enzymes released by bacteria, called β-lactamases, which degrade the antibiotic molecules; (B) Reduced binding affinities between the antibiotics and receptors in the bacterial cells. These antibiotic resistance mechanisms are of great clinical concern as their development and spread across many species of bacteria has led to the erosion of the efficacy of many commonly prescribed antibiotics, in particular penicillin and its derivatives.

Tests were carried out to validate the Micro-Gen model by using kinetic parameters applicable to some common antibiotics (penicillin, ampicillin, and cephalothin) versus the clinically important multi-drug resistant bacterial strain methicillin-resistant *Staphylococcus aureus* (MRSA). The cellular and molecular parameters for this model were derived from the biological literature for three different strains of MRSA, and the model was used to predict the Minimum Inhibitory Concentration (MIC), which is a key clinical measure of antibiotic efficacy, of each antibiotic versus the three strains. The MIC of an antibiotic is the minimum effective dose of antibiotic that will succeed in inhibiting the growth of the bacterial colony. When the predicted MICs from the model were compared with experimentally derived MICs for MRSA, they were found to be in close quantitative agreement.

As such, the model represents a good tool for informing antibiotic treatment strategies since it can be used to investigate the principal parameters affecting antibiotic resistance in bacteria and relate this to key clinical indicators such as the MIC of a drug. There is a significant logistical burden associated with growing bacterial cultures and testing novel candidate drug compounds in the lab. However, the ability to simulate a wide variety of different conditions and parameters in a simulated environment could be used to inform rational drug design strategies.

In conclusion, Micro-Gen represents a robust tool for modelling the complex interactions of bacterial cells in colonies and their interactions with extra-cellular molecules such as antibiotics. In particular, the ability to investigate the antibiotic efficacy and predict an important clinical parameter such as the MIC using basic low-level cellular/molecular information represents a significant, novel contribution to the field.

Future work will include expanding the model to represent more complex, three-dimensional bacterial communities, such as biofilms, that form in nature. In these structured communities, dynamic community interactions take place between multiple species of bacteria forming a complex interdependent microbial ecosystem. The agent-based modelling approach is particularly suited for modelling highly heterogeneous and dynamic structures such as these.

**Web Services for Accessing Explicit State Space Verification Tools**

by María del Mar Gallardo, Christophe Joubert, Pedro Merino and David Sanán

Formal verification tools generally require users to deal with tedious and time-consuming installation, licensing issues, configuration, documentation, frequent updates and other hardware-related issues. This is the case even if all that is required is a quick check of a tool’s adequacy for solving specific a problem. A current joint effort inside the ERCIM Working Group on Formal Methods for Industrial Critical Systems (FMICS) is promoting the use of an electronic tool integration (ETI) platform that allows remote connection through Web services to widespread and numerous verification toolboxes, among them Construction and Analysis of Distributed Processes (CADP).

The purpose of the project is to integrate in a remote and simple way new research tools developed at the University of Málaga. This will allow the static analysis and model checking of C programs into CADP, a popular toolbox for the design of communication protocols and distributed systems. An unexpected result of this project was the development of a Web service that remotely executes any verification tool (of which there are more than 42) or case study (more than 95) of CADP. This research consists in an FMICS Working Group contribution to the Verified Software Initiative (VSI), and resulted from a strengthened cooperation between the FMICS-jETI development group (University of Potsdam and Dortmund, Germany - Tiziana Margaria and Christian Kubczak) and the FMSE group (University of Málaga, Spain - Maria del Mar Gallardo, Jesús Martínez, Pedro Merino, David Sanán, and Christophe Joubert, the latter being now at Technische Universität Valencia, Spain), in June 2006 at Málaga (Spain), June 2006 at IDPT’06 (San Diego, USA), November 2006 at ISOLA’06 (Paphos, Cyprus), and July 2007 at ICECCS’07 (Auckland, New Zealand). The research lines are also part of the Development of Automatic Techniques for Software Verification tasks of the SELF projects.

Our current research is working towards the direct connection of well-established verification toolboxes in a common environment, allowing easier access to efficient (unofficial/unreleased extensions of) verification tools and direct combinations of different formal technologies to solve a given problem. It is based on the FMICS-jETI platform for program verification, which is the new
Plug and Play with FMICS-jETI: Beyond Scripting and Coding

by Christian Kubczak, Tiziana Margaria, Ralf Nagel and Bernhard Steffen

The aim of new technology in software analysis is to save time and money and to help organizations and businesses carry out their core topics and processes more effectively. Whether compliance, governance, auditing, risk management or optimization, any theme that targets quality and efficiency in businesses and organizations relies on software and IT platforms to ensure a fast and accurate response. The FMICS-jETI platform makes this as easy as a plug-and-play solution.

The analysis of safety-critical and business-critical software and systems is the core topic of the ERCIM Working Group on Formal Methods for Industrial Critical Systems (FMICS). Accurate mathematical analysis of industrial systems is greatly supported and simplified with the help of computers. In spite of the use of advanced technology, extensive and error-prone software adaptations are required for the development of new programs and processes, and even the implementation of small changes and adaptations. This mandates extensive validation and testing which must be delegated to programming experts: a costly detour in terms of precious time and absorbed capacity, and a threat to the fast responses demanded by market competitiveness.

FMICS promotes the development and the fast industrial adoption of precise and efficient automated analysis methods. These can help businesses govern their software, harness their risks, and in this way improve their software products. But once the analysis algorithms and tools are there, how can they best be used, customized or combined? Efficient, targeted analyses nearly always require complex combinations of heterogeneous algorithms and transformations, and without a community that shares its knowledge and tools as services; without a repository that knows where such algorithms are available and what capabilities they offer; without a platform that supports the simple, intuitive composition of problem-specific analyses that are immediately executable; the potential user is lost.

The FMICS-jETI framework developed at the Chair of Service and Software