em 71 proteínas. Com base na estatística da rede, as seguintes proteínas conectoras foram selecionadas: CDH5 e NOS3, da "antiangiogênese"; CUL4A e CRBN da "ligação a Cereblon"; FGFR1, do "desenvolvimento de membros"; GSK3B, MAPK8 e NFKB1, do "estresse oxidativo"; CYP2C19 do "metabolismo"; TNF da "imunomodulação"; TBX5, SALL4, ESCO2, RECQL4 e RBM8A, das "fenocópias" e CTNNB1 como nó central da rede. A partir do estudo de Sievers, foram obtidos 415 TF degradados significativamente por Tal-CRBN, Len-CRBN ou Pom-CRBN. De acordo com o TF2DNA, 35/415 TF são reguladores dos genes codificantes das proteínas selecionadas na análise de redes. ZNF48 regula cinco proteínas: CTNNB1, FGFR1, NOS3, RBM8A e SALL4. A proteína FGFR1 é regulada por 11 TF (maior número obtido na análise), incluindo ZNF48 e ZNF84. O ZNF84 é o único dos 35 TF obtidos que é degradado pelos três medicamentos. Os resultados permitiram a identificação de dois TF, ZNF48 e ZNF84, como potenciais neosubstratos de Tal-CRBN. Há poucas informações sobre ontologias e vias de sinalização em que esses dois TF estão envolvidos. Mais estudos são necessários para entender o efeito desses TF nas proteínas sabidamente afetadas por talidomida, e como esses neosubstratos podem estar conectados às propriedades já bem estabelecidas desse medicamento.

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A FRAMEWORK FOR ARCHITECTURAL COMPONENTS UPDATES IN LARGE-SCALE HEALTHCARE SYSTEMS
ALAN BARONIO MENEGOTTO; CLAUDIO FERNANDO VAGHETI; DANIEL CERQUEIRA DEVILLA; GABRIEL ALABARSE HERNANDEZ; RENATO FALSARELLA MARTINS MALVEZZI
HCPA - Hospital de Clínicas de Porto Alegre

Introduction
Software architecture is the discipline within software engineering related to the project and design of the core components of a computer system. Enterprise software design often comprises reusing modular components to facilitate the development process.
During a software development process, errors can happen. Moreover, security breaches can be found, compromising all the technology infrastructure of a healthcare institution.
The core components of an enterprise system should be updated regularly to mitigate these points of failures and bring extra features for the development of healthcare software.
Since 2014, the HCPA software architecture team has been responsible for creating and maintaining the core components of the AGHUse, a large-scale Hospital Information System (HIS).
Objectives
The process of updating architectural components of the AGHUse ecosystem has been improving at each iteration over the years. Development frameworks are updated every six months at most, and major components such as the programming language version, application server or UI framework are updated yearly.
The expertise acquired by all the teams involved in the update process can be summarized in fixed steps, allowing the creation of a framework which other IT professionals can use during the update of fundamental components of large-scale healthcare systems.
The framework was created aiming to document these steps and share the HCPA knowledge.
Methods
- Knowledge gathering and summary;
- Framework design;
- Preliminary evaluation of the framework application.
Results
The framework is divided into six sequential steps, each one composed by subtasks which were removed from this document for brevity:
1) Component modification
2) Quality Assurance tests
3) System Analysts tests
4) Candidate-Release tests
5) Deploy in Production
6) Evaluate the dos and don'ts of the process
Conclusions
The framework described has been used in the last two major architectural components updates of the AGHUse ERP and brought benefits to the IT team such as the predictability of the update impact, minimum downtime, near-zero unknown situations and decreased number of bugs.
These benefits also have a direct impact on the ERP customers, healthcare professionals and patients, which uses a better and more secure version of the same software without even noticing.

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BIOLOGIA DE SISTEMAS COMO ABORDAGEM PARA SELEÇÃO DE GENES PARA A INVESTIGAÇÃO DE VIAS ENVOLVIDAS NAS MALFORMAÇÕES DA EMBRIOPATIA DA TALIDOMIDA
BRUNA DUARTE RENGEL; THAYNE WOYCINCK KOWALSKI; LUCAS ROSA FRAGA; FERNANDA SALES LUIZ VIANNA
UFRGS - Universidade Federal do Rio Grande do Sul

A embriopatia da talidomida (TE), conhecida por causar várias anomalias, tem entre seus principais fenótipos malformações de membros e coração. Os mecanismos moleculares da TE ainda não são totalmente elucidados. Um estudo recente