

## "What is the scope of bioinformatics?" Do we really need to ask this?

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“What is the scope of bioinformatics?” This is the question which is most frequently asked by some students and scholars. The real question is do we really need to ask this? Bioinformatics is an interdisciplinary field including computer science, chemistry, mathematics, physics, and many disciplines. Bioinformatics is a fast emerging field which has been grown immensely in the last decade. There are more than a thousand databases and multiple bioinformatics tools/software available which are frequently used to extract or develop new information for further use. We are capable of visualizing the biological data easily, ease tedious tasks, develop advanced methods, study the phylogeny of organisms, solve essential problems, and so on. With the application of programming skills in bioinformatics, new innovations can be made easily.

Though there are a few limitations in bioinformatics such as lack of data connectivity, redundant data, accurate prediction of protein-protein interaction. These limitations can be overcome by developing and applying new methods and techniques. For example, a few years ago, bioNerDS [1], a recognition system for databases’ and software names have been developed which is capable of identifying mentions of named-entities in the literature. This is helpful in exploring various things in bioinformatics on a single platform.

Exploration is another aspect which is quite helpful in answering that question as exploration leads to learning which further leads to innovation. The things which exist now were non-existent once but the curiosity and exploration are the reasons for these realities. It is not about the scope, it’s about the possibilities and discovering new opportunities.

It is better to find solutions to the existing problems and overcoming the limitations either by utilizing the available resources or inventing new ones. That’s what science and research are all about.

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Please write to us at [info@bioinformaticreview.com](mailto:info@bioinformaticreview.com).

## References

1. Duck, G., Nenadic, G., Brass, A., Robertson, D. L., & Stevens, R. (2013). bioNerDS: exploring bioinformatics' database and software use through literature mining. *BMC bioinformatics*, 14(1), 194.

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