**A stochastic approach for modeling cell mass distribution of microalgae culture**

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**1.Introduction**

Microalgae are considered an important source to produce innovative foods, because they have several advantages in terms of the consumption of resources and energy when compared to traditional foods. Furthermore, they are rich in bioactive compounds, including pigments and polyunsaturated fatty acids [1]. The composition of microalgal biomass depends on the strain, the composition of the culture medium, and the operative conditions. Mathematically modeling microalgae growth can provide an effective tool for optimizing the biochemical process and maximize the production of specific high-value compounds. Several authors showed that the microalgae growth can be successfully described by the Droop model [2,3], that considers the dynamic behavior of biomass, substrate and quota. It has been observed that some bi-active compounds, e.g. astaxanthin, are produced by the microalgae during a particular phase of their growth, therefore the obtainment of cell-mass distribution can improve the value of the model. The cell population balance approach has recently been reported for microalgae in [4], showing a rather good correspondence with measurement data for extracellular substrate (i.e., nitrate) concentration, biomass concentration and cell–size distribution. The proposed approach led to good results but the modeling and identiﬁcation was associated to a high experimental and analytic eﬀort, the identiﬁcation process and the model analysis showed to be rather complex, and the resulting model was diﬃcult to be used for monitoring and control purposes. In this work, a different method based on Fokker-Planck equation is used to model the cell-size distribution.

**2. Methods**

Following the results reported in [5], the cell growth has been modelled by the following stochastic equation

$\frac{dm}{dt}=f\left(m,t\right)+g\left(m\right)η\left(t\right)=r m\left(1-\frac{m}{K}\right)+\sqrt{g(m)}η(t)$ (1)

where $m$ is the mass of a single cell, $r$ and $K$ are the parameters of the deterministic growth process and $\sqrt{g(m)}η(t)$ is the noise term, with $g(m)$ representing the diffusion term. It is assumed that

$E\left[η\left(t\right)\right]=0 $ $E\left[η\left(t\right)η\left(t'\right)\right]=δ\left(t-t^{'}\right)$ (2)

according to [5], the following law has been used for the noise term

$g\left(m\right)=\frac{q\_{v}}{2}m^{2}$ (3)

Eqs. (1) and (2) implies that the cell mass behaves as a random variable, which is characterized by a certain probability density function $ψ\left(m,t\right).$ The dynamic behavior of the distribution can be calculated by resorting to the Fokker-Planck equation in Stratonovich form (4)

$\frac{∂ψ}{∂t}=\frac{∂}{∂m}\left[\frac{q\_{v}}{2}m^{2}\frac{∂ψ}{∂x}-\left(f\left(m,t\right)-\frac{q\_{v}}{2}m\right)ψ\left(m,t\right)\right]$ (4)

along with the boundary and initial conditions

$\frac{q\_{v}}{2}m^{2}\frac{∂ψ}{∂x}-\left(f\left(m,t\right)-\frac{q\_{v}}{2}m\right)ψ\left(m,t\right)=0 at m=0$ $\frac{∂ψ}{∂t}=0 at m\rightarrow 0$ $ψ=ψ\_{0} at t=0$ (5)

**3. Results and discussion**

Model parameters [r,K,q/2] has been calculated using experimental data obtained during the growth of microalga *Chlamydomonas Reinhardtii.* Results are reported in Figure 1, where a good agreement is shown between experimental histogram and calculated cell-size density (CSD) function.

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Figure 1. Experimental histograms (grey) and calculated CSD (blue line) at different sampling time.

**4. Conclusions**

The comparison of the model predictions with the experimental measurement data shows that this approach provides a valid tool for approximating cell-mass distribution. It is worth to noting that the resulting model is considerably simpler than alternative cell population balance equations, that have been previously applied to model the time evolution of the process.

**References**

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