Юля! Вот посмотри на результаты. Я брал в качестве критерия для отбора проб в тестинг датасет те, у кого Ptros были наиболее близки к 0.2, 0.4, 0.6, 0.8 квантилям распределения Ptros в соответствующем Subset. Сразу скажу, что в качестве границ для отбора не стоит брать Ptros = 0.5 или около того, та как мы выьиваем серединку и от этого все модели сильно едут.

# Regression models parameters

In all models outcome variables were supposed as binomialy disributed (). Logit was used as a linck function in all models. In all cases full models including all terms and their inteactions were constructed. After the full models were constructed they were simplified accordingly to backward selection protocol (Zuur et al., 2009).

Model1:

Model2:

Model3:

Model4:

Model5:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Terms | Estimate | SE | z-statistic | p-value |
| NA | NA | NA | NA | NA |
| (Intercept) | -2.7 | 0.17 | -16.10 | < 0.001 |
| Ptros | 4.6 | 0.30 | 15.45 | < 0.001 |
| Subset(BL) | -0.1 | 0.32 | -0.46 | 0.643 |
| Subset(BH) | 2.3 | 0.21 | 11.00 | < 0.001 |
| Ptros:Subset(BL) | 0.6 | 0.56 | 1.02 | 0.307 |
| Ptros:Subset(BH) | -2.1 | 0.46 | -4.46 | < 0.001 |
| NA | NA | NA | NA | NA |
| (Intercept) | -3.8 | 0.36 | -10.42 | < 0.001 |
| Ptros | 3.4 | 0.57 | 5.96 | < 0.001 |
| Subset(BL) | -0.3 | 0.51 | -0.49 | 0.625 |
| Subset(BH) | 3.1 | 0.42 | 7.31 | < 0.001 |
| Species(*M.trossulus*) | 3.0 | 0.28 | 10.70 | < 0.001 |
| Subset(BL):Species(*M.trossulus*) | 0.7 | 0.46 | 1.43 | 0.152 |
| Subset(BH):Species(*M.trossulus*) | -2.2 | 0.34 | -6.26 | < 0.001 |
| sd\_(Intercept).pop | 0.8 | NA | NA | NA |
| NA | NA | NA | NA | NA |
| (Intercept) | 2.5 | 0.17 | 14.47 | < 0.001 |
| Ptros | -1.6 | 0.29 | -5.63 | < 0.001 |
| Subset(BL) | -0.2 | 0.34 | -0.65 | 0.517 |
| Subset(BH) | -2.5 | 0.21 | -11.63 | < 0.001 |
| Ptros:Subset(BL) | 1.3 | 0.57 | 2.20 | 0.028 |
| Ptros:Subset(BH) | 2.7 | 0.43 | 6.25 | < 0.001 |
| NA | NA | NA | NA | NA |
| (Intercept) | 3.6 | 0.25 | 14.30 | < 0.001 |
| Morph(T) | -4.3 | 0.35 | -12.46 | < 0.001 |
| Ptros | -4.7 | 0.42 | -11.23 | < 0.001 |
| Subset(BL) | 0.2 | 0.31 | 0.55 | 0.58 |
| Subset(BH) | -0.6 | 0.27 | -2.23 | 0.025 |
| Morph(T):Ptros | 9.0 | 0.56 | 16.28 | < 0.001 |
| Morph(T):Subset(BL) | 0.4 | 0.44 | 0.98 | 0.327 |
| Morph(T):Subset(BH) | -0.7 | 0.32 | -2.13 | 0.033 |
| sd\_(Intercept).pop | 0.3 | NA | NA | NA |
| NA | NA | NA | NA | NA |
| (Intercept) | -2.6 | 0.14 | -19.19 | < 0.001 |
| PT | 5.5 | 0.26 | 21.32 | < 0.001 |
| Subset(BL) | 0.2 | 0.16 | 1.08 | 0.278 |
| Subset(BH) | -1.5 | 0.14 | -10.45 | < 0.001 |

In all models Ptros - proportion of *M.trossulus* in population; Subset - sampling area (*W*, *BL*, *BH*); PT - proportion of T-morphotype in population; Species - mussel genotype (*M.edulis* or *M.trossulus*). *M.edulis* and *W* where used as basic levels for categorical predictors.

## Regression models visualisation

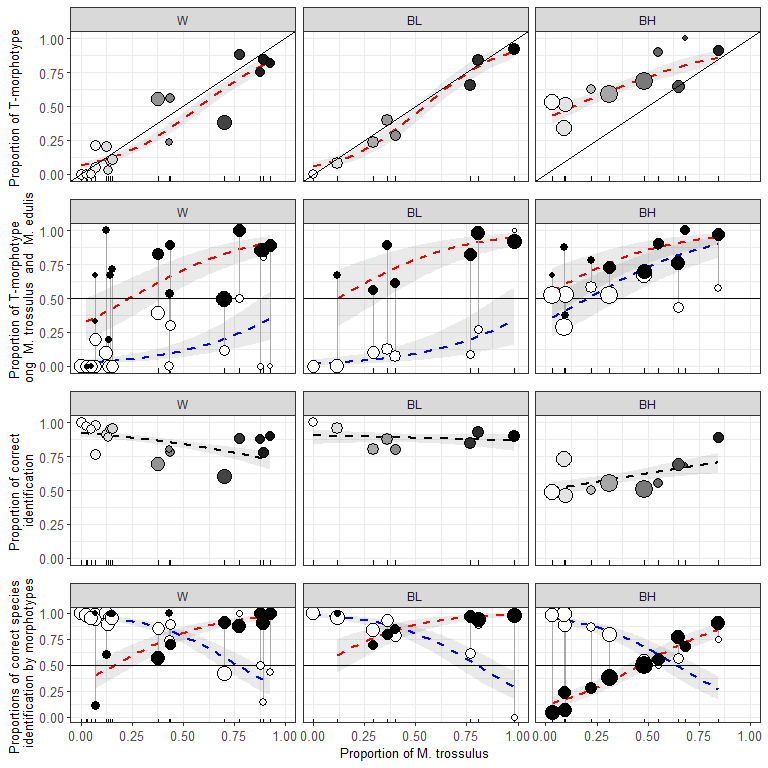


Figure ++. Visualisation of regression models. Initial data are presented as proportions of positive outcome in particular populations. Size of points is proportional to number of mussels in the particular sample. (A) Model1: the fill intensity is proportional to Ptros (**А то этого не видно из значений абсциссы?…**). (B) Model2: filled points - *M.trossulus* with T-morphotype; emty points - *M.edulis* with T-morphotype. (C) Model3: filled points - *M.trossulus* with T-morphotype; empty points - *M.edulis* with E-morphotype.

## Strategy for finding of calibration samples

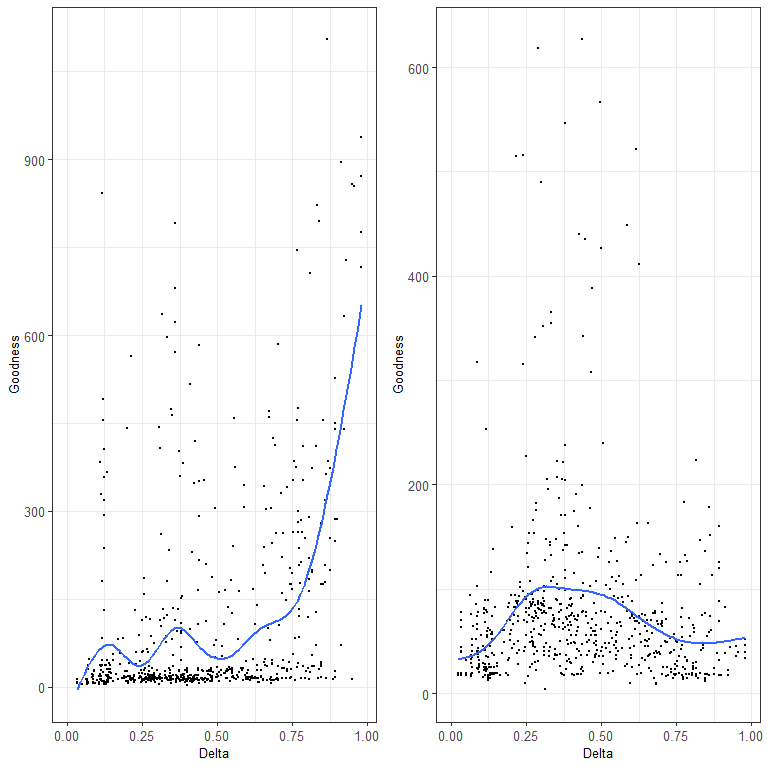


Figure +. Correspondence between regression and theoretical models. Each point corresponds to one of the possible pairs of populations from modelling data set. OX axis represents the differencу in genetic structre for each pair of populations. OY axis represents correspondence between prediction of regression model and theoretical model. Lines represent loess-smoother. (A ) Model 5 describing the dependence of proportion of M.trossulus (Ptros) on proportion of T-morphotype (P\_T) ; (B) Model 4 describing the dependence of probability of correct species identification (Pcorrect) on proportion of M.trossulus (Ptros) and morphotype (Morph).

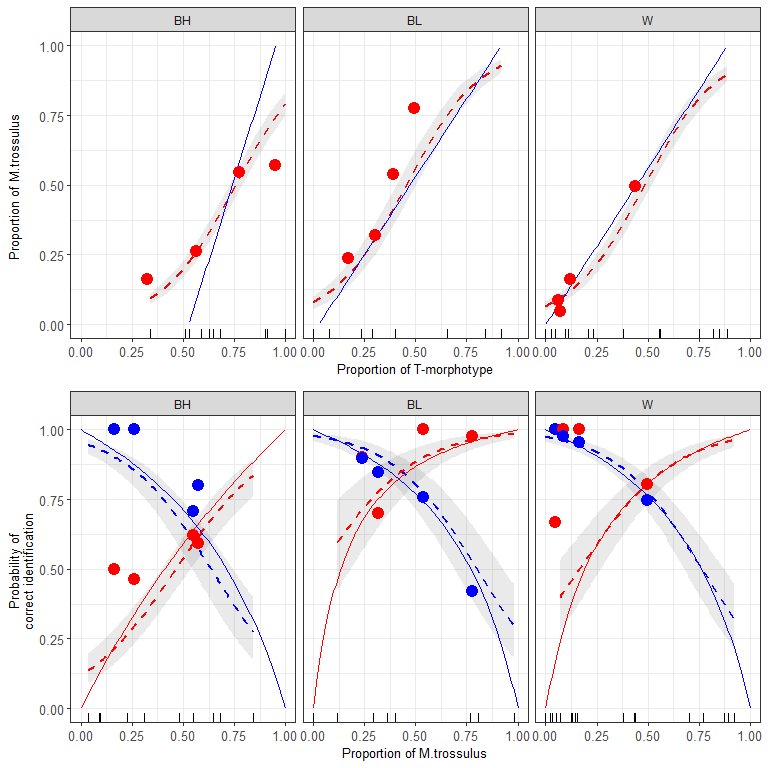


Figure +. Visualisation of regression models and theoretical models. Points represent the testing data set.