courseName

authorName

telegram: @authorName

Github: mainRepoLink

March 16, 2022

Contents

Part I

nameOfPart01

Chapter 1

Introduction

1.1 Transcriptomics

Transcriptome: collection of mRNA species/transcripts in a cell at a given time

    Microarrays can be used to measure levels of mRNA in a high-throughput fashion. Results of microarrays have to be normalized (Smyth & Speed, 2003) (Caddeo, Boffito, & Sartori, 2017)
(Devlin & Nagahama, 2002)

Part II

nameOfPart02

Chapter 2

chapterName

2.1   sectionName

References

Caddeo, S., Boffito, M., & Sartori, S. (2017). Tissue Engineering Approaches in the Design of Healthy and Pathological In Vitro Tissue Models. *Frontiers in Bioengineering and Biotechnology*, *5*, 40. doi: 10.3389/fbioe.2017.00040

Devlin, R. H., & Nagahama, Y. (2002). Sex determination and sex differentiation in fish: an overview of genetic, physiological, and environmental influences. *Aquaculture*, *208*(3-4), 191–364.

Smyth, G. K., & Speed, T. (2003, December). Normalization of cDNA microarray data. *Methods (San Diego, Calif.)*, *31*(4), 265–273. doi: 10.1016/s1046-2023(03)00155-5