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Mathematical tranformation to faciliate the proper calculation and presentation of specific rates in cell culture

Mammalian cell culture automation relies on timely detection of cultural parameters, such as cell densities, metabolic concentrations as well as waste build-up, and a reliable algorithm for timely intervention to sustain cellular well-being and desired productivity. The conventional approach for calculating cell growth and metabolic rates is mostly time-based. However, if cell densities, metabolite concentrations and product titer are plotted against IVCC (Integral of Viable Cell Count) then the slopes would show their specific rates. The IVCC conversion can not only provide direct visual cues for the investigators but is also more accurate than the time-based analysis for specific rate computation since it is not affected by the fluctuations in cell viability during the cell culture batch. In this presentation, we will show how parameters such as glucose, lactate, glutamine and glutamate can be used to determine cell densities, viability and cell growth rate without counting cells, once the correlation for the cell line is established. We will also show that the IVCC approach can demonstrate distinct phase changes for cell growth, death and product formation which correspond to different metabolic phase changes for 12 individual CHO clones expressing the same therapeutic antibody investigated. In addition, the efficiency of cell making is shown to determine the maximal cell density and the duration of cell culture of the fed-batches. In conclusion, IVCC approach can be a key for cell culture automation which requires simplicity, sensitivity, accuracy and predictability.

Biography

Yung shyeng Tsao received his PhD from the University of Tennessee, specialized in Liposome and Membrane Technologies. He was a Post-doctoral Fellow in New York University, specialized in Membrane Trafficking and Protein Secretion Mechanisms. He joined Schering-Plough Research Institute Merck in 1988 and developed cell lines for gene therapy and recombinant protein production. He has published in the area of protein isolation and characterization, membrane biophysics and fusion mechanisms, liposome drug targeting, membrane trafficking, protein secretion and degradation mechanisms, animal cell culture media, serum-free virus production, aggregated cell monitoring, cell growth-protein productivity-metabolic modeling, cell culture miniaturization and automation, and transcriptome and integrative pathway analysis.

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