

Preface

The MICCAI community needs data with known ground truth to develop, evaluate, and validate image analysis and reconstruction algorithms. Since synthetic data are ideally suited for this purpose, over the years, a full range of models underpinning image simulation and synthesis have been developed: (a) simplified mathematical models to test segmentation and registration algorithms; (b) detailed mechanistic models (top–down), which incorporate priors on the geometry and physics of image acquisition and formation processes; and (c) complex spatiotemporal computational models of anatomical variability, organ physiology, or disease progression. Recently, cross-fertilization between image computing and machine learning gave rise to data-driven, phenomenological models (bottom–up) that stem from learning directly data associations across modalities, resolutions, etc. With this, not only the application scope has been expanded but also the underlying model assumptions have been refined to increasing levels of realism.

The goal of the Simulation and Synthesis in Medical Imaging (SASHIMI) Workshop aims to put all those interested in these problems in the same room, for the purpose of invigorating research and stimulating new ideas on how to best proceed and bring these two worlds together. The objectives were to: (a) hear from invited speakers in the areas of transfer learning and mechanistic models and cross-fertilize across fields; (b) bring together experts of synthesis (via phenomenological machine learning) and simulation (via explicit mechanistic models) to raise the state of the art; and (c) identify challenges and opportunities for further research. We also wanted to identify how we can best evaluate synthetic data and if we could collect benchmark data that can help the development of future algorithms.

The first workshop on “Simulation and Synthesis in Medical Imaging — SASHIMI 2016”¹ was held in conjunction with the 19th International Conference on Medical Image Computing and Computer-Assisted Intervention — MICCAI 2016 as a satellite event in Athens, Greece, on October 21, 2016. Submissions were solicited via a call for papers that was circulated by the MICCAI organizers, through known mailing lists (e.g., ImageWorld, MIUA) but also by directly e-mailing several colleagues and experts in the area. Each submission underwent a double-blind review by at least two members of the Program Committee consisting of researchers who actively contribute in the area. At the conclusion of the review process, 17 papers were accepted. Overall, the contributions span the following broad categories in alignment with the initial call for papers: fundamental methods for image-based biophysical modeling and image synthesis, biophysical and data-driven models of disease progression or organ development, biophysical and data-driven models of organ motion and deformation, biophysical and data-driven models of image formation and acquisition, segmentation/registration across or within modalities to aid the learning of model parameters, cross-modality (PET/MR, PET/CT, CT/MR, etc.) image synthesis, simulation and synthesis from large-scale

¹ <http://www.cistib.org/sashimi/>.

image databases, automated techniques for quality assessment of simulations and synthetic images, and several applications of image synthesis and simulation in medical imaging such as image registration and segmentation, image denoising and information fusion, image reconstruction from sparse data or sparse views, and real-time simulation of biophysical properties. The accepted papers were divided into two general topics of “Simulation and Its Applications in Computational Medical Imaging” and “Synthesis and Its Applications in Computational Medical Imaging” and presented during two oral and one poster sessions, overall covering eight and nine papers, respectively.

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