### Anova table for pH

<table>
<thead>
<tr>
<th>Source</th>
<th>Sum Sq</th>
<th>D.F</th>
<th>Mean Sq</th>
<th>F</th>
<th>Prob&gt;F</th>
</tr>
</thead>
<tbody>
<tr>
<td>Dye-Type</td>
<td>0.8533</td>
<td>4</td>
<td>0.21332</td>
<td>5.61</td>
<td>0.0013</td>
</tr>
<tr>
<td>Dose</td>
<td>20.9644</td>
<td>3</td>
<td>6.98814</td>
<td>183.82</td>
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</tr>
<tr>
<td>Cons</td>
<td>0.1099</td>
<td>2</td>
<td>0.05495</td>
<td>1.45</td>
<td>0.249</td>
</tr>
<tr>
<td>Error</td>
<td>1.3686</td>
<td>36</td>
<td>0.03802</td>
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<td></td>
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<tr>
<td>Total</td>
<td>23.5875</td>
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</tr>
</tbody>
</table>

Constrained (Type-III) sums of squares

### Anova table for IAU

<table>
<thead>
<tr>
<th>Source</th>
<th>Sum Sq</th>
<th>D.F</th>
<th>Mean Sq</th>
<th>F</th>
<th>Prob&gt;F</th>
</tr>
</thead>
<tbody>
<tr>
<td>#Dye-Type</td>
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<td>65.24</td>
<td>2.05</td>
<td>0.2262</td>
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<tr>
<td>#Dose</td>
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<td>4509.73</td>
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<td>#Cons</td>
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<td>0</td>
<td>0</td>
<td>0</td>
<td>NaN</td>
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<tr>
<td>#Dye-Type*Dose</td>
<td>76.1</td>
<td>7</td>
<td>10.87</td>
<td>0.34</td>
<td>0.9036</td>
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<tr>
<td>#Dye-Type*Cons</td>
<td>105.7</td>
<td>7</td>
<td>15.11</td>
<td>0.47</td>
<td>0.8213</td>
</tr>
<tr>
<td>#Dose*Cons</td>
<td>1689.3</td>
<td>2</td>
<td>844.66</td>
<td>26.48</td>
<td>0.0022</td>
</tr>
<tr>
<td>Error</td>
<td>159.5</td>
<td>5</td>
<td>31.89</td>
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<tr>
<td>Total</td>
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</table>

Constrained (Type-III) sums of squares. Terms marked with # are not full rank

### Anova table for ADMI

<table>
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<th>Source</th>
<th>Sum Sq</th>
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<th>Mean Sq</th>
<th>F</th>
<th>Prob&gt;F</th>
</tr>
</thead>
<tbody>
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<td>#Dye-Type</td>
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<td>NaN</td>
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<tr>
<td>#Dye-Type*Dose</td>
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</tbody>
</table>
In order to plot max $R^2$ that satisfies null hypothesis against value of parameter $a$ in equation $y/x = a$, (Figure 2 of manuscript) the following steps should be performed:

1. Specify parameter $a$ and the number of data points (here Data No=50, 100 or 150).
2. Generate x data (here using x=linspace (0, 2000, Data No); in MATLAB)
3. Assume $R^2=1$.
4. Generate random $y_{new}$ similar to $y=ax$ with $[R^2(y_{new},x) – R^2] <\epsilon$ (here 0.01).
5. If paired comparison of $y_{new}$ and x rejects null hypothesis (here $h=ttest (y_{new}, x) = 1$) then $R^2$-limit(a)=$R^2(y_{new},x)$ else $R^2=R^2 – 0.01$ and go to step 4.

This algorithm produces repeatable results independent of the selected random $y_{new}$. 