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D6.4 Report on selected emerging use cases for existing solutions

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Lead beneficiary for this deliverable: *USFD*

Contributors: UPF, UvA, UNIGE, LTG

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CO	Confidential, only for members of the consortium (including the Commission Services)	
CI	Classified, as referred to in Commission Decision 2001/844/EC	

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1 Version Log

Version	Date	Released by	Nature of Change
V1.0	15/07/2018	Marco Viceconti	First Draft
V1.2	03/08/2018	Marco Viceconti	Final version before revision
V1.3	15/09/2018	Marco Viceconti	Pre-final version, to address internal reviewer comments
V1.4	15/09/2018	Marco Viceconti	Pre-final version, revised by all contributors
V1.5	27/09/2018	Marco Viceconti	Final version, revised by all coordinator office

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3 Definition and Acronyms

Acronyms	Definitions
BME	Budapest University of Technology and Economics
CFD	Computational Fluid Dynamics
CoE	Centre of Excellence
CT (mircoCT/CT scan	Computerised Tomography
DEM	Digital Elevation Model
DICOM	Digital Imaging & Communications in Medicine
DPS	Data Publication Suite
EM	Electromagnetic
EPCC	Edinburgh Parallel Computing Centre
FEM/FEA	Finite Element Method/Analysis
GEC	Genetic Engineering of Cells
GPU	Graphics Processing Units
HPC	High Performance Computing
HRpQCT	High Resolution Peripheral Quantitative Computed Tomography
HTBAC	High Throughput Binding Affinity Calculator
LBM	Lattice Boltzmann Method
LBS	Language for Biochemical Systems
LHHM	Living Heart Human Model
LRZ	Leibniz Rechenzentrum
MPI	Message Passing Interface
MUSCLE	Multiscale Simulation Coupling Library & Environment
NA	Not Applicable
NTU	Nanhang Technological University
PaaS	Platform-as-a-Service
PSNC	Poznan Supercomputing and Networking Center
RF	Radio Frequency
SAR	Specific Absorption Rate
STHFTSME	Sheffield Teaching Hospital NHS Foundation TrustSmall and Medium Enterprises

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STL	Standard Template Library
UCL	University College London
UEDIN	University of Edinburgh
UNIGE	University of Geneva
UOXF	University of Oxford
UPF	Universitat Pompeu Fabra
CBMUSFD	CompBioMedUniversity of Sheffield
UvA	University of Amsterdam
VPHWP	Virtual Physiological HumanWork Package
VPH-HFPM	VPH-Hypermodelling Framework Project Month

4 Executive Summary

The purpose of this deliverable is to update the description of existing end-user applications provided in deliverable D6.1, in order to include the further developments and implementations made up to M24 in the project. The deliverable provides a taxonomy used to annotate Computational Medicine end-user solutions; the annotation includes a layperson description, a technical description, the access modality, the HPC systems that can run it, the version, the type of end-users, etc. Using this set of information, the deliverable then described the 23 end-user solutions that are available to date through the CompBioMed Centre of Excellence.

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5 Introduction

Deliverable D6.4 provides a report on selected emerging use cases for existing solutions. While D6.1 reported on the solutions that were already available at the project's outset, this report describes the end-user solutions available by M24, including those developed/exposed in the meanwhile. A further update will be provided at the end of the project (M36), in D6.6. The activity reported here is relative to work being done in WP6, in particular task T6.2:

Task 6.2: Emerging Use Cases for Existing Solutions (M12-M36) [Deep Track]

Leader: USFD (6 PM), Partners: UPF (5 PM), UvA (5), UNIGE (5), LTG (5)

In this task we seek to use existing tools, services and datasets for new purposes and applications. We will initiate this task in year 2, once the existing solutions have been made readily exposed as part of task 6.1. We will formulate a set of emerging use cases for existing solutions, and work on making these use cases fully functional using high-end computing and data service infrastructures. We will also explore how the Data Publication Suite (DPS) technology STHFT developed as part of the VPH-Share project can help in servicing research hospitals. Using the VPH-HF execution environment, or any other middleware that become available on the CoE infrastructure, we will expose new simulation workflows useful for academic, industrial or clinical research. Tentatively, USFD will serve as application expert for neuro-musculoskeletal, UvA and USFD for cardiovascular, and UCL and UPF for molecularly-based problems. But this separation will not be rigid: all domain experts in the consortium will be involved case-by-case depending on the expertise a new use case requires; for each, a small workgroup of specialists will be formed, who will provide the primary interface to the end users during service activation. As these new end-user solutions emerge, the public document will be updated again at M24 (D6.2.1) and M36 (D6.2.2).

It should be noted that due to a clerical error D6.4 was marked as D.6.2.1 in the task description, whereas D6.6 was marked as D.6.2. Hereinafter we shall refer to this deliverable with the correct numbering, D6.4.

As D6.4 and D6.6 are updates to D6.1, one could present only changes since the last update. However, we think it is more useful, since these are public deliverables, that each provides the complete picture of all end-user solutions, and thus not only updates the previous deliverable but also replaces it.

Similarly, in D6.1 there was a first attempt to taxonomise the end-user solutions; this work has been further extended in the meanwhile, and it is now being used to monitor all developments. Thus, even if it is a partial repetition of what was reported in D6.1, we think it is less confusing to present it here in its extended version, which is now being used.

The new taxonomy has been used to provide a coherent description of the 23 solutions currently supported by the CompBioMed Centre of Excellence. While we tried to be as consistent as possible, each developer provided the information that they thought most useful at this moment in time, given the specific status of their solution. Also, different developers have more or less detailed tracking of

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who uses their solutions, and for-profit organisations may consider part of this information confidential. As a result, there is an unavoidable heterogeneity in the information provided for each solution, especially under "Current Users".

6 Taxonomy of end-user solutions

6.1 Who are the users?

The top level of our tentative taxonomy is quite simple: the VPH Institute has proposed that all Computational Medicine applications can be divided by type of end user:

- Digital Patient: these are all predictive medicine solutions that are used by **medical professionals** to do clinical research or to support decisions towards an individual patient; these include diagnostic technologies, prognostic / risk assessment technologies, treatment planning technologies, etc.
- *In Silico* Clinical Trials: these are all predictive solutions using individualised computer simulation used by **biomedical companies, clinical research organisations, and regulators** in the discovery, development, or regulatory evaluation of a medicinal product, medical device, or medical intervention, both pre-clinical and clinical.
- Personal Health Forecasting: these are all predictive medicine solutions that are used by the **individual citizens/patients** in their daily living to monitor their health status and self-manage their chronic condition, alone or in collaboration with remote medical professionals.

From these three macro-applications, we can derive a number of User Scenarios, that have emerged so far:

- Non-clinical research: all research on the development of computational medicine models which advances the basic science of medicine, as well as computational medicine in support of fundamental research in biology, physiology, biochemistry, and biophysics.
- Clinical research: computational medicine technologies used to refine and empower clinical research, disease mechanisms, observational studies, intervention efficacy assessment, etc.
- Clinical decision support: use of patient-specific models to support the clinical decision on diagnosis, prognosis, or treatment.
- Drug discovery: model mechanisms of disease, support for the discovery of potential druggable targets, support for the elucidation of the mechanism of action.
- Design & optimisation: support for all biomedical products (drugs, devices, combinatory, biological), the design and the optimisation in term of safety, efficacy, synthesis/manufacturability, etc.
- *In silico* preclinical trials: use of individualised computer simulation in the regulatory pre-clinical evaluation of any biomedical product; models can reduce or replace the use of bench, in vitro, or

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ex vivo tests; they can also be used to reduce, refine, and partially replace animal experimentation (non-animal technologies).

- *In silico* clinical trials: use of individualised computer simulation in the regulatory clinical evaluation of any biomedical product. Models can reduce the number of patients involved, or the duration of a clinical trial, or mitigate the risks involved. Models can also be used to augment clinical trials where conventional approaches are impossible, i.e. in rare diseases.
- Personal Health Forecasting: predictive medicine solutions that are used to advise or monitor individual citizens/patients.

6.2 Why use HPC?

Hereinafter we will use the term High-Performance Computing (HPC) in a relatively loose sense, indicating anything that accelerates the solution of predictive models by use of computational resources that go beyond the desktop. This may involve classic HPC, Exascale systems, Cloud computing, High-throughput Computing, etc.

In our exploration, we have identified a number of reasons why Computational Medicine users need to scale-up to HPC:

- Run full order model to:
    - Solve unreducible model
    - Validate reduced-order model
- Scale full order model to:
    - Test convergence
    - Model larger space-time regions
    - Include more detailed physics, chemistry, biology
- Run model repeatedly to:
    - Do sensitivity analysis and uncertainty quantification
    - Train surrogate model
    - Explore parameter spaces
- Combinatory explosion in:
    - Orchestrated composite models (including stochastic multiscale)
    - Strongly coupled models
- Run model urgently to:
    - Provide time-constrained clinical decision support

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6.3 Who does what?

If we combine these user motivations with the use case scenarios above, not all possible combinations are relevant. The result is represented in the table below. It should be recognised that this is largely speculative, and based on the collective experience of what it is a very young sector; we cannot exclude that particular additional use motivations, use scenarios, or combinations of the two that we have now excluded might turn out to be relevant in the future. Until then, they provide a useful starting point to orient prospective users on which problems we can help them with.

	Solve unreducible model	Validate reduced-order model	Test model convergence	Larger space-time regions	Do uncertainty quantification	Inform surrogate model	Multiscale models	Strongly coupled models
Non-clinical research	X	X	X	X	X	X	X	X
Clinical research	X	--	--	X	X	--	X	X
Clinical decision support	--	--	--	--	X	X	X	X
Drug discovery	--	--	--	X	X	--	X	X
Design & optimisation	--	--	--	X	X	X	X	X
In silico preclinical trial	--	--	--	X	X	X	X	X
In silico clinical trial	--	--	--	X	X	--	X	X
Personal Health Forecasting	--	--	--	--	X	X	--	--

6.4 Taxonomy of Computational Medicine solutions

Based on the concepts exposed above, each solution is annotated with the following information:

Field	Tab	Explanation	Values
Name	Solutions	Short acronym used as unique identifier in all communications to refer to this end-user solution	
Layperson Description	Solutions	Full name and layperson description of the solution from an end-user point of view	
Technical description	Solutions	Technical description of the solution, including key information on solvers, etc.	
Access mode	Solutions	Type of access to the solution offered to end-users: Source indicates Open or licensed access to the source code, via GitHub or similar; Direct indicates direct access to all end-users with an account on the target HPC system; Service indicate and end-user interface that has an HPC backend; Indirect indicates access via consulting service, typically, the user sends the data and gets back the solution	Source, Direct, Service, Indirect
HPC system	Solutions	List of all HPC systems available in CompBioMed that can be used to access the solution	
Version	Solutions	Version of the solution, and/or of the underlying solvers; multiple versions can be listed if their features of HPC systems availability differs	

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End-users	Solutions	List end-users that are already using the solution; for each user listed here there should be a match in the Needs tab	
Web site	Solutions	URL to access the solution, or a description of the solution	
Provider	Solutions	Acronym of the partner organisation that provides this solution	
Contact email	Solutions	e-mail of the person(s) to be contacted for more information or access to the solution	

7 Cardiovascular solutions

7.1 Alya

Perform Cardiac Computational Mechanics simulations, from tissue to organ level. FEM-based electro-mechanical coupling solver, specifically designed for the efficient use of supercomputing resources. The contact is mariano.vazquez@bsc.es.

Provider: BSC

Current users: 40 internal and 40 external users

Access mode: Direct

URL: https://www.bsc.es/research-and-development/software-and-apps/software-list/alya

Use scenario: Non-clinical research; Clinical research; Clinical decision support; Design & optimisation for medical devices; In silico clinical trial.

HPC Systems: MareNostrum, Archer, Cartesius

HPC motivation: Solve unreducible model; Multiscale model; Strongly coupled multiphyisics model.

7.2 HemeLB

This code simulates the blood flow through a stent (or other flow diverting device) inserted in a patient's brain. The aim is to discover how different stent designs (surface patterns) affect the stress the blood applies to the blood vessel, in particular in the region of the aneurysm being treated. The pipeline also allows the motion of magnetically steered particles, for example coated with drugs, to be simulated and estimates made as to where they might statistically end up. More technically, the pipeline takes as input an STL file of the surface geometry of the patient, generally obtained via segmentation of DICOM images from a CT-scan. Also required is the (peak) velocity-time profile of fluid flow at each of the inlets to the simulated region. If inserting a stent, the start and end points of the stent in the vessel must be specified, as well as an image file containing a black and white representation of the surface pattern (black signifying 'solid'). The HemeLB setup tool voxelises the

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geometry bounded by the input STL at the given resolution, and HemeLB (lattice-Boltzmann CFD solver) then simulates the fluid flow within that geometry, using the given velocity-time profiles for each inlet. Once complete, the simulation output is analysed using the hemeXtract utility, which can produce images of cross-sectional flow, or 3D shots of wall shear stress distribution in the geometry using ParaView visualisation software. The contact is robin.richardson@ucl.ac.uk.

Provider:	UCL
Current users:	40 users (mostly academia)
Access mode:	Direct
URL:	https://github.com/UCL/hemelb
Use scenario:	Open Source software used primarily in academia. Clinical research; Clinical decision support; In silico clinical trial.
HPC Systems:	EPCC ARCHER, LRZ SuperMUC, PSNC Prometheus
HPC motivation:	Solve unreducible model.

7.3 PolNet

PolNet is a software tool for the computer simulation of blood flow in realistic microvascular networks imaged with a wide variety of microscopy and clinical imaging techniques. To date, PolNet has contributed to: a) uncovering the relationship between blood flow and blood vessel biology and its importance for correct vascularisation of tissues, and b) developing ways of predicting retinal vascular damage in diabetic retinopathy patients. PolNet facilitates the adoption of cutting-edge computer simulation technology by non-experts in the Biosciences. PolNet provides a complete workflow for image processing, three-dimensional vascular network reconstruction, and blood flow simulation with the HemeLB software. In addition, it provides tools for studying the relationship between the flow simulated and cellular/molecular readouts quantified in the same images. To date, PolNet has contributed to establishing the relationship between blood flow and endothelial cell polarisation and migration during vascular development. In addition, PolNet is being used to develop novel methods for the prediction of sight-threatening complications in diabetic retinopathy. PolNet uses the Docker platform to facilitate deployment in experimental biology laboratories and hospitals. PolNet allows execution of HemeLB simulations in both commodity software and High Performance Computing resources. Ongoing work is aimed at enabling HemeLB execution in Cloud resources. The contact is miguel.bernabeu@ed.ac.uk.

Provider:	UEDIN
Current users:	Computational scientists, experimental biologists, clinicians
Access mode:	Source
URL:	https://github.com/mobernabeu/polnet

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Use scenario: Non-clinical research; Clinical research; Clinical decision support

HPC Systems: ARCHER

HPC motivation: Solve unreducible model

7.4 Flow Diverter Simulator

This solution, currently in its final stage of development, uses Palabos to provide a vertical solution for the pre-operative planning for the insertion of flow diverters. CT scan images of blood vessels with aneurysms or other anomalies are converted into an LBM model. Different types of flow diverters are numerically inserted to test their impact on the blood flow pattern. Simulation output includes wall shear stress distribution in the aneurysm to predict the rate of blood clotting. The contact is jonas.latt@unige.ch.

Provider: UNIGE

Current users: NA

Access mode: Source

URL: NA

Use scenario: Clinical research, Clinical decision support, In silico clinical trial.

HPC Systems: BAOBAB, CADMOS

HPC motivation: Solve unreducible model; Multiscale model; Strongly coupled model.

7.5 Palabos

Code to simulate blood flow and more in patient specific geometries. Lattice Boltzmann solver, open source and massively parallel. Comes with specific features to deal with biomedical problems, reading medical images, etc. The contact is jonas.latt@unige.ch.

Provider: UNIGE

Current users: NA

Access mode: source

URL: http://www.palabos.org

Use scenario: Non-clinical research; Clinical research; Clinical decision support; Drug discovery; Design & optimisation; In silico preclinical trial; In silico clinical trial; Personal Health Forecasting

HPC Systems: BAOBAB, CADMOS, ARCHER, MARE NOSTRUM, ARCHIMEDES

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HPC motivation: Solve unreducible model, Validate reduced-order model, Test model convergence, Larger space-time regions, Uncertainty quantification, Inform surrogate model, Multiscale models, Strongly coupled models.

7.6 OpenBF

Calculate pulse waveform transmission and reflection in the cardiovascular system. One-dimensional finite volume solver for 1D non homogeneous hyperbolic equations describing pulsatile blood flow in network of elastic vessels. The contact is a.melis@sheffield.ac.uk.

Provider: USFD

Current users: USFD

Access mode: Source

URL: https://INSIGNEO.github.io/openBF

Use scenario: Non-clinical research; Clinical research; Clinical decision support; *In silico* preclinical trial; *In silico* clinical trial

HPC Systems: ShARC, SURFSara cloud, Cartesius

HPC motivation: Uncertainty quantification, Inform surrogate model, Multiscale models, Strongly coupled models.

7.7 HemoCell

High-performance library to simulate the transport properties of dense cellular suspensions, such as blood. It contains validated material models for red blood cells and additional support for further cell types (white blood cells, platelets). The blood plasma is represented as a continuous fluid simulated with an open-source LBM solver (Palabos, see 7.5). The cells are represented as DEM membranes coupled to the plasma flow through a tested in-house immersed-boundary implementation. HemoCell is computationally capable of handling a large domain size with high number of cells (> 10^4-10^6 cells). The contact is g.zavodszky@uva.nl.

Provider: UvA

Current users: UvA, NTU, BME, University of Queensland, Brisbane

Access mode: Source

URL: http://www.hemocell.eu

Use scenario: Clinical research, Clinical decision support, In silico clinical trial.

HPC Systems: Cartesius, Lisa, SuperMUC, MareNostrum, Eagle (PSNC Poland), Sanam (KACST), Lomonosov (Moscow).

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HPC motivation: Solve unreducible model; Multiscale model; Strongly coupled model.

7.8 Virtual Assay

Predicts a variety of responses of the human cardiac behaviour under pharmacological drugs to help with drug safety and efficacy. Virtual Assay starts with well-understood human cellular biology models and modulates the variables to generate a range, or population, of models, which will respond differently to the same inputs. These populations are then calibrated against experimental data, retaining only those models in Calibrated Model Populations range with experimental observations. Once calibrated, these populations can be used to analyse the effects of different pharmaceutical agents on cellular response at the population level. The contact is elisa.passini@cs.ox.ac.uk.

Provider: UOXF

Current users: Industry

Access mode: Source, Indirect

URL: http://www.cs.ox.ac.uk/ccs/virtual-assay

Use scenario: Non-clinical Research, In silico preclinical trial

HPC Systems: NA

HPC motivation: Multiscale models.

7.9 SIMULIA LHHM

The SIMULIA Living Heart Human Model (LHHM) is a high-fidelity multi-physics model of a healthy, 4-chamber adult human heart and proximal vasculature. The LHHM was developed within The Living Heart Project, a translational initiative to advance the use of simulation in the delivery of safe and effective cardiovascular devices and clinical treatments. This is a finite element model of a human heart backed by the power of Abaqus within the SIMULIA Realistic Simulation software suite. The response of the LHHM is governed by realistic electrical, structural and fluid-flow physics. The model comprises a ready-to-execute dynamic, electro-mechanical simulation; refined geometry; a blood flow model, and a complete characterisation of cardiac tissues including passive and active behaviours, its fibrous nature and the electrical pathways. The contacts are clint.davies-taylor@3ds.com; steve.levine@3ds.com.

Provider: Dassault Systemes

Current users: Academia, Industry, Clinicians and Regulatory Authorities

Access mode: Source, Direct

URL: https://www.3ds.com/products-services/simulia/solutions/life-sciences/living-heart-human-model/

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Use scenario:	Clinical Research; Non-clinical Research; Clinical decision support; in-silico clinical trials
HPC Systems:	ARCHER, ShARC clusters
HPC motivation:	Solve unreducible model; Multiscale model; Strongly coupled multiphyisics model.

8 Molecular medicine solutions

8.1 ACEMD

Molecular Dynamics simulations software that allows to simulate molecular biosystems at the atomic level. ACEMD is a production level molecular dynamics software specially optimized to run on NVIDIA graphics processing units (GPUs) and it is one of the world's fastest molecular dynamics engines. The contact is compbiomed@acellera.com.

Provider:	Acellera
Current users:	744 (~15% industry)
Access mode:	Download
URL:	https://www.acellera.com/products/molecular-dynamics-software-gpu-acemd/
Use scenario:	Non-clinical research; Drug discovery; Design & optimisation; In silico preclinical trial
HPC Systems:	Clusters, AWS, GPUGRID
HPC motivation:	Solve unreducible model.

8.2 HTMD

Programmable environment to prepare, execute, visualize and analyse Molecular Dynamic simulations. Python-based programmable environment to perform system preparation and building, execution of simulations with different MD codes using adaptive sampling schemes and generate Markov State models to analyse simulations. The contact is compbiomed@acellera.com.

Provider:	Acellera
Current users:	500 registered academic users; 5 commercial users
Access mode:	Source
URL:	https://www.acellera.com/products/high-throughput-molecular-dynamics/
Use scenario:	Non-clinical research; Drug Discovery; Design & optimisation.

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HPC Systems: Clusters, AWS

HPC motivation: Solve unreducible model; Do uncertainty quantification.

8.3 Playmolecule

Intuitive platform to access a diverse set of web applications for molecular discovery. Repository of free best-in-kind applications with a diverse set of solutions like molecular predictors and modelling tools. The contact is compbiomed@acellera.com.

Provider: Acellera

Current users: 180 registered users; 13% from industry; >8.000 sessions

Access mode: Service

URL: http://playmolecule.org/

Use scenario: Non-clinical research; Drug discovery; Design & optimisation.

HPC Systems: GPUGRID, AWS

HPC motivation: Solve unreducible model; Do uncertainty quantification.

8.4 BAC

Workflow tool that runs and analyses simulations designed to assess how well drugs bind to their target proteins and the impact of changes to those proteins. A collection of scripts which wrap around common molecular dynamics codes to facilitate free energy calculations. Use of ensemble simulations to robust, accurate and precise free energy computations from both alchemical and end-point analysis methodologies. EnsembleMD are commercially developing user friendly interfaces to replace existing prototypes produced at UCL. The contact is dave.wright@ucl.ac.uk.

Provider: UCL and EnsembleMD

Current users: UCL, GSK, Janssen

Access mode: Service (Source available to academic collaborators only at present)

URL: No current website - DNAnexus app available only to UCL/GSK at present

Use scenario: Non-clinical research; Drug discovery; Design & optimization.

HPC Systems: DNAnexus, AWS, Azure (academic collaborators use multiple resources including ARCHER and Cartesius within CompBioMed)

HPC motivation: Solve unreducible model; performs uncertainty quantification.

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8.5 Antibiotic Resistance

The Fowler Lab has developed a computational techniques, based on GROMACS, to evaluate the potential antibiotic resistance of various bacterial strains mutations. The contact is philip.fowler@ndm.ox.ac.uk.

Provider:	UOXF
Current users:	John Radcliffe Hospital
Access mode:	Service
URL:	http://fowlerlab.org/
Use scenario:	Clinical research
HPC Systems:	ARCHER
HPC motivation:	Solve unreducible model.

8.6 Visual GEC

A software tool for designing engineered cells and simulating biochemical interactions. The Genetic Engineering of Cells (GEC) software, developed by the Biological Computation team at Microsoft Research (Cambridge, UK), is a modelling tool that can be used to design and simulate synthetic genetic circuits. At the core is a domain-specific programming language for biochemical systems (LBS), originally developed at the University of Edinburgh. The tool supports stochastic and deterministic simulation of the temporal dynamics of chemical reaction networks, but also spatio-temporal dynamics via reaction-diffusion equations. Parameter inference can also be performed using Metropolis-Hastings Markov chain Monte Carlo with time-series data. The contact is ndalchau@microsoft.com.

Provider:	Microsoft
Current users:	Not tracked
Access mode:	Direct
URL:	https://www.microsoft.com/en-us/research/project/genetic-engineering-of-living-cells/
Use scenario:	Non-clinical research
HPC Systems:	Azure
HPC motivation:	Solve unreducible model.

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8.7 HTBAC

High throughput binding affinity calculator (HTBAC): scalable solution for adaptive personalised drug discovery. High level python object abstractions for defining simulations, physical systems and ensemble-based free energy protocols. The Runner class as part of the HTBAC abstraction uses underlying building blocks middleware developed by the RADICAL team to create and execute multiple concurrent executions of protocols on supercomputing cyberinfrastructures while abstracting and handling execution management, and data transfer. The contact is jdakka@scarletmail.rutgers.edu, kristof.farkas-pall.14@ucl.ac.uk.

Provider:	UCL and Rutgers
Current users:	UCL
Access mode:	Source
URL:	https://github.com/radical-cybertools/htbac
Use scenario:	Drug discovery
HPC Systems:	NCSA-Blue Waters, ORNL-Titan
HPC motivation:	Test model convergence.

8.8 DNAnexus

A data agnostic platform which allows one to store, manage, analyse and share data. DNAnexsus is a cloud-based Platform-as-a-Service (PaaS) which supports the ingestion of any type of data and any type of Linux-based software (your own, commercial or open-source) for the analysis of said data. Most of the current applications are in the genomics space but do include a few in the Computational Chemistry space. The contact is info@dnanexus.com.

Provider:	DNAnexus
Current users:	NA
Access mode:	Source
URL:	www.dnanexus.com
Use scenario:	Non-clinical research; Clinical research; Drug discovery
HPC Systems:	Cloud-based
HPC motivation:	NA

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9 Neuromusculoskeletal solutions

9.1 Vertebroplasty Simulator

Provides patient-specific numerical simulation for medical procedures. Currently covered procedures are (1) the injection of cement into a vertebral bone and (2) insertion of a flow diverter into an artery. The numerical tool reads patient-specific data, including the geometry of a vertebral bone obtained from a Micro CT Scan, or the geometry of an artery section and flow diverter. For vertebroplasty, cement injection is simulated efficiently with help from a free-surface model, and is represented at pore scale without Darcy-type continuum model. For insertion of flow diverters, the pulsatile blood flow is computed over several pulsations. The flow diverter is fully resolved. The simulated data can be post-processed with Paraview, and provides detailed insights into flow mechanical values like shearing forces on arterial walls, which help medical decision making. The tool uses a lattice-Boltzmann model is massively parallel. The simulations run on a high resolution. They require the usage of a large parallel computer with at least 100 cores, and require several hours to several days to complete. The contact is jonas.latt@unige.ch.

Provider:	UNIGE
Current users:	NA
Access mode:	Source
URL:	NA
Use scenario:	Clinical research, Clinical decision support, In silico clinical trial.
HPC Systems:	BAOBAB, CADMOS
HPC motivation:	Solve unreducible model; Multiscale model; Strongly coupled model.

9.2 CT2S

Predict the strength of a patient's bone from a CT scan of that bone. Stochastic Finite element Analysis of subject-specific model generated from CT data. The contact is ct2s-support@insigneo.org.

Provider:	USFD
Current users:	STHFT
Access mode:	Service
URL:	https://ct2s.insigneo.org
Use scenario:	Clinical research; Clinical decision support; In silico clinical trial
HPC Systems:	ShARC
HPC motivation:	Uncertainty quantification; Multiscale model.

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9.3 Bone Tissue Suit

Calculate displacement field in bone tissue specimens under axial compression by means of finite element analysis. A 3D cartesian mesh is obtained from microCT images of the bone specimen. The mesh is used to perform the FEA. The contact is phil.tooley@sheffield.ac.uk.

Provider:	USFD
Current users:	USFD
Access mode:	Source
URL:	TBA
Use scenario:	Non-clinical research
HPC Systems:	ShARC
HPC motivation:	Solve unreducible model.

9.4 XCT2FE

This service predicts stiffness and strength of the distal humerus or of the distal tibia from High Resolution peripheral Computed Tomography images. Stochastic Finite element Analysis of subject-specific model generated from High Resolution Peripheral Quantitative Computed Tomography (HRpQCT) data. The contact is hrpqct@sheffield.ac.uk.

Provider:	USFD
Current users:	USFD
Access mode:	Service
URL:	https://xct2fe.insigneo.org/
Use scenario:	Clinical research; Clinical decision support; In silico clinical trial
HPC Systems:	ShARC
HPC motivation:	Solve unreducible model.

10 Other solutions

10.1 MuscleHPC

Middleware to set up a pipeline between numerical solvers for biomedical problems. The MUSCLE toolkit (Multiscale Simulation Coupling Library and Environment) consists of Java and C++ libraries

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which facilitate the implementation of coupled multiscale applications. MUSCLE-HPC uses MPI communication interfaces to couple diverse codes. It provides an MPI native interface for C/C++ and the concept can also be applied to other languages which implement the MPI-2.2 features, including Fortran and Python (the current API is developed and tested using C++ language). The contact is jonas.latt@unige.ch.

Provider:	UNIGE
Current users:	NA
Access mode:	Source
URL:	https://gitlab.com/benbelga/muscleHPC
Use scenario:	Non-clinical research; Clinical research; Clinical decision support; Drug discovery; Design & optimisation; In silico preclinical trial; In silico clinical trial; Personal Health Forecasting
HPC Systems:	NA
HPC motivation:	Solve unreducible model, Validate reduced-order model, Test model convergence, Larger space-time regions, Uncertainty quantification, Inform surrogate model, Multiscale models, Strongly coupled models.

10.2 pFIRE

Image Registration Code, used to evaluate the difference between a pair of image and express them as a mapping field. This allows measurement of e.g changes to organs over time, or how a bone changes shape when force is applied. Parallel Elastic Image Registration based on the method of Barber and Hose (https://doi.org/10.1080/03091900412331289889). The Dask framework (flexible library for parallel computing in Python) is used to distribute the problem over many nodes to allow registration of multi-gigabyte to terabyte images. Out-of-core execution is also supported to facilitate registration of large images on memory limited machines. The contact is phil.tooley@sheffield.ac.uk.

Provider:	USFD
Current users:	USFD
Access mode:	Source
URL:	TBA
Use scenario:	Non-clinical research; Clinical research; Clinical decision support
HPC Systems:	Desktop, ShARC, Archer
HPC motivation:	Solve unreducible model.

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10.3 InSilicoMRI

Predicts the overheating of a medical device during an MRI scan. Radiofrequency (RF) safety analysis of a passive device exposed to a 3T MRI birdcage coil field following the directives of ASTM F2182 standard. The simulation calculates the EM fields, SAR, and thermal heating after 900s of RF exposure. The contact is project@insilicotrials.com.

Provider:	InSilicoTrials
Current users:	Industry
Access mode:	Service
URL:	https://insilicomri.com
Use scenario:	Non-clinical research Design & optimisation
HPC Systems:	Microsoft Azure
HPC motivation:	Solve unreducible model.

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