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Towards a web resource for quantitative renal physiology

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We present a two-pronged project: 1) a Quantitative Kidney DataBase (QKDB), and 2) an interactive website presenting a coherent and comprehensive set of mathematical models covering the major aspects of renal physiology.

1. The QKDB will contain the data needed for quantitative evaluation of hypotheses of renal function, from the cellular, through the epithelial and tubular, to whole organ levels. It will thus put legacy measurements, as well as recent and new data, at the ready disposal of renal researchers, facilitating comparisons among different species and under various experimental conditions. It will include especially (list to be extended as needed): transport parameters, tubular concentrations and flow rates along the various nephron segments, and anatomical details, in human kidneys, in experimentally studied species, and in model epithelia such as cultured cells and amphibian skin and urinary bladder.

2. The modeling resource, a dynamic website, will be grounded in the experience of the project participants, all of whom are established modelers of kidney physiology. The site will provide an interactive user interface to a collection of published models at all levels of renal physiology, thus enabling non-modelers to interactively exploit the models, altering the key parameters according to hypotheses of their own and visualizing the simulation results, thus permitting quantitative exploration of new hypotheses. The site will include all existing types of models relevant to renal physiology, including kinetic models of transporters and channels, transport models of individual cell types, of flat model epithelia (such as bladder and cultured epithelia), and of tubular segments along the nephron, models of the microcirculation, models of tubuloglomerular feedback, and models of inner and outer medulla at various levels of detail.

Implementation of the web resource will be facilitated by translation of the models into a common markup language (such as CellML and SBML). There will thus be a modular separation of model descriptions from their numerical solution methods.

This two-pronged web resource, by leveraging the efforts of the community of renal modelers and thus facilitating general access to hypothesis-driven modeling, will enhance the evaluation of new hypotheses in renal physiology and the effects of disease-related defects of transport proteins, renal metabolism, and anatomical features. The development strategy will use, as far as possible, a generic approach so that conversion of this effort for application to other organ systems will be straightforward.

Where applicable, the experiments described here conform with Physiological Society ethical requirements.