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Convergence Medical Research using Bioinformatics

Recently, studies using bioinformatics has been actively performed in various fields, especially in the medical research. Data sharing and cooperation among experts in clinical medicine, bioinformatics, molecular biology, and engineering are necessary to successfully conduct convergence medical research. Efficient convergence research has the benefits of not only being able to find unmet needs of other fields, but also making high-quality results in a short period of time. In this study, I will explain the types and roles of data handled by bioinformatics in convergence medical research with some examples. The types of data mainly dealt with in bioinformatics are omics data (transcriptome, whole genome, epigenome, metagenome etc), image data (X-ray, CT, MRI, histology, bone scan etc), and text data (EMR, published data, health care data, health and nutrition survey etc). Informaticians use various data to develop potential biomarkers for diagnosis, treatment, and prognosis for specific diseases. In this way, I have improved the efficiency and success rate of co-work by using bioinformatics techniques. Therefore, collaboration of experts from various fields including bioinformatics is one of the best options to overcome the limitations of individual laboratories.

References

1. Role of PCK2 in the proliferation of vascular smooth muscle cells in neointimal hyperplasia. Int J Biol Sci 2022; 18(13):5154–5167.
2. Single-cell RNA sequencing demonstrates the molecular and cellular reprogramming of metastatic lung adenocarcinoma. Nat Commun. 2020 May 8;11(1):2285

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