

Appendix A

Glossary

List of acronyms

| | |
|----------|--|
| BHI | Brain Heart Infusion |
| BioTeC | Bioprocess Technology and Control group |
| CFU | Colony Forming Unit |
| ESAB | <i>Escola Superior d'Agricultura de Barcelona</i> |
| FC | Flow Cytometer |
| FS | Forward Scattered light (flow cytometry) |
| IbM | Individual-based Modelling |
| IbMs | Individual-based Models |
| INDISIM | INDividual DIScrete SIMulation |
| MOSIMBIO | Modelling and Computer Simulation of Biological Systems group |
| MSE | Mean sum of Squared Errors |
| MSZ | Multisizer |
| NMTA | Nelder-Mead Threshold Accepting |
| PBC | Periodic Boundary Conditions |
| RBC | Red Blood Cells |
| SCT-UB | Scientific-Technical Services of the <i>Universitat de Barcelona</i> |
| SS | Side Scattered light (flow cytometry) |

| | |
|-----|---|
| SSE | Sum of Squared Errors |
| TIP | Thermodynamics of Irreversible Processes |
| TA | Threshold Accepting |
| UB | <i>Universitat de Barcelona</i> |
| UPC | <i>Universitat Politècnica de Catalunya</i> |

List of abbreviations

| | |
|-------------------------|-----------------------------|
| <i>beg</i> | beginning |
| <i>bib</i> | bibliography |
| <i>ENV</i> ⁻ | pre-inoculation environment |
| <i>ENV</i> ⁺ | present environment |
| <i>exp</i> | exponential phase |
| <i>inf</i> | inferior |
| <i>max</i> | maximum |
| <i>min</i> | minimum |
| <i>ref</i> | reference |
| <i>s.u.</i> | simulation units |
| <i>sup</i> | superior |
| X_0 | initial value of 'X' |
| X_f | final value of 'X' |

List of symbols

| | |
|------------------|---|
| λ | lag parameter |
| μ | growth rate |
| $D(t)$ | product distance |
| $D_{\bar{m}}(t)$ | mean mass distance |
| $D_{pk}(t)$ | mass distribution distance |
| m | bacterial individual mass |
| $\bar{m}(t)$ | bacterial mean mass of a culture |
| m_d | individual bacterial mass at division |
| m_R | individual mass to initiate reproduction cycle |
| $N(t)$ | cell density |
| $p_{k_m}(t)$ | instantaneous cell's biomass relative frequency |
| t_{FD} | time to the first division |
| t_G | generation time or doubling time |
| t_R | reproduction cycle duration |
| U | uptaken nutrient particles |

Chapter 1

| | |
|--------------------------|--|
| $\alpha(t)$ | adjustment function |
| τ_i | individual adjustment period |
| b, c, T_{min}, T_{max} | parameters of Equation 1.4 |
| $G(t)$ | growing fraction population |
| g_1, g_2 | mathematical attractors for defining lag parameter |
| k_n | constant for Equation 1.9 |
| M | cell biomass |
| $NG(t)$ | non-growing fraction population |
| $Q(t)$ | physiological |
| s | excess biomass per cell |
| s^* | total biomass per cell |
| s_{min} | minimum biomass per cell |
| t_{a_i} | individual adjustment period |
| t_{LAG_i} | individual lag time |
| t_{m_i} | individual generation time |

Chapter 2

| | |
|------------------------|---|
| ρ | parameter to fix an interval of the growth curve |
| σ | standard deviation |
| (x, y) | coordinates of a spatial cell |
| B | increase in bacterial biomass |
| b | parameter of Equation 2.2 |
| B_i | vector that describes a bacterium |
| c_s | concentration of substance s |
| d | mean distance between neighbouring cells |
| d_{max} | maximum movement radius |
| D_s | diffusion coefficient of a substance |
| E_{xy} | vector that describes a spatial cell |
| E_{enz} | enzyme particles in a bacterial cell |
| I | maintenance constant |
| I_{gen} | index to control the extracellular enzyme particles synthesis |
| J_s | flux of a substance between neighbouring cells |
| m_1, m_2 | individual bacterial masses after division |
| n_{enz} | enzyme particles synthesized by a bacterial cell |
| N_{mon} | number of monomers contained in a polymer |
| p_{mov} | probability for a bacteria to move |
| t_{enz} | time duration of extracellular enzyme particles |
| V_{enz} | enzyme synthesis rate per unit of mass and time step |
| Y | metabolic efficiency |
| Y_{enz} | energy cost of enzyme synthesis |
| Z_1, α, c, k, n | parameters of the uptake model |

Chapter 3

| | |
|-------------|--|
| \bar{E}_k | mean kinetic energy of the nutrient particles |
| r | radius of the accessible volume of nutrient particles around a bacterium |
| T | temperature |

Chapter 4

| | |
|--------------------|---|
| Δm | biomass interval to define the classes of biomass |
| λ_{pseudo} | apparent lag or pseudolag of a culture |
| λ_{real} | real lag of a culture |
| μ_B | total biomass growth rate |
| μ_N | cell density growth rate |
| ρ | parameter to fix an interval of the growth curve |
| τ_B, t_B | parameters to distinguish the balanced growth |
| a | parameter of Equation 4.10 |
| $B(t)$ | total biomass of a culture |
| m_i | class of biomass |
| $p(m_i)$ | biomass probability distribution of a bacterial culture |
| P_{EXP} | exponential phase |
| $P_{I(B)}$ | initial phase in total biomass |
| $P_{I(N)}$ | initial phase in cell density |
| $P_{T(B)}$ | transition phase in total biomass |
| $P_{T(N)}$ | transition phase in cell density |
| R | mean of duplications per hour of an individual cell |
| t_1, t_2 | temporal limits of transition phase in cell density |
| t_e, N_e | coordinates of an exponential point of the growth curve |
| Z, γ, β | parameters of Equation 4.4 |

Chapter 5

| | |
|------------------|---|
| d | equivalent diameter |
| $D_{\bar{d}}(t)$ | mean diameter distance |
| $D_{pk_d}(t)$ | diameter distribution distance |
| $D_d(t)$ | product distance |
| fs | forward scatter channels |
| N | number of channels |
| $p_{km}(t)$ | instantaneous cell's diameter relative frequency |
| R | mean of duplications per hour of an individual cell |
| ss | side scatter channels |

Chapter 6

| | |
|------------------------------|---|
| Γ, α, β | parameters to fix the thresholds (NMTA) |
| $\gamma, \rho, \chi, \sigma$ | coefficients of NMTA geometric operations |
| ξ | random simplex shift probability (NMTA) |
| ρ | radius of the trust region (NEWUOA) |
| $\hat{\rho}$ | re-scaled radius of the trust region (NEWUOA) |
| τ_r | threshold value for round r (NMTA) |
| A, B, C | parameters of a Weibull distribution |
| $C_{exp}(t)$ | experimentally measured cell concentration |
| $C_{sim}(t)$ | simulation output of cell concentration |
| $f(m; A, B)$ | Weibull distribution |
| $F(\vec{x})$ | objective function (NEWUOA) |
| g | number of generations per hour |
| m | number of interpolation points (NEWUOA) |
| n | total number of data points |
| n_{pi} | number of points to be tested for each parameter (grid search) |
| n_R | number of stepping rounds (NMTA) |
| $n_{S,r}$ | number of simplex steps in round r (NMTA) |
| p_i | parameters to be estimated |
| \hat{p}_i | re-scaled parameters to be estimated (NEWUOA) |
| $Q(\vec{x})$ | quadratic model (NEWUOA) |
| R_1, R_2, R_3 | number of evaluations of the objective function at each simplex vertex (NMTA) |
| t_s | time step |
| u_{max} | mean maximum uptake rate |
| V_d | bacterial volume at division |
| \vec{x} | vector with a combination of parameters to be estimated (NEWUOA) |
| Y | yield |