**Formatting of the input data.**

**Look@Rates** reads input data from an Excel spreadsheet (xlsx). 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 assimilated element (i.e., it considers 13C atom fractions and carbon density). For other elements, replace C with that element and the corresponding isotope (e.g., specify 15N atom fractions and N density). Approaches, equations, and supplementary method sections referred to in the table are described in Polerecky et al. (submitted to Frontiers in Microbiology).

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| **Column** | **Description** |
| ***t*** | **Duration** of the SIP incubation. A value in h will yield rates in h-1. |
| ***x*** | Best estimate of the **13C** **atom** **fraction** 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*** | **Error** (uncertainty) of the 13C atom fraction of the measured cell, Δ*x*. Value determined from the nanoSIMS measurement. It can be quantified by analyzing the nanoSIMS data with programs such as Look@NanoSIMS. |
| ***xSeff*** | 13C atom fraction of the **effective** **C** **source**, *xS,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 13C-labelled substrate. |
| ***x\_ini*** | **Initial 13C atom fraction** of the cell, *xi*. Ideally determined from the measurement of control cells. If not available, the value corresponding to the natural 13C abundance (*xi* ≈ 0.011) can be used. |
| ***rho*** | **Carbon** **density** of the cell from the same species as the measured cell. A value reflecting the average C content per μm3 of the cell, (in fmol C μm-3). |
| ***avgVcell*** | **Average** **biovolume** of the cell from the same species as the measured cell, (in μm3). This value is required for calculating the rate according to Approach A and C. Values of and are used to calculate the average C content of the cell as . Note that calculated must represent the C content of the cell averagedacrossthe *entire* cellcycle. See **Supplementary Methods, Section 1.3**, for more details. |
| ***Vcell*** | **Biovolume** of the **measured** cell, *V* (in μm3). This value is required for calculating the rate according to Approach B and C. *V* can be estimated from the dimensions of the cell determined from the same nanoSIMS image as *x*. Values of and *V* are used to calculate the C content of the cell at the end of the SIP incubation, (in fmol C cell-1). Values of *C* and are combined to calculate the cell cycle stage of the cell, *s* = *C*/(*Cmax*/2) – 1, where (Eq. **17**). Note that calculated *s* 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 and *V* yields or , the function will change *V* to the value of by default. |
| ***dVcell*** | **Error** (uncertainty) of the measured cell’s biovolume, Δ*V* (in μm3). This value is required for calculating the rate according to Approach B and C. Δ*V* can be estimated from the dimensions of the cell determined from the same nanoSIMS image as *x*. Values of and Δ*V* are used to calculate the uncertainty of the cell’s C content, . |
| **Comment** | Optional comment, such as name of the sample, treatment, etc. |