

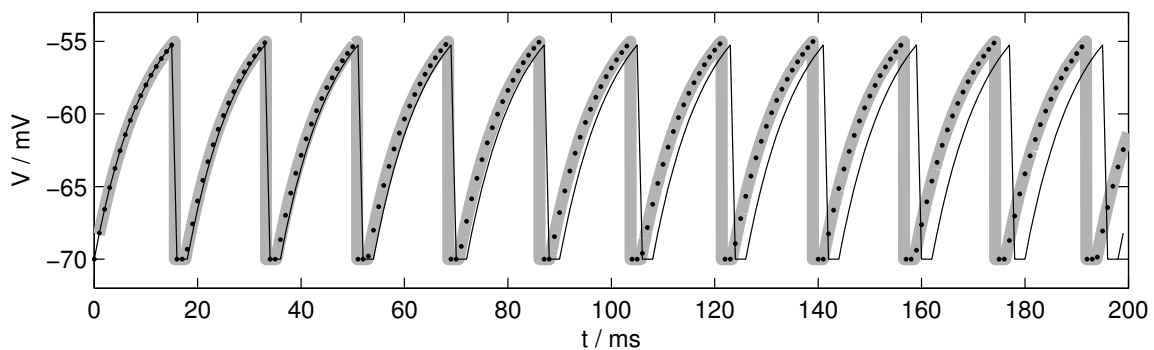
Precise spike timing with exact subthreshold integration in discrete time network simulations

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The subthreshold dynamics of a wide class of integrate-and-fire type neuron models can be integrated exactly [1]. It has previously been shown that even very large networks of spiking neurons can be simulated efficiently under the constraint that spike times are bound to an equidistant time grid [2]. This simulation scheme has two drawbacks: Firstly, it introduces artificial synchronisation by forcing all threshold crossings occurring in the integration interval $(t - h, t]$ to the point t on the time grid, potentially distorting the synchronisation dynamics of a network model. Secondly, restricting spikes to the time grid introduces an integration error which declines only linearly with the resolution h . Several authors have discussed the advantages of interpolating spike times within the grid based simulation of neural networks [3,4]. Based on an implementation in our simulation tool NEST [5], we demonstrate that the exact integration scheme can be naturally combined with off-grid spike events found by interpolation. This facilitates the precise simulation of large networks for which event-driven simulation schemes are inherently inefficient.



The figure shows the exact solution for the membrane potential of an integrate-and-fire neuron driven by a supra-threshold DC current (grey curve). Using exact integration with a resolution of $h = 1\text{ms}$ incurs a progressive error (black curve). Combining exact integration with interpolated spike timing essentially eliminates the progressive error (dotted curve).

We evaluate the new scheme in a relevant scenario of a neuron receiving input from a large network. A cost/benefit analysis of the integration error is provided parameterised by the resolution and the interpolation order. Cross-correlation analysis is used to characterise the error in spike train structure. The advantages and limitations of the approach are discussed.

This research is part of our long term project to provide the technology for neural systems simulations. Partially funded by DAAD/NFR 313-PPP-N4-1k, BMBF-DIP F1.2, GIF, and Honda Research Institute.

- [1] Rotter S, & Diesmann M (1999) *Biol Cybern* **81**:381–402.
- [2] Morrison A, Mehring C, Geisel T, Aertsen A, & Diesmann M (2004) submitted.
- [3] Hansel D, Mato G, Meunier C, Neltner L (1998) *Neural Comput* **10**:467–483.
- [4] Shelley MJ, & Tao L (2001) *J Comp Neurosci* **11**:111–119.
- [5] www.nest-initiative.org.

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