

Julia SIM

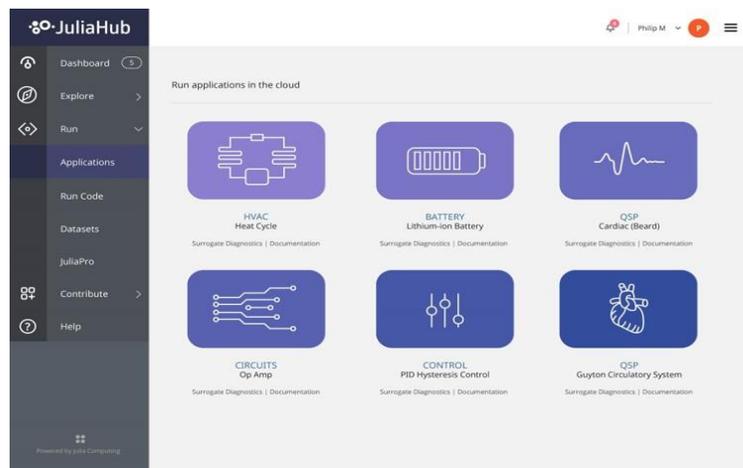


Simulating Reality

MAIN FEATURES

JuliaSim is a next generation cloud-based simulation platform, combining the latest techniques in scientific machine learning (SciML) with equation-based digital twin modeling and simulation. Our modern ML-based techniques accelerate simulation up to 500x, changing the paradigm of what is possible with computational design.

JuliaSim allows the user to directly import models from its Model Store into the Julia environment, making it easy to build large complex simulations. Pre-trained machine learning models leveraging SciML are seamlessly integrated into the engineer's workflow, reducing model development and simulation time. JuliaSim offers dramatic acceleration with surrogates, model discovery, parameter estimation, optimal control, and specialized numerical environments

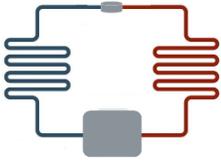


Contact us

sales@juliacomputing.com

www.Juliacomputing.com

REQUEST A DEMO 



SIMULATING HVAC SYSTEMS

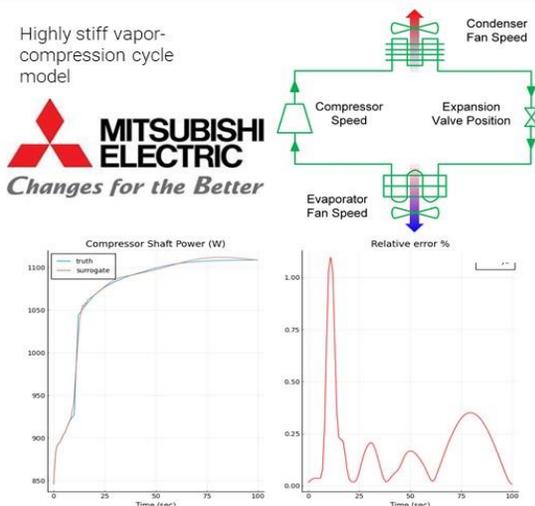
HOW JULIASIM IMPROVES HVAC MODELING

Buildings account for 40% of energy consumption, which means that the next frontier of energy savings will come from the construction of more efficient buildings. Better engineering requires high precision modeling and simulation. Phase transitions in the refrigerant media mean that these models can be difficult to simulate. Moreover, large-scale models require significant computational expense.

JuliaSim provides a suite of tools for improving the stability and efficiency of HVAC simulations. Using the SciML ecosystem, JuliaSim dramatically outperforms leading Modelica implementations and accelerates simulation. Using the proprietary Continuous-Time Echo State Network (CTESN) surrogates, we have demonstrated acceleration up to 570x in 8,000-equation heat cycle models, with gains scaling as the model grows. New discontinuity-

aware differential equation solvers, DiscoDiffEq.jl, improve the ability to properly handle the internal phase transitions while JuliaHub provides automatic parallelism.

ARPA-E: Accelerated Simulation of Building Energy Efficiency



The Julia implementation is 6x faster than Dymola for the full cycle simulation.

- Dymola reference model: 35.3 s
- Julia equivalent model: 5.8 s

Using CTESNs as surrogates improves simulation times between 10x-95x over the Julia baseline. Acceleration depends on the size of the reservoir in the CTESN.

Training set size	Reservoir size	Prediction time	Speedup over baseline
100	1000	0.06 s	95x
1000	2000	0.56 s	10x

Error is < 5% in all cases.

Total speedup over Dymola: 60-570x

Selected details of simulation results, which highlight the considerable acceleration achieved by means of CTESN surrogates.

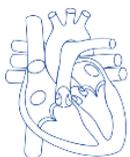


Contact us

sales@juliacomputing.com

www.juliacomputing.com





QUANTITATIVE SYSTEMS PHARMACOLOGY

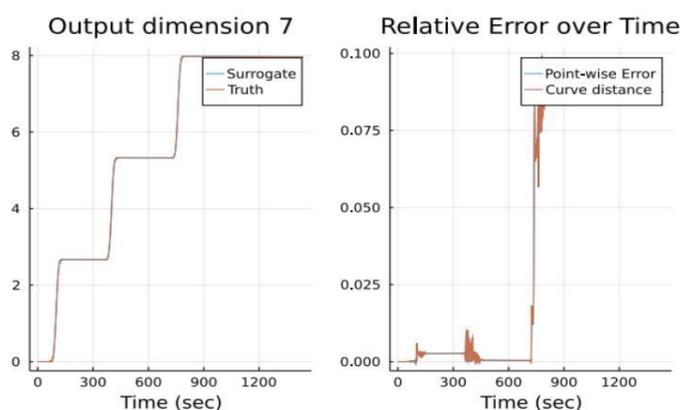
Pumas-QSP, powered by JuliaSim, has also proved highly successful in the domain of systems pharmacology. QSP modeling assists in identifying issues with pharmaceutical efficacy and safety before commencing the next phase of trials. This technique has been employed to help predict trial failures and potentially save valuable resources by allowing the company to focus on therapies with the highest probabilities of clinical success.

HOW JULIASIM IMPROVES PHARMACOLOGICAL MODELS

Julia's fast runtime and unique libraries gave Pfizer a special efficiency advantage in the field of quantitative pharmacology. Pfizer used Julia to accelerate several models:

- Steady state calculations of a cardiac model were reduced from nearly a day to just 40 minutes - an improvement of 26x. With multithreading, the total simulation time was reduced to just 9 minutes - an improvement of 115x.
- Global sensitivity analysis of the Tewari-Beard 2016 model was accelerated by 2x over the highly optimized C code, showing that even well-optimized code can be improved through Julia's specialized differential equation solver algorithms.
- A 7x acceleration on CPUs and 175x acceleration on GPUs for simulations of a 14 ODE Leucine model compared with the original optimized C code.

Other partners achieved similar results, such as a 250x acceleration for internal models with Sanofi, and similar gains at United Therapeutics and Moderna.



Validation of the CTESN surrogate accuracy using the Leucine model. The surrogate achieved predictions with a relative error < 4% across a wide range of parameters.

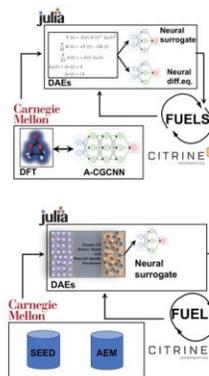


BATTERIES

In order to improve efficiency and achieve the reduction of global greenhouse gas emissions, alternative electrochemical materials are required. However, the candidate solutions must be thoroughly evaluated before being adopted on a large scale. Unfortunately, purely theoretical analyses often fail to model realistic operating conditions. Fast and accurate models can greatly reduce the time needed to perform the evaluation of new materials.

HOW JULIASIM IMPROVES ENERGY MATERIAL DEVELOPMENT

As part of the ARPA-E ACED project (Accelerated Computational Electrochemical systems Discovery), JuliaSim was used to accelerate the solutions of differential and algebraic equations describing the microkinetics of the electrochemical systems. The outcome was then applied to optimize the materials for battery-powered aircraft. Digital twins of batteries were trained to incorporate data which captured the unknown physics, significantly increasing the ability to predict battery degradation from the material properties. Physics-informed neural network surrogates of pseudo-2D (P2D) partial differential equations allow for complex property simulations to run faster than real-time. Notably, the scientific machine learning approach of JuliaSim was able to outperform state-of-the-art alternatives while standard machine learning methods failed.



ARPA-E ACED: closed loop optimization of materials for battery-powered aircraft

19% Increase in Degradation Modeling Accuracy Where ML Has Failed to Recover the State of the Art





JULIASIM MODEL LIBRARY

The JuliaSim Model Library is a collection of acausal components that includes pre-trained surrogates of models so that users can utilize the acceleration without having to pay for the cost of training locally. The specialized and fully customizable models are accessible via an intuitive GUI, and are accompanied by ample documentation and usage examples. The models comprise entries from the Modelica Standard Library, CellML Physiome model repository, and other benchmark problems defined by means of ModelingToolkit.jl. Each model is also accompanied by a detailed diagnostic report that provides, amongst other features, surrogate accuracy, the training parameter space, and the performance of the surrogate against the original model. In order to facilitate searching for a particular model, the entries contain metadata that can be queried by the user.

