**S1 Text**

**DEFINITION OF IN SILICO MEDIA**

**1.1 Definition of *in silico* rich medium**

The rich medium described below is based on the *in silico* LB medium described previously (Nogales et al., 2017) and also on conditional essential genes of *Bdellovibrio*. The default Exchange reactions were constrained as follow.

**Oxygen:** model=changeRxnBounds(model,'EX\_o2(e)',-10,'l')

**Amino acids**

model=changeRxnBounds(model,'EX\_val\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_leu\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_ile\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_ser\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_thr\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_ala\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_glu\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_tyr\_L(e)',-5,'l')

model=changeRxnBounds(model,'EX\_gln\_L(e)',-5,'l')

**Amino acids from dipeptides**

The major carbon and energy source for *Bdellovibrio* are amino acid from the breakdown of proteins, preferentially dipeptides of alanine (Odelson et al., 1982)

model=changeRxnBounds(model,'EX\_ALAHIS',-5,'l')

model=changeRxnBounds(model,'EX\_ALAMET',-5,'l')

model=changeRxnBounds(model,'EX\_ALAASN',-5,'l')

model=changeRxnBounds(model,'EX\_ALAPRO',-5,'l')

model=changeRxnBounds(model,'EX\_ALAARG',-5,'l')

model=changeRxnBounds(model,'EX\_ALAPHE',-5,'l')

model=changeRxnBounds(model,'EX\_ALATYR',-5,'l')

model=changeRxnBounds(model,'EX\_ALATRP',-5,'l')

model=changeRxnBounds(model,'EX\_ALAASP',-5,'l')

model=changeRxnBounds(model,'EX\_ALALYS',-5,'l')

model=changeRxnBounds(model,'EX\_ALAALA',-5,'l')

model=changeRxnBounds(model,'EX\_ALAGLU',-5,'l')

model=changeRxnBounds(model,'EX\_ALATHR',-5,'l')

model=changeRxnBounds(model,'EX\_ALACYS',-5,'l')

model=changeRxnBounds(model,'EX\_ALAGLY',-5,'l')

model=changeRxnBounds(model,'EX\_ALAILE',-5,'l')

model=changeRxnBounds(model,'EX\_ALASER',-5,'l')

model=changeRxnBounds(model,'EX\_ALAVAL',-5,'l')

model=changeRxnBounds(model,'EX\_ALAGLN',-5,'l')

**Vitamins.** This medium only provides the auxotrophic metabolites of *B. bacteriovorus* HD100*.*

**Folic Acid (B9):** model=changeRxnBounds(model,'EX\_thf(e)',-0.1,'l')

**Pantotenate:** model=changeRxnBounds(model,'EX\_ptth(e)',-0.1,'l')

**Piridoxal phosphate:** model=changeRxnBounds(model,'EX\_pdx5p(e)',-0.1,'l')

**Biotine (B8):** model=changeRxnBounds(model,'EX\_btn(e)',-0.1,'l')

**Lipoate:** model=changeRxnBounds(model,'EX\_lipoate(e)',-0.1,'l')

**1.2 Definition of *in silico* minimal medium**

In order to define an *in silico* minimal medium, the lower bounds of several exchange reactions were constrained as follows and only the essential reactions have been included.

**Oxygen:** model=changeRxnBounds(model,'EX\_o2(e)',-10,'l')

**Essential amino acids**

model=changeRxnBounds(model,'EX\_val\_L(e)',-0.1,'l')

model=changeRxnBounds(model,'EX\_leu\_L(e)',-0.1,'l')

model=changeRxnBounds(model,'EX\_ile\_L(e)',-0.1,'l')

model=changeRxnBounds(model,'EX\_ser\_L(e)',-0.1,'l')

**Dipeptides.** The rest of amino acid will be providing in form of dipeptides

model=changeRxnBounds(model,'EX\_ALAHIS',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALACYS',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALAMET',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALAASN',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALAPRO',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALAARG',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALAPHE',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALATYR',-0.1,'l')

model=changeRxnBounds(model,'EX\_ALATRP',-0.1,'l')

Threonine and glycine will be obtained from serine. Aspartic acid and lysine will be obtained from asparagine. Tyrosine will be obtained from phenylalanine.

**Vitamins.** This medium only provides the auxotrophic metabolites of *B. bacteriovorus* HD100*.*

**Folic Acid (B9):** model=changeRxnBounds(model,'EX\_thf(e)',-0.1,'l')

**Pantotenate:** model=changeRxnBounds(model,'EX\_ptth(e)',-0.1,'l')

**Piridoxal phosphate:** model=changeRxnBounds(model,'EX\_pdx5p(e)',-0.1,'l')

**Biotine (B8):** model=changeRxnBounds(model,'EX\_btn(e)',-0.1,'l')

**Lipoate:** model=changeRxnBounds(model,'EX\_lipoate(e)',-0.1,'l')

Definition of *in silico* CAV medium to simulate the growth of BdQ10

In the following, a detailed *in silico* composition of the CAV medium used to verify the possible growth of *Bdellovibrio* cells in CAV medium axenically with *i*CH457 metabolic model, is described. The default Exchange reactions were constrained as follow

**Oxigen:** model=changeRxnBounds(model,'EX\_o2(e)',-10,'l')

**Amino acids**

The amount of each amino acid is select based on the experimental data obtained from the target analysis by GC-MS.

model=changeRxnBounds(model,'EX\_ala\_L(e)',-0.018,'l')

model=changeRxnBounds(model,'EX\_val\_L(e)',-0.011,'l')

model=changeRxnBounds(model,'EX\_leu\_L(e)',-0.011,'l')

model=changeRxnBounds(model,'EX\_ile\_L(e)',-0.01,'l')

model=changeRxnBounds(model,'EX\_pro\_L(e)',-0.004,'l')

model=changeRxnBounds(model,'EX\_gly(e)',-0.01,'l')

model=changeRxnBounds(model,'EX\_ser\_L(e)',-0.02,'l')

model=changeRxnBounds(model,'EX\_thr\_L(e)',-0.009,'l')

model=changeRxnBounds(model,'EX\_asp\_L(e)',-0.02,'l')

model=changeRxnBounds(model,'EX\_glu\_L(e)',0.012,'l')

model=changeRxnBounds(model,'EX\_phe\_L(e)',-0.0064,'l')

model=changeRxnBounds(model,'EX\_lys\_L(e)',-0.0032,'l')

model=changeRxnBounds(model,'EX\_arg\_L(e)',-0.0028,'l')

model=changeRxnBounds(model,'EX\_trp\_L(e)',-0.001,'l')

model=changeRxnBounds(model,'EX\_tyr\_L(e)',-0.00248,'l')

**Dipeptides**

Conditional essential genes found in Barabote et al., 2009.

model=changeRxnBounds(model,'EX\_ALAHIS',-0.0001,'l')

model=changeRxnBounds(model,'EX\_ALACYS',-0.0001,'l')

model=changeRxnBounds(model,'EX\_ALAMET',-0.0001,'l')

model=changeRxnBounds(model,'EX\_ALAASN',-0.0001,'l')

model=changeRxnBounds(model,'EX\_ALATYR',-0.01,'l')

model=changeRxnBounds(model,'EX\_ALATRP',-0.01,'l')

**Vitamins.** This medium only provides the auxotrophic metabolites of *B. bacteriovorus* HD100*.*

**Folic Acid (B9):** model=changeRxnBounds(model,'EX\_thf(e)',-0.1,'l')

**Pantotenate:** model=changeRxnBounds(model,'EX\_ptth(e)',-0.1,'l')

**Piridoxal phosphate:** model=changeRxnBounds(model,'EX\_pdx5p(e)',-0.1,'l')

**Biotine (B8):** model=changeRxnBounds(model,'EX\_btn(e)',-0.1,'l')

**Lipoate:** model=changeRxnBounds(model,'EX\_lipoate(e)',-0.1,'l')

**Other chemicals included in all the media based on Nogales et al., 2017**

|  |  |  |  |
| --- | --- | --- | --- |
| **Reaction Name** | **Reaction Description** | **Lower bond (mmol·gDW-1·h-1)** | **Lower bond (mmol·gDW-1·h-1)** |
| EX\_co2(e) | Exchange of CO2 | -30 | 1000 |
| EX\_fe2(e) | Exchange of Fe2 | -30 | 1000 |
| EX\_h(e) | Exchange of H | -50 | 1000 |
| EX\_h2o(e) | Exchange of H2O | -30 | 1000 |
| EX\_hco3(e) | Exchange of HCO3 | -30 | 1000 |
| EX\_na1(e) | Exchange Na | -30 | 1000 |
| EX\_nh4(e) | Exchange NH4 | -30 | 1000 |
| EX\_pi(e) | Exchange Pi | -30 | 1000 |
| EX\_so4(e) | Exchange SO4 | -30 | 1000 |