varied in strength with sex, we carried out a fourth
 115 model (model 4), which was the same as model 1 except the individual random term was split
 116 between the sexes. Repeatability for each sex was estimated by dividing the sex specific
 117 variance by the total variance (e.g., male repeatability: variance of individual effects (male) /
 118 variance of individual effects (male) + population variance + residual variance).

119 Models 2-4 were each compared with model 1 using a *likelihood-ratio test* (LRT) with 1
 120 df to assess whether models were significantly different on removing particular random
 121 components (Zuur *et al.* 2009). A significant difference between the models would indicate
 122 that the term removed was important, and should therefore be retained. In all of the random
 123 models, days were coded as days since June 6th 2009, when sampling began, running
 124 continuously until the end of sampling on 31st May 2011. Detailed model descriptions are as
 125 follow:

126

127 *model 1*

128 daily foraging time (h) = sex+wind speed+wind direction+year+date+date²+breeding status+
 129 brood size+days since laying+days since laying²+days since laying³+age+age²+sex*(wind
 130 speed+wind direction+breeding status+brood size); random model = variance of individual
 131 effects (individual) + individual correlation + population correlation + population variance +
 132 residual variance

133

134

135 *model 2*

136 daily foraging time (h) = sex+wind speed+wind direction+year+date+date²+breeding status+
137 brood size+days since laying+days since laying²+days since laying³+age+age²+sex*(wind
138 speed+wind direction+breeding status+brood size); random model = variance of individual
139 effects (individual) + population correlation + population variance + residual variance

140

141 *model 3*

142 daily foraging time (h) = sex+wind speed+wind direction+year+date+date²+breeding status+
143 brood size+days since laying+days since laying²+days since laying³+age+age²+sex*(wind
144 speed+wind direction+breeding status+brood size); random model = variance of individual
145 effects (individual) + individual correlation + population variance + residual variance

146

147 *model 4:*

148 daily foraging time (h) = sex+wind speed+wind direction+year+date+date²+breeding status+
149 brood size+days since laying+days since laying²+days since laying³+age+age²+sex*(wind
150 speed+wind direction+breeding status+brood size); random model = variance of individual
151 effects (male) + variance of individual effects (female) + individual correlation + population
152 correlation + population variance + residual variance

153

154 **Results**

155

156 Table S3.1 shows the variance components and standard errors of the different random
157 models (models 1-4). The covariance of foraging time between successive days within
158 individuals was high (0.86) and the effect was highly significant ($\Delta LL = 2626$, $p < 0.001$;
159 Table S3.1). The covariance of the average daily foraging time across all individuals
160 (population) between successive days was also high (0.61) and highly significant (ΔLL
161 $= 254$, $p < 0.001$; Table S3.1). The total correlation between successive foraging times, or
162 temporal correlation, was 0.40. There was no evidence that accounting for sex specific
163 variation in the random effects structure of model 4 was important ($\Delta LL = 0.8$, $p = 1.0$;
164 Table S3.1), suggesting that the sexes did not differ in their overall variance. In line with
165 this, the overall repeatability of male and female daily foraging time was similar (male:
166 0.044; female: 0.063). Thus, model 1 was favoured and is presented in Table 1 in the main
167 text.

168

169 **References**

170 Zuur, A.F., Ieno, E.N., Walker, N., Saveliev, A.A. & Smith, G.M. (2009) *Mixed Effects*
171 *Models and Extensions in Ecology with R*. Springer, New York.

172

173 Table S3.1. Variance components \pm standard errors (s.e.) and z ratio for the different random
 174 effect models and the likelihood ratio tests (LRTs) comparing the fit of models on daily
 175 foraging time in shags on the Isle of May from 2009-2011.

176

| model | random effects: | variance component | s.e. | z ratio |
|--------------|---|---------------------------|-----------------|------------------|
| 1 | variance of individual effects | 0.186 | 0.029 | 6.368 |
| | individual correlation | 0.316 | 0.004 | 83.393 |
| | population variance | 0.799 | 0.078 | 10.274 |
| | population correlation | 0.760 | 0.022 | 33.836 |
| | residual variance | 2.720 | 0.019 | 145.785 |
| 2 | variance of individual effects | 0.196 | 0.030 | 6.567 |
| | population variance | 0.797 | 0.082 | 9.747 |
| | population correlation | 0.783 | 0.022 | 35.632 |
| | residual variance | 2.717 | 0.017 | 158.300 |
| 3 | variance of individual effects | 0.186 | 0.029 | 6.362 |
| | individual correlation | 0.317 | 0.004 | 83.760 |
| | population variance | 0.686 | 0.039 | 17.634 |
| | residual variance | 2.725 | 0.019 | 145.522 |
| 4 | variance of individual effects (male) | 0.160 | 0.031 | 5.173 |
| | variance of individual effects (female) | 0.239 | 0.064 | 3.707 |
| | individual correlation | 0.316 | 0.004 | 83.392 |
| | population variance | 0.799 | 0.078 | 10.273 |
| | population correlation | 0.761 | 0.022 | 33.839 |
| | residual variance | 2.720 | 0.019 | 145.786 |
| model | | log Likelihood | delta LL | p (chisq) |
| 1 | Main model | -49404.570 | * | * |
| 2 | Testing individual correlation | -52031.180 | 2626.610 | 0.000 |
| 3 | Testing population correlation | -49658.220 | 253.650 | 0.000 |
| 4 | Comparing sexes | -49403.820 | 0.750 | 1.000 |

177