

Accepted Manuscript

Title: Differential Evolution with Sensitivity Analysis and the Powell's Method for Crowd Model Calibration

Author: Jinghui Zhong Wentong Cai

PII: S1877-7503(15)00051-4

DOI: <http://dx.doi.org/doi:10.1016/j.jocs.2015.04.013>

Reference: JOCS 356

To appear in:



Please cite this article as: Jinghui Zhong, Wentong Cai, Differential Evolution with Sensitivity Analysis and the Powell's Method for Crowd Model Calibration, *Journal of Computational Science* (2015), <http://dx.doi.org/10.1016/j.jocs.2015.04.013>

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Differential Evolution with Sensitivity Analysis and the Powell's Method for Crowd Model Calibration

Jinghui Zhong and Wentong Cai

School of Computer Engineering, Nanyang Technological University, Singapore
{jinghuizhong, ASWTCAI}@ntu.edu.sg

Abstract

This paper proposes a novel evolutionary algorithm named differential evolution with sensitivity analysis and the Powell's method (DESAP) for model calibration. The proposed DESAP owns three main features. First, an entropy-based sensitivity analysis operation is introduced to dynamically identify important parameters of the model as evolution progresses online. Second, the Powell's method is performed periodically to fine-tune the important parameters of the best individual in the population. Finally, in each generation, the evolutionary operators are performed on a small number of better individuals in the population. These new search mechanisms are integrated into the differential evolution framework to improve the search efficiency. To validate its effectiveness, the proposed DESAP is applied to two crowd model calibration cases. The results demonstrate that the proposed DESAP outperforms several model calibration methods in terms of solution accuracy and search efficiency.

Keywords: Crowd Modeling and Simulation, Differential Evolution, Evolutionary Algorithm, Model Calibration, Sensitivity Analysis

1 Introduction

Crowd modeling and simulation has now become an active research field that has drawn increasing attention from industry, academia and government [1, 10, 14]. One fundamental issue in crowd modeling and simulation is model calibration, which aims to tune the parameter settings of the model so that the simulation can match what is observed from the real system. Traditionally, crowd model calibration is done manually using the trial-and-error method which is time consuming and tedious. Recently, Evolutionary Algorithms (EAs) such as Genetic Algorithm (GA) have attracted increasing attention of researchers and using EAs has become a popular and powerful approach for automatic crowd model calibration [3, 11].

However, crowd model calibration through EAs is quite computationally intensive. This is because that EAs iteratively evolve a population of chromosomes to search for a near global optimal solution. In each iteration, a number of fitness evaluations are required and each fitness evaluation requires a few simulation runs which can be quite time consuming. Hence, reducing

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