

## Modified Fürth equation describes cell crawling experiments and simulations

Ismael Fortuna<sup>1</sup>, Gabriel C. Perrone<sup>1</sup>, Monique S. Krug<sup>1</sup>, Eduarda Susin<sup>1</sup>, Julio M. Belmonte<sup>2,3</sup>,  
Gilberto L. Thomas<sup>1</sup>, James A. Glazier<sup>2</sup>, and Rita M.C. de Almeida<sup>1,4</sup>

<sup>1</sup>*Instituto de Física and* <sup>4</sup>*Instituto Nacional de Ciência e Tecnologia: Sistemas Complexos,*  
*Universidade Federal do Rio Grande do Sul, Caixa Postal 15051, 91501-970 Porto Alegre, RS, Brazil*

<sup>2</sup>*Biocomplexity Institute and Department of Intelligent Systems Engineering, University of Indiana,*  
*Bloomington, Simon Hall MSB1, 047G, 212 South Hawthorne Drive, Bloomington, IN 47405–7003,*  
*USA*

<sup>3</sup>*European Molecular Biology Laboratory Heidelberg, Meyerhofstr. 1, 69117 Heidelberg, Germany*

### ABSTRACT

Cell crawling plays important roles in development, wound healing and the inflammatory response, and is a key process in tissue engineering. While we know many of the biochemical components which lead to crawling cells, we lack both a proper mathematical description of cells' large-scale movements and a 3D simulation approach which reproduces these movements at low computational cost. We develop a modified Fürth equation to quantify cell center-of-mass motion and a computationally tractable 3D simulation of cells crawling on a flat stiff substrate. The modified Fürth equation generates three temporal regimes: short-range and long-range diffusion and mid-range ballistic motion. Rescaling time and length scales by fits of two of the modified Fürth equation parameters collapses both experimental and simulated mean-squared displacements of cells onto a single-parameter family of curves. These fitting parameters provide a direct translation between simulation and experimental length and time units. Our 3D simulation of migrating cells also replicate the spontaneous symmetry breaking that initiates cell migration, spontaneous changes in cells' directions of motion due to the loss and reformation of the cells' leading edges, and the velocity auto correlation functions seen in experiments. The speed of the simulations should allow their use in multi-scale virtual-tissue simulations of tissue and organ formation.

