

### Formatting of the input data.

**Look@Rates** reads input data from a spreadsheet (xlsx format). The required data are organized in columns, with rows corresponding to individual cells. Table below describes the required data. The description assumes carbon to be the element assimilated by the cell (i.e., it considers  $^{13}\text{C}$  atom fractions and carbon density). For other elements, replace C with that element and the corresponding isotope (e.g., specify  $^{15}\text{N}$  atom fractions and N density). Approaches, equations, and supplementary method sections referred to in the table are described in Polerecky et al. (2021).

Column	Description
$t$	<b>Duration</b> of the SIP incubation. A value in h will yield rates in $\text{h}^{-1}$ .
$x$	Best estimate of the <b><math>^{13}\text{C}</math> atom fraction</b> of the measured cell, $x$ . Value determined from the nanoSIMS measurement. It can be quantified by analyzing the nanoSIMS data with programs such as Look@NanoSIMS.
$dx$	<b>Error</b> (uncertainty) of the $^{13}\text{C}$ atom fraction of the measured cell, $\Delta x$ . Value determined from the nanoSIMS measurement. It can be quantified by analyzing the nanoSIMS data with programs such as Look@NanoSIMS.
$x_{\text{Seff}}$	$^{13}\text{C}$ atom fraction of the <b>effective C source</b> , $x_{S,\text{eff}}$ (see Eq. 6). Ideally obtained from a direct measurement. Alternatively, the value can be calculated from the known concentration of substrate in the medium and the known concentration and amount of added $^{13}\text{C}$ -labelled substrate.
$x_{\text{ini}}$	<b>Initial <math>^{13}\text{C}</math> atom fraction</b> of the cell, $x_i$ . Ideally determined from the measurement of control cells. If not available, the value corresponding to the natural $^{13}\text{C}$ abundance ( $x_i \approx 0.011$ ) can be used.
$\rho$	<b>Carbon density</b> of the cell from the same species as the measured cell. A value reflecting the average C content per $\mu\text{m}^3$ of the cell, $\rho$ (in $\text{fmol C } \mu\text{m}^{-3}$ ).
$\text{avgVcell}$	<p><b>Average biovolume</b> of the cell from the same species as the measured cell, <math>\langle V \rangle</math> (in <math>\mu\text{m}^3</math>). This value is required for calculating the rate according to Step 3, Approach A and C.</p> <p>Values of <math>\rho</math> and <math>\langle V \rangle</math> are used to calculate the average C content of the cell as <math>\langle C \rangle = \rho \cdot \langle V \rangle</math>. Note that calculated <math>\langle C \rangle</math> must represent the C content of the cell averaged across the <i>entire</i> cell cycle. See <b>Supplementary Methods, Section 1.3</b>, for more details.</p> <p>If <math>\langle V \rangle</math> cannot be constrained by experimental data, leave the cell <i>empty</i>. In this case, the rate will only be calculated by Step 2 and Step 3, Approach B (the latter approach will only yield a result if <math>V_{\text{cell}}</math> is not empty; see below).</p>

<b><i>V<sub>cell</sub></i></b>	<p><b>Biovolume</b> of the <b>measured</b> cell, <math>V</math> (in <math>\mu\text{m}^3</math>). This value is required for calculating the rate according to Step 3, Approach B and C. <math>V</math> can be estimated from the dimensions of the cell determined from the same nanoSIMS image as <math>x</math>. Values of <math>\rho</math> and <math>V</math> are used to calculate the C content of the cell at the end of the SIP incubation, <math>C = \rho \cdot V</math> (in fmol C cell<sup>-1</sup>).</p> <p>In Approach C, values of <math>C</math> and <math>\langle C \rangle</math> are combined to calculate the cell cycle stage of the measured cell, <math>s = C/(C_{\text{max}}/2) - 1</math>, where <math>C_{\text{max}} = \langle C \rangle \cdot 2 \cdot \ln(2)</math> (Eq. 17). Note that calculated <math>s</math> must be between 0 (beginning of the cell cycle, i.e., cell just after division) and 1 (end of the cell cycle, i.e., cell just before division). If the entered combination of values of <math>\langle V \rangle</math> and <math>V</math> yields <math>s</math> below 0 or above 1, the function will change <math>V</math> to the value of <math>\langle V \rangle</math> by default.</p> <p>If <math>V</math> cannot be constrained by experimental data, leave the cell <i>empty</i>. In this case, the rate will only be calculated by Step 2 and Step 3, Approach A (the latter approach will only yield a result if avg<i>V<sub>cell</sub></i> is not empty; see above).</p>
<b><i>dV<sub>cell</sub></i></b>	<p><b>Error</b> (uncertainty) of the measured cell's biovolume, <math>\Delta V</math> (in <math>\mu\text{m}^3</math>). This value is required for calculating the rate according to Step 3, Approach B and C. <math>\Delta V</math> can be estimated from the dimensions of the cell determined from the same nanoSIMS image as <math>x</math>. Values of <math>\rho</math> and <math>\Delta V</math> are used to calculate the uncertainty of the cell's C content, <math>\Delta C = \rho \cdot \Delta V</math>.</p>
<b>Comment</b>	Optional comment, such as name of the sample, treatment, etc.