

Biological process model and SoftGene: a novel software process model and a CASE tool

D A I P Fernando^{1*} and A S Karunananda²

^{1,2}Department of Mathematics and Computer Science, Open University, Nawala

Current software processes face high cost, scarcity of experts and failures leading to substantial losses, and also, lack a proper theoretical basis. As a solution, we have introduced Biological Process Model, for achieving a substantial automation using a knowledge-based approach. This model is based on three concepts, *Genes*, *Component Hierarchy*, and *Requirement Hierarchy* derived from biological systems.

The software analogy of a Gene has been proposed as encapsulation of knowledge to generate a cohesive set of program codes (which is defined as a *Component*) for meeting a specified user requirement. A Gene essentially contains a set of customizable program codes designed according to the generic nature of a set of user requirements. Given a specific requirement from this set, these codes are customized to generate a Component. In biological systems, its structural hierarchy of components, which implicates a corresponding requirement hierarchy, is generated using genetic information. Similarly, in our approach, given user requirements as a hierarchy corresponding Genes generates the entire system in a bottom-up approach, recursively by combining child components to form parent components.

Domains are analyzed to derive generic user requirements and they are engineered as building blocks of various complexities, which can be matched with specific user requirements so that they can be used as templates during requirement analysis. Furthermore, they pave the skeleton for preparing requirements as hierarchies. These generic user requirements are stored in a repository. Likewise, for each generic user requirements, a Gene is developed according to predetermined system architecture that can be viewed as a hierarchy of components, so that the would-be generated Component will fit in to a one of its location. Genes are also stored in a repository. This approach for automation was developed as a CASE tool, SoftGene based on an object-oriented framework, where those three concepts were implemented as classes