Online Resource 1: Non-linear models

This supplementary file details several common non-linear models. Equations and parameter definitions are given in Table A1.1, and the results of fitting these models to experimental data are shown in Table A1.2 and Figure A1.1.
### Table A1.1: Parameters for several non-linear developmental models

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Definition</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Sharpe</strong></td>
<td>$\rho = \frac{T e^{\left(\phi - \left(\Delta H_A^<em>/T\right)\right) / R}}{1 + e^{\left[\left(\Delta S_A - \Delta H_A^</em>/T\right) / R\right]} + e^{\left[\left(\Delta S_L - \Delta H_A^*/T\right) / R\right]}}$</td>
<td>Sharpe and DeMichele 1977</td>
</tr>
<tr>
<td>$T$</td>
<td>Absolute temperature (Kelvin)</td>
<td></td>
</tr>
<tr>
<td>$K$</td>
<td>Boltzmann constant</td>
<td></td>
</tr>
<tr>
<td>$h$</td>
<td>Planck’s constant</td>
<td></td>
</tr>
<tr>
<td>$R$</td>
<td>Gas constant</td>
<td></td>
</tr>
<tr>
<td>$\epsilon_e$</td>
<td>Relative enzyme concentration</td>
<td></td>
</tr>
<tr>
<td>$\Delta H_A^*$</td>
<td>Enthalpy of activation</td>
<td></td>
</tr>
<tr>
<td>$\Delta H_A$</td>
<td>Difference in enthalpy of activation between first inactive and active enzyme states at equilibrium</td>
<td></td>
</tr>
<tr>
<td>$\Delta H_H$</td>
<td>Difference in enthalpy of activation between active and second inactive enzyme states at equilibrium</td>
<td></td>
</tr>
<tr>
<td>$\Delta S_A^*$</td>
<td>Entropy of activation</td>
<td></td>
</tr>
<tr>
<td>$\Delta S_A$</td>
<td>Difference in entropy of activation between first inactive and active enzyme states at equilibrium</td>
<td></td>
</tr>
<tr>
<td>$\Delta S_H$</td>
<td>Difference in entropy of activation between active and second inactive enzyme states at equilibrium</td>
<td></td>
</tr>
<tr>
<td>$\phi$</td>
<td>Simplying parameter, equal to $\Delta S_A^* + \ln\left(\epsilon_e / h\right)$</td>
<td></td>
</tr>
<tr>
<td><strong>Logan</strong></td>
<td>$\rho = \psi \cdot \left(e^{rT} - e^{(rT_{max} - (\delta_{max} - T) / \Delta T)}\right)$</td>
<td>Logan et al. 1976</td>
</tr>
<tr>
<td>$T$</td>
<td>Air temperature – minimum temperature threshold</td>
<td></td>
</tr>
<tr>
<td>$\delta_{max}$</td>
<td>Lethal maximum temperature</td>
<td></td>
</tr>
<tr>
<td>$\Delta T$</td>
<td>Difference between maximum and optimal temperatures</td>
<td></td>
</tr>
<tr>
<td>$\psi$</td>
<td>Developmental rate at a given base temperature above the minimum developmental temperature</td>
<td></td>
</tr>
<tr>
<td>$r$</td>
<td>Rate increase up to optimal temperature</td>
<td></td>
</tr>
<tr>
<td><strong>Holling</strong></td>
<td>$\rho = \psi \cdot \left(\frac{T^2}{T^2 + D^2} - e^{(\delta_{max} - T) / \Delta T}\right)$</td>
<td>Hilbert and Logan 1983</td>
</tr>
<tr>
<td>$T$</td>
<td>Air temperature – minimum temperature threshold</td>
<td></td>
</tr>
<tr>
<td>$\delta_{max}$</td>
<td>Lethal maximum temperature</td>
<td></td>
</tr>
<tr>
<td>$\Delta T$</td>
<td>Difference between maximum and optimal temperatures</td>
<td></td>
</tr>
<tr>
<td>$\psi$</td>
<td>Developmental rate at a given base temperature above the minimum developmental temperature</td>
<td></td>
</tr>
<tr>
<td>$D$</td>
<td>Fit parameter</td>
<td></td>
</tr>
<tr>
<td><strong>Lactin</strong></td>
<td>$\rho = e^{rT} - e^{(rT_{max} - (\delta_{max} - T) / \Delta T)} + \lambda$</td>
<td>Lactin et al. 1995</td>
</tr>
<tr>
<td>$T$</td>
<td>Air temperature – minimum temperature threshold</td>
<td></td>
</tr>
<tr>
<td>$\delta_{max}$</td>
<td>Lethal maximum temperature</td>
<td></td>
</tr>
<tr>
<td>$\Delta T$</td>
<td>Difference between maximum and optimal temperatures</td>
<td></td>
</tr>
<tr>
<td>$r$</td>
<td>Rate increase up to optimal temperature</td>
<td></td>
</tr>
<tr>
<td>$\lambda$</td>
<td>Fit parameter</td>
<td></td>
</tr>
</tbody>
</table>
Table A1.2: Goodness of fit of models to empirical *N. bisignatus* developmental data, using two metrics of model fit: $R^2$, the coefficient of determination or nonlinear regression, for linear or nonlinear models, respectively, and RSS, the residual sum of squares. High $R^2$ and low RSS indicate good model fit. Model fit analysis conducted by Kontodimas et al. (2004).

<table>
<thead>
<tr>
<th>Model</th>
<th>$R^2$</th>
<th>RSS (x10⁶)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Linear</td>
<td>0.9965</td>
<td>1.152</td>
</tr>
<tr>
<td>Sharpe</td>
<td>0.9998</td>
<td>0.8661</td>
</tr>
<tr>
<td>Logan</td>
<td>0.9983</td>
<td>0.6503</td>
</tr>
<tr>
<td>Holling</td>
<td>0.9985</td>
<td>5.7955</td>
</tr>
<tr>
<td>Lactin</td>
<td>0.9997</td>
<td>1.0767</td>
</tr>
</tbody>
</table>
Figure A1.1 Representative plots of the linear and several non-linear developmental models, with points indicating empirical developmental data of *N. bisignatus*. All parameter values and data were obtained from Kontodimas et al. (2004). Additionally, Kontodimas et al. (2004) assessed the goodness of fit for these models using two metrics ($R^2$ and RSS). Their results are shown in Table A1.2.
References


