

# A Platform for *insilico* Modeling of Physiological Systems II

## CellML Compatibility and Other Extended Capabilities



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### INTRODUCTION

Physiome and systems biology have been recognized as emerging and important research areas that can integrate growing experimental data at multiple levels and scales of the human body for better understanding of human physiological functions<sup>[1,2]</sup>. The number of mathematical models describing biological functions published in peer reviewed journals is rapidly increasing. Moreover, complexity of each of those published models increases as the computational performance increases. In this situation, following problems have been occurred.

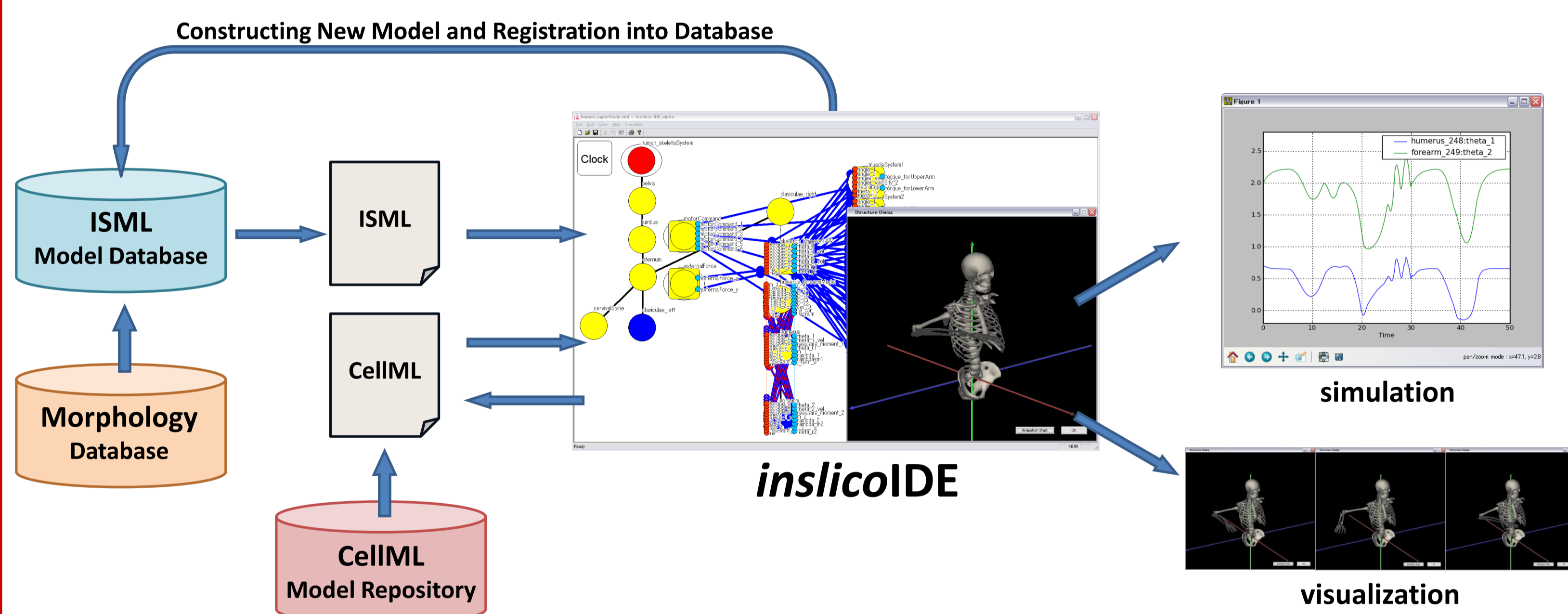
- Difficulty to reproduce simulation results of the published models
- Difficulty to reuse the models

These problems are obstructing promotion of sciences and the knowledge integration. The pioneering effort to overcome these has been promoted by CellML project<sup>[3,4]</sup> as a part of IUPS Physiome Project. CellML is a XML based markup language which aims at describing mathematical models of biological functions. The model written in the CellML format includes all information necessary to reproduce simulated results described in the corresponding to publication about the model.

This study is a continuation of our previous report<sup>[5]</sup>. We have proposed a XML based model description format referred to as *insilicoML* (abbreviated as ISML). For ISML, *insilicoIDE* is used to support the user for model and for automatic generation of C++ source codes to numerically simulate dynamics of the models. The *insilicoIDE*, together with model databases, is on the development to play a role as a platform for *in silico* modeling of physiological systems.

We describe progresses of our platform development.

### SYSTEM OUTLINE

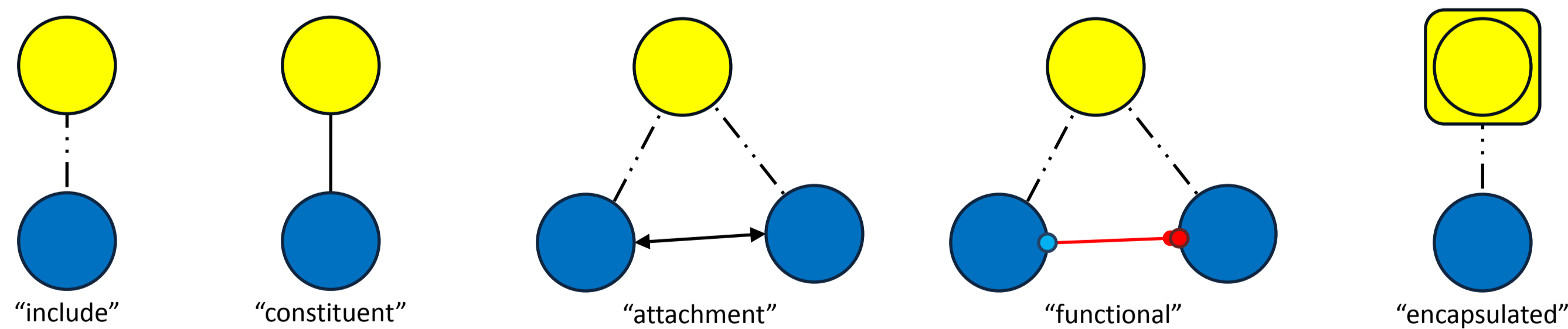


Our platform is composed of three parts.

- Markup Language
- Integrated Development Environment
- Model Database

(*insilicoML*, ISML)  
(*insilicoIDE*, ISIDE)  
(*insilicoDB*, ISDB)

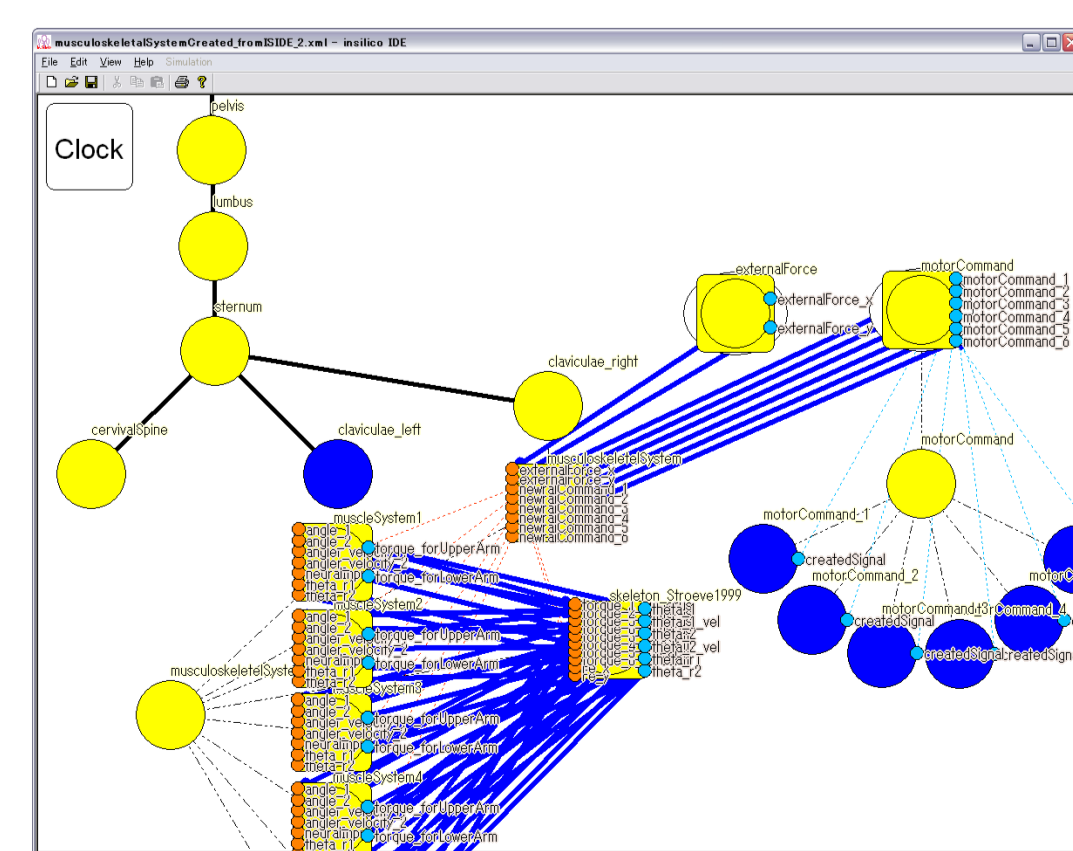
	Type	Aspect on <i>insilicoIDE</i>
module	not encapsulated	A ball-like object
	encapsulated	A ball-like object with square
edge	structural relationship : "include"	dash-dot line
	structural relationship : "constituent"	straight line
	structural relationship : "attachment"	straight line with arrow
	functional relationship	Red line



We consider that a target biological system as an aggregate of elements referred to as modules, and these modules are connected with relationships referred to as edges. The user can edit modules and relationships between modules using mouse operated GUI.

On *insilicoIDE*, the user

- can create a new module
- can edit module property
- can connect edges between modules
- can edit edges between modules



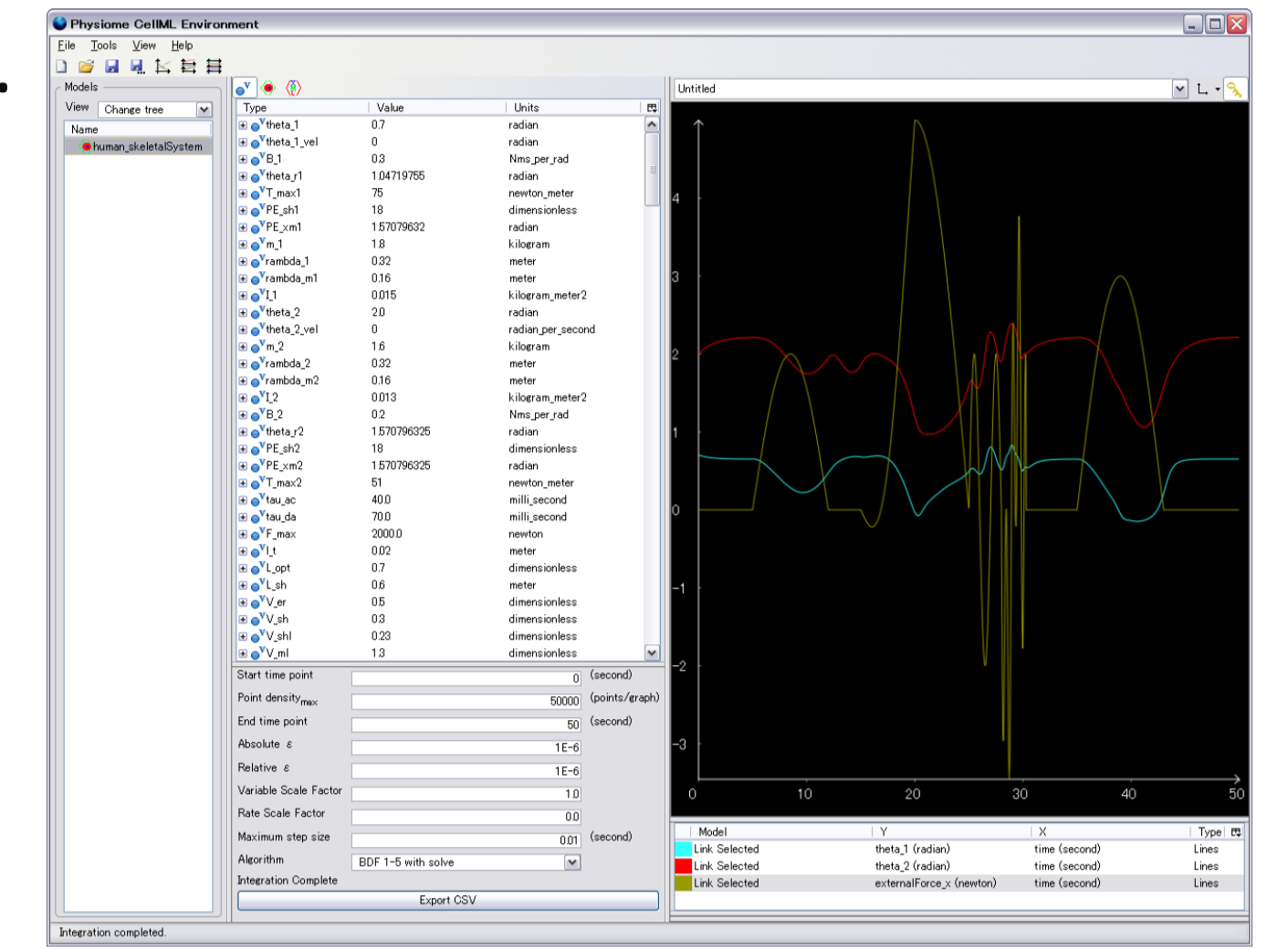
Once, the model construction is completed, the *insilicoIDE* can export the model either as a C++/MPI-C++ source code or as a ISML file.

### CellML COMPATIBILITY

*insilicoIDE* has high compatibility with CellML. *insilicoIDE*

- can load CellML formatted models
- can export CellML formatted models
- can create a model which has interaction with module which is written in ISML

This compatibility enhances the reusability of existing models.

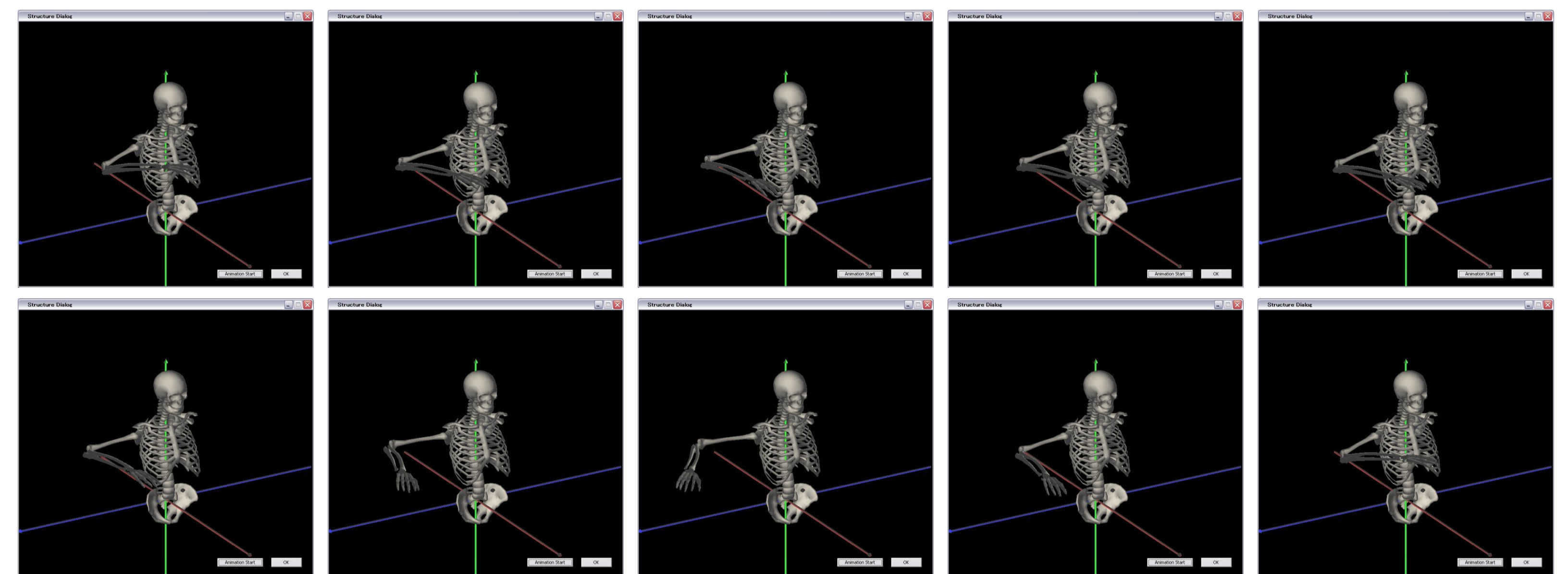
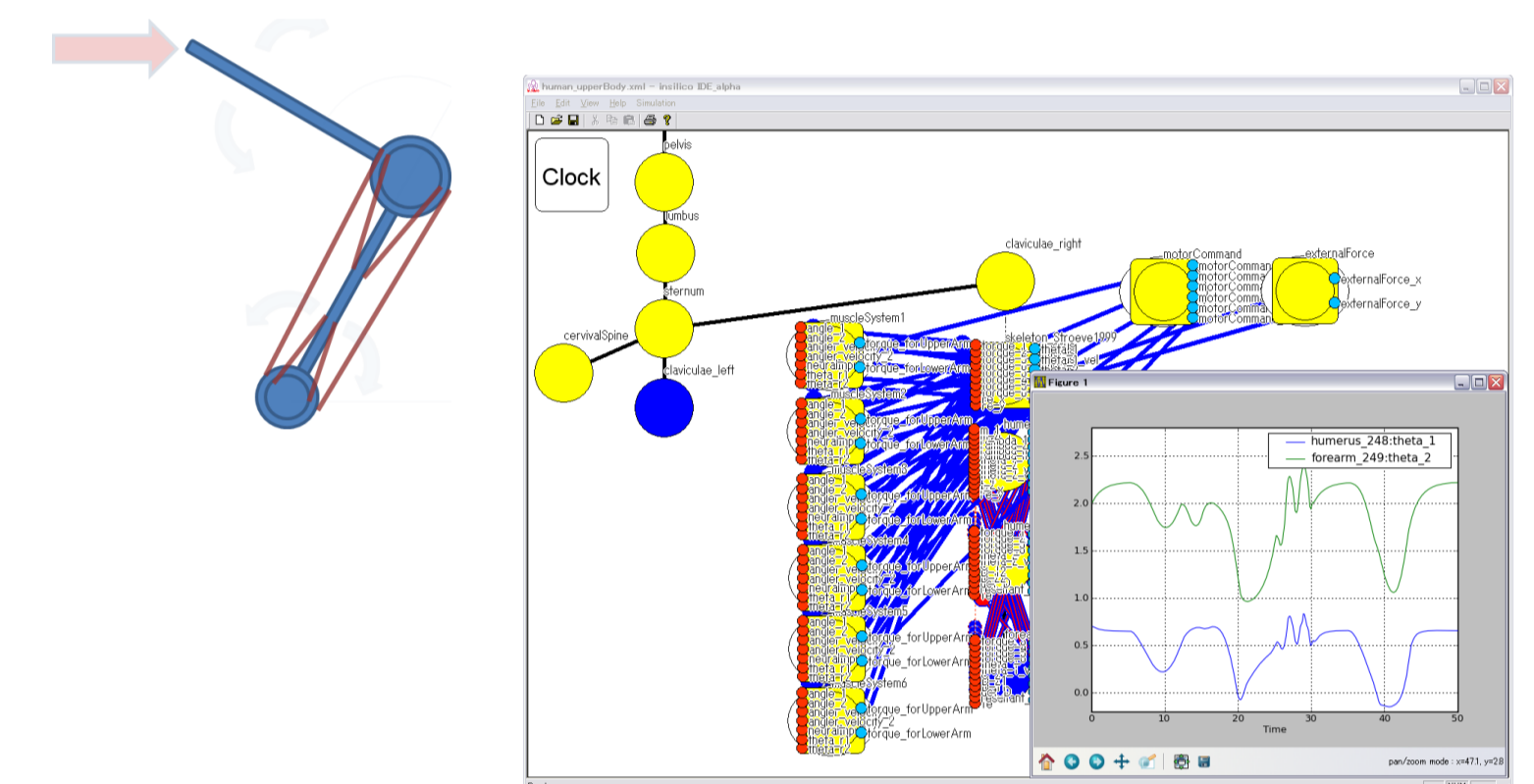


### USE OF MORPHOLOGY AND TIME SERIES DATA

*insilicoIDE* can deal with the morphology data and time series data.

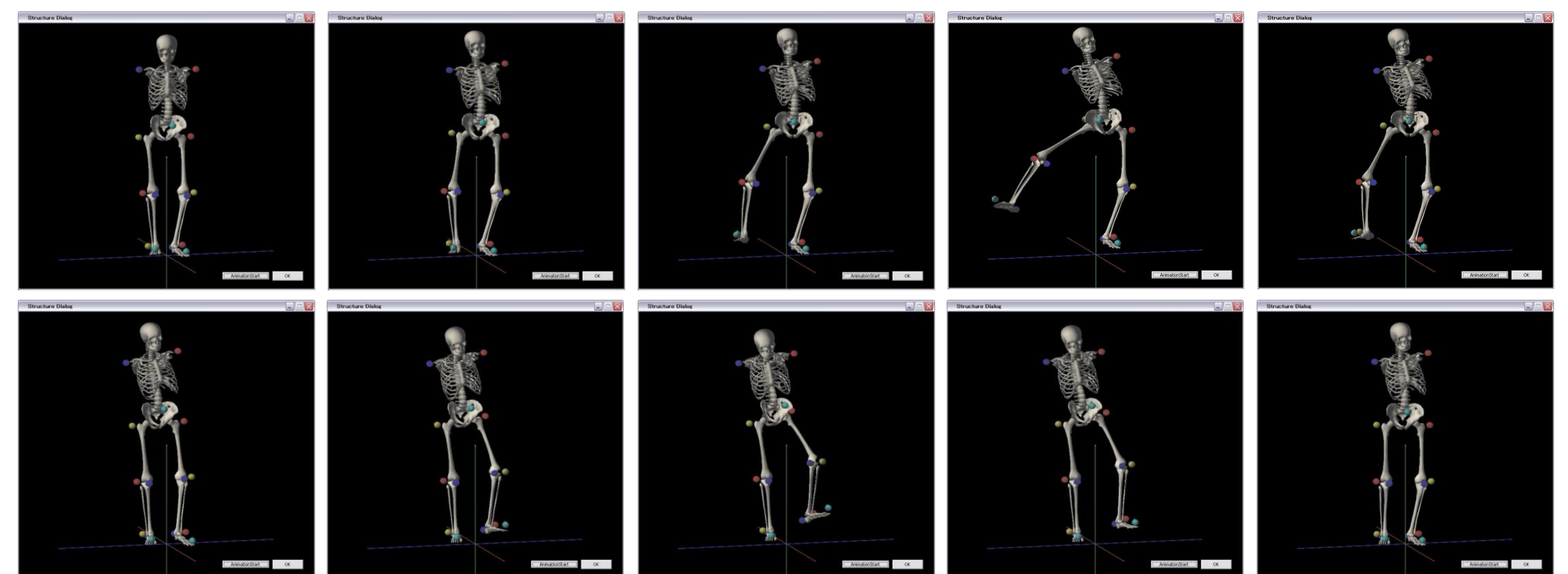
The following pictures are snapshots of the *insilicoIDE*. *insilicoIDE* can show the simulation result as two ways :

- as a waveform
- as a morpho dynamics



*insilicoIDE* can deal with time series data which is obtained from experiment too.

The following pictures are snapshots of the *insilicoIDE* which loads time series data of captured human motion.



### CONCLUSION

Several functionalities such as importing and simulating published models in the CellML model repository, browsing and editing a CellML model and then exporting it as a new model either with the CellML or ISML format, and newly constructing large scale models by connecting numbers of CellML/ISML models are demonstrated. Benefits to use both ISML and CellML are described. ISML can deal with morphology of models, enabling the user to perform geometry dependent modeling and simulations. ISML with the *insilicoIDE* can deal with time series data, both simulated and experimentally acquired data, for visualization of dynamics.

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