

Proceedings of the Workshop on the Advances of Information Technology 2021

Editors: Bálint Kiss and László Szirmay-Kalos

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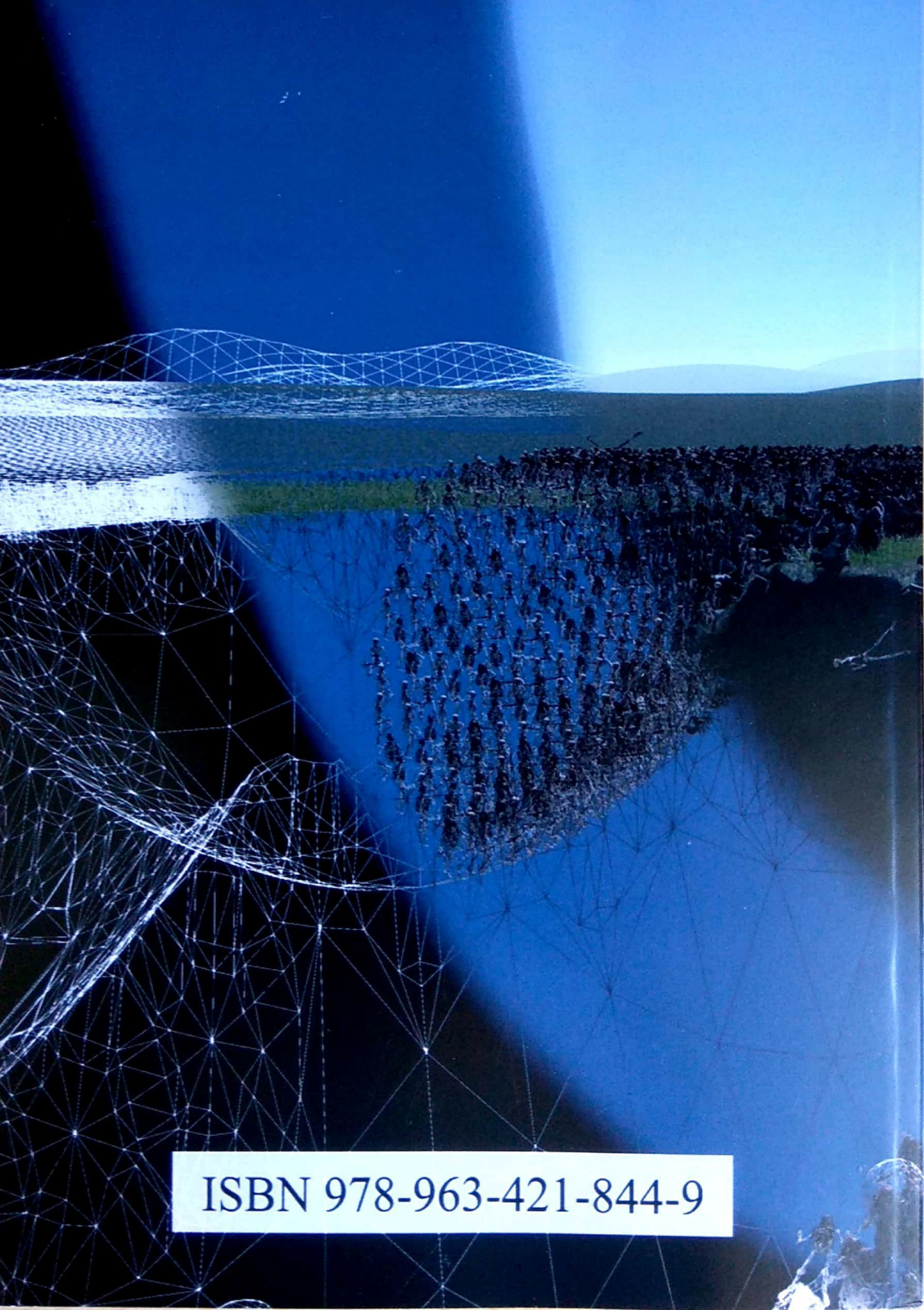


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*Workshop on the
Advances of Information Technology*

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Preface

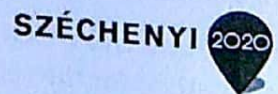
This book is the proceedings of the *Sixth Workshop on the Advances of Information Technology* (WAIT 2021), organized as an annual conference by the *Department of Control Engineering and Information Technology (IIT)* of the *Budapest University of Technology and Economics (BME)*. The presented papers of the conference cover the fields of research of this institution, including deep learning, autonomous and assisted driving, robotics, computer graphics, games, computer aided geometric design, medical imaging and simulation, user interfaces.

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László Szécsi prepared the proceedings for printing. The cover image has been created by Károly Hupján, showing a scene from his real-time tactical battle RTS, capable of simulating, animating and rendering tens of thousands of troops on deformable terrain covered in vegetation.

Budapest, January 28, 2021.

Bálint Kiss and László Szirmay-Kalos
WAIT 2021 chairmen



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Determination of the Blood Input Function for Dynamic Emission Tomography with Deep Learning

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Abstract

Dynamic tomography reconstructs a Time Activity Curve (TAC) for every voxel assuming that the algebraic form of the function is known a-priori. Practical kinetic models include the blood input function that may be scaled, integrated, derivated or convolved during the calculation of kinetic parameters. In direct dynamic tomography, the kinetic parameter calculation and reconstruction happen simultaneously, which either requires the blood input function from the beginning or obtains the kinetic parameters and the blood input function simultaneously as a joint optimization. In the latter case, we still need the approximation of the blood input function to serve as a starting point for the iterative optimization. This paper proposes a deep-learning-based approach to find a good guess for the non-linear blood input parameters from which the iterative process can start its refinement.

1. Introduction

With dynamic Positron Emission Tomography, we can determine the dynamics of radiotracer spreading and accumulation in tissues. The determined TAC function is expected to be consistent with biology, therefore it is searched in a pre-defined algebraic form that reflects the biological model.

The most popular approach is the *compartmental analysis* ^{8, 19, 20, 18}, in which the algebraic form is based on the solution of differential equations expressing the tracer exchange between n compartments ⁶. The solution has an algebraic form that is a non-negative linear combination of convolutions of the *blood input function* $C_p(t)$ and the *impulse response* $w(t)$ of the tissue. The impulse response is the non-negatively weighted sum of exponentials of unknown, non-negative *rate constants* α_i and constrained only for positive time values t by the Heaviside step function $\varepsilon(t)$:

$$w(t) = \varepsilon(t) \sum_{i=1}^n c_i e^{-\alpha_i t},$$

where c_i are the non-negative weights. Taking into account that a voxel is a mixture of tissue and blood, we obtain

$$\mathcal{K}(\mathbf{p}, t) = f_v C_W(t) + (1 - f_v) w(t) * C_p(t), \quad (1)$$

where $f_v \in [0, 1]$ is the unknown *fraction of blood* and C_W is the *total blood concentration function* taking into account

also the portion of the radiotracer that cannot diffuse into the tissues. The blood input function for tissues, $C_p(t)$, may be different from the radioactivity of the whole blood, $C_W(t)$, because metabolism is limited. The two functions may be fitted separately, or we can assume that one of them can be obtained from the other with a tracer-dependent metabolic correction. In this paper, we assume that a known tracer-dependent factor γ can be used to express total blood concentration $C_W(t)$ from the blood input $C_p(t)$ as $C_W(t) = \gamma C_p(t)$.

In PET, we use radiotracer isotopes decaying with positron emission. The positron emitted at the decay of an isotope wanders a few millimeters in the tissues and then collides with an electron. As a result, both particles annihilate, and two oppositely directed gamma-photons are born, which might be detected by the tomograph. A PET/CT system collects the *events* of simultaneous photon incidents in detector pairs. An event is a composition of the identification of the detector pair, also called *Line Of Response* or *LOR*, and its time of occurrence. The raw input data of the reconstruction is the list of events, which is processed directly in list mode, or binned in *frames* (t_F, t_{F+1}) .

Using the concentration function $\mathcal{K}(\mathbf{p}_V, t)$ of voxel V , the expected number of radioactive decays, i.e. number of