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Scientific software solution modelling using Butterfly model

Zeeshan Ahmed University of Wuerzburg, Germany

Scientific software solution development involves different steps requiring specific information to be gathered and implemented. A successful, comprehensive, flexible, futuristic and on demand, software development can only be achieved, if the system is properly designed, following the software engineering principles, modelling approaches and implementation life cycles. Most of the existing bioinformatics software modelling approaches suffer from design short comings though their impact depends on professional, user friendly, sustainable and high quality solution.

This abstract/presentation identifies and discusses how we can overcome the deficiencies during the effective software development life cycle execution, human computer interaction design and in choosing the technologies, especially when we are developing agile prototype solutions. Moreover it elaborates the concepts on the usage of existing solution's requirement analysis, design modelling, implementation, testing and deployment, and resolving conflicts between traditional, professional and scientific applications.

After the critical software engineering analysis, a new science oriented bioinformatics approach is proposed i.e. *Butterfly* model, towards an advanced, designed, mocked, flexible, reliable, futuristic, reusable scientific solutions implementation. The potential of newly proposed approach is strongly validated by modelling five (intelligent, statistical, real time embedded, distributed, mobile and data management) scientific software solutions e.g. DroLIGHT, Isotopo, Lipid-Pro, Ant App Database and LS-MIDA.

Conceptual hypothesis; with the use of *Butterfly* modelling concepts, not only the comprehensive software solution development will be achieved but it will also expedite the processes of application' usage, maintenance and future extensions. Moreover in return, it will not only save the time and efforts but will also help in efficient experimental data analysis, storage, manipulation, maintenance, sharing and reuse.

Biography

Zeeshan Ahmed works at the University of Wuerzburg with a strong interest in scientific software solution design and development. He is Post Doc. and Scientific Software Engineer and in the central computation support project of the collaborative research center SFB 1047 at the Biocenter, Department of Neurobiology and Genetics. He did PhD in Bioinformatics from the University of Wuerzburg Germany. His profile details are given at http://zeeshanahmed.info/

zeeshan.ahmed@uni-wuerzburg.de