Table ++. Parameters of regression models fitted

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Terms | Estimate | SE | z-statistic | p-value |
| **Model 1** | = 0.38 |  |  |  |
| (Intercept) | -2.7 | 0.15 | -18.23 | < 0.001 |
| Ptros | 4.7 | 0.28 | 16.58 | < 0.001 |
| Subset(BL) | 0.2 | 0.26 | 0.62 | 0.537 |
| Subset(BH) | 2.2 | 0.19 | 11.30 | < 0.001 |
| Ptros:Subset(BL) | -0.5 | 0.45 | -1.03 | 0.302 |
| Ptros:Subset(BH) | -1.4 | 0.43 | -3.38 | 0.001 |
| **Model 2** | = 0.57 | = 0.64 |  |  |
| (Intercept) | -4.2 | 0.38 | -10.89 | < 0.001 |
| Ptros | 4.7 | 0.82 | 5.80 | < 0.001 |
| Subset(BL) | 0.3 | 0.75 | 0.40 | 0.688 |
| Subset(BH) | 3.5 | 0.57 | 6.18 | < 0.001 |
| Species(*M.trossulus*) | 4.2 | 0.45 | 9.34 | < 0.001 |
| Ptros:Subset(BL) | -1.9 | 1.51 | -1.24 | 0.214 |
| Ptros:Subset(BH) | -1.8 | 1.29 | -1.36 | 0.174 |
| Ptros:Species(*M.trossulus*) | -2.5 | 0.83 | -3.02 | 0.003 |
| Subset(BL):Species(*M.trossulus*) | -0.5 | 0.77 | -0.61 | 0.54 |
| Subset(BH):Species(*M.trossulus*) | -3 | 0.62 | -4.87 | < 0.001 |
| Ptros:Subset(BL):Species(*M.trossulus*) | 2.2 | 1.46 | 1.52 | 0.129 |
| Ptros:Subset(BH):Species(*M.trossulus*) | 2.5 | 1.25 | 1.96 | 0.05 |
| sd\_(Intercept).pop | 0.8 |  |  |  |
| **Model 3** | = 0.17 |  |  |  |
| (Intercept) | 2.6 | 0.16 | 16.58 | < 0.001 |
| Ptros | -1.9 | 0.28 | -6.82 | < 0.001 |
| Subset(BL) | -0.4 | 0.28 | -1.53 | 0.127 |
| Subset(BH) | -2.4 | 0.2 | -12.29 | < 0.001 |
| Ptros:Subset(BL) | 1.1 | 0.47 | 2.26 | 0.024 |
| Ptros:Subset(BH) | 2.6 | 0.39 | 6.66 | < 0.001 |
| **Model 4** | = 0.4 | = 0.42 |  |  |
| (Intercept) | 3.8 | 0.28 | 13.99 | < 0.001 |
| Morph(T) | -3.8 | 0.41 | -9.12 | < 0.001 |
| Ptros | -5.2 | 0.55 | -9.57 | < 0.001 |
| Subset(BL) | -0.4 | 0.47 | -0.88 | 0.377 |
| Subset(BH) | -0.6 | 0.47 | -1.21 | 0.226 |
| Morph(T):Ptros | 8.1 | 0.78 | 10.40 | < 0.001 |
| Morph(T):Subset(BL) | 0.8 | 0.73 | 1.09 | 0.276 |
| Morph(T):Subset(BH) | -1.6 | 0.58 | -2.71 | 0.007 |
| Ptros:Subset(BL) | 0.8 | 0.9 | 0.91 | 0.361 |
| Ptros:Subset(BH) | 0.4 | 1.02 | 0.36 | 0.72 |
| Morph(T):Ptros:Subset(BL) | -0.3 | 1.37 | -0.21 | 0.83 |
| Morph(T):Ptros:Subset(BH) | 1.4 | 1.2 | 1.16 | 0.244 |
| sd\_(Intercept).pop | 0.3 |  |  |  |
| **Model 5** | = 0.42 |  |  |  |
| (Intercept) | -2.5 | 0.14 | -17.97 | < 0.001 |
| PT | 5.3 | 0.32 | 16.73 | < 0.001 |
| Subset(BL) | 0.3 | 0.25 | 1.12 | 0.264 |
| Subset(BH) | -1.3 | 0.33 | -4.06 | < 0.001 |
| PT:Subset(BL) | 0.3 | 0.58 | 0.54 | 0.588 |
| PT:Subset(BH) | -0.3 | 0.53 | -0.54 | 0.591 |
| **Model 6** | = 0.5 | = 0.51 |  |  |
| (Intercept) | 3.7 | 0.21 | 17.23 | < 0.001 |
| Morph(T) | -3.5 | 0.33 | -10.50 | < 0.001 |
| Ptros | -4.9 | 0.41 | -12.00 | < 0.001 |
| Subset(BH) | -0.4 | 0.43 | -1.00 | 0.318 |
| SubsetGOM | 1 | 0.58 | 1.78 | 0.074 |
| SubsetBALT | -0.9 | 0.41 | -2.28 | 0.023 |
| SubsetNORW | -0.6 | 0.61 | -1.00 | 0.315 |
| Morph(T):Ptros | 8.1 | 0.63 | 12.90 | < 0.001 |
| Morph(T):Subset(BH) | -1.8 | 0.53 | -3.43 | 0.001 |
| Morph(T):SubsetGOM | -1.8 | 0.84 | -2.18 | 0.029 |
| Morph(T):SubsetBALT | 0.4 | 1.54 | 0.23 | 0.82 |
| Morph(T):SubsetNORW | -1.1 | 1.17 | -0.95 | 0.343 |
| Ptros:Subset(BH) | 0.1 | 0.93 | 0.09 | 0.928 |
| Ptros:SubsetGOM | -3.2 | 1.08 | -2.92 | 0.003 |
| Ptros:SubsetBALT | -0.5 | 0.72 | -0.72 | 0.47 |
| Ptros:SubsetNORW | 0 | 0.95 | -0.05 | 0.959 |
| Morph(T):Ptros:Subset(BH) | 1.4 | 1.1 | 1.27 | 0.204 |
| Morph(T):Ptros:SubsetGOM | 4.8 | 1.88 | 2.57 | 0.01 |
| Morph(T):Ptros:SubsetBALT | 1.2 | 2.2 | 0.55 | 0.579 |
| Morph(T):Ptros:SubsetNORW | 3.6 | 1.94 | 1.86 | 0.063 |
| sd\_(Intercept).pop | 0.3 |  |  |  |

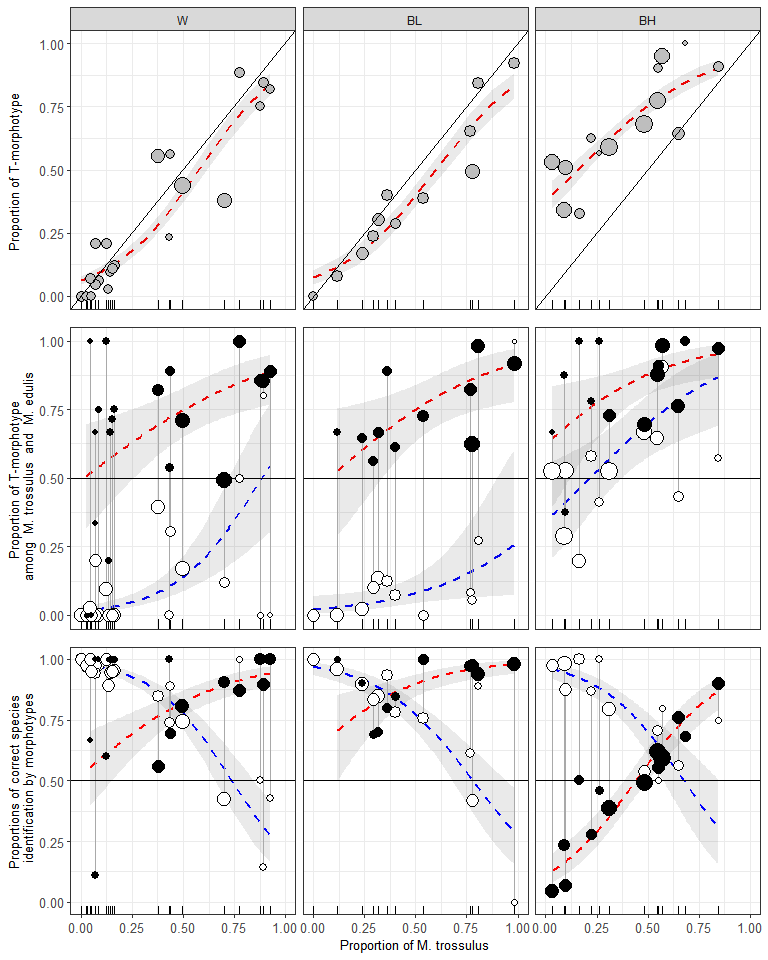


Figure ++. Variation of PT, P(T|tros), P(E|edu), P(tros|T), P(edu|E) as functions of Ptros in the White Sea (WS), brackish Barents Sea (BL) and saline Barents Sea (BH). Points - empirical estimates, size is proportional to sample sizes. Lines – regression model predictions, grey filling – 95% confidence intervals of regressions. (A) Proportions of T-morphotypes (PT) (Model 1). (B). Proportions of T-morphotypes among M. trossulus (filled points) and M. edulis (empty points) (Model 2). (C) Frequencies of M. trossulus among T-morphotypes (filled points) and of M. edulis among E-morphotypes (Model 4). Vertical lines on B and C connect subsamples of *M. trossulus* and *M. edulis* from the same samples.

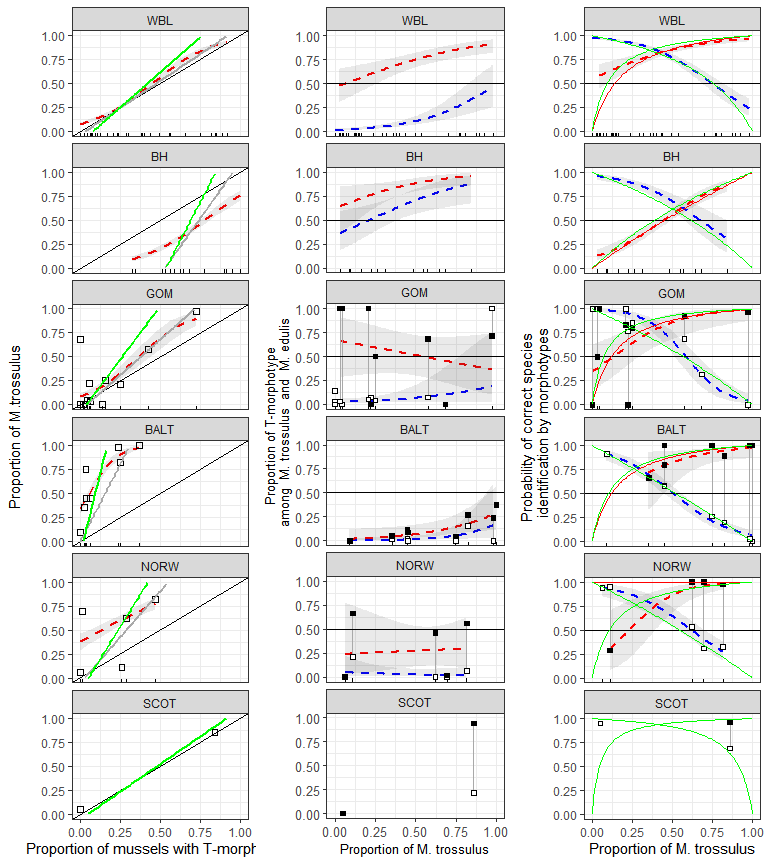


Figure ++. Predictive power of morphotype test in different regions. (A) Dependence of Ptros on proportion of T-morphotype mussels. Dotted line is empirical regression line (Model 7). Solid gray line - prediction accordingly to Eq. 3. Solid black lines represent Y=X dependence. (B) Probability to find a mussel with T-morphotype among M.edulis and M.trossulus. Dotted lines correspond to regression Model 8. Black squares - M.trossulus, white - M.edulis. (C) Probability of correct species identification by morphotype-test. Dotted lines are empirical regression lines (Model 6). Sold red line - prediction by Eq.1, Solid blue line - prediction by Eq.2. Shedded areas around regression lines represent 95% CI. For WBL and BH dots represent testing data sets in all other cases dots represent data used for constructing corresponding regression models.

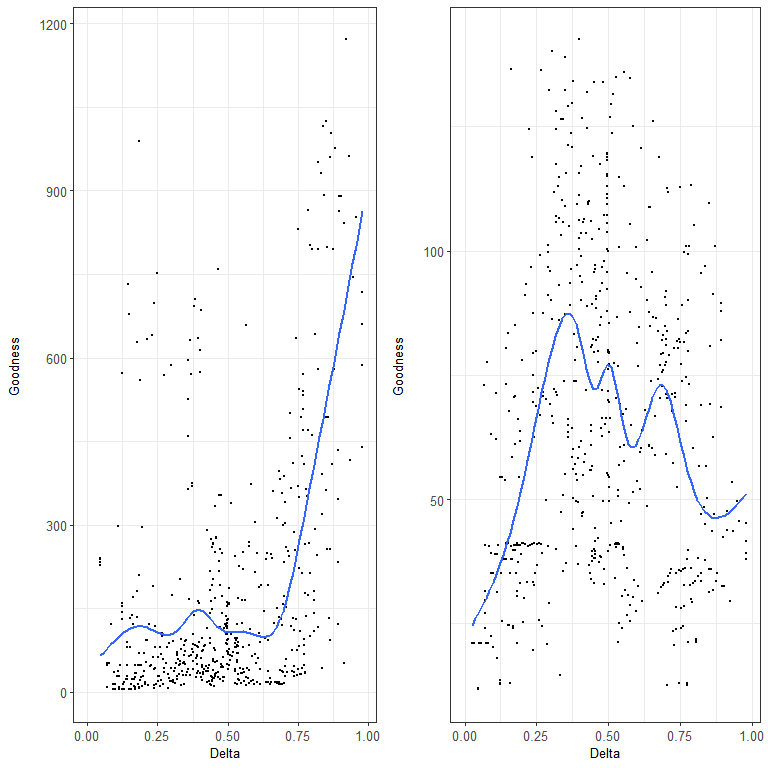


Figure +. Correspondence between regression and theoretical models. Each point corresponds to one of the possible pairs of populations from modelling data set (White Sea joined with low salinity Barens Sea). OX axis represents the differencу in genetic structre for each pair of populations. OY axis represents correspondence between prediction of regression model and theoretical model. Lines represent LOESS-smoother. (A ) Model 7 describing the dependence of proportion of M.trossulus (Ptros) on proportion of T-morphotype (P\_T) ; (B) Model 6 describing the dependence of probability of correct species identification on proportion of M.trossulus and morphotype.