PERFUSION-DIFFUSION GAS CONTENT COMPARTMENTAL MODELS AS A PREDICTOR OF DECOMPRESSION SICKNESS

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Introduction

Probabilistic models of decompression sickness (DCS) typically rely upon a collection of parallel, mono-exponential perfusion-limited compartments which describe gas content kinetics and in some cases bubble volume within theoretical tissue compartments. Doolette, Upton, and Grant proposed a collection of perfusion-diffusion based models as descriptors of the helium uptake and washout kinetics they observed in cerebral blood flow and skeletal muscle of sheep [1,2]. They found that their data were best fit for both skeletal muscle and cerebral blood flow using a combination of coupled perfusion- and diffusion-limited compartments. We are investigating whether these and similar multi-exponential model structures lead to a better prediction of the incidence of DCS in Navy divers.

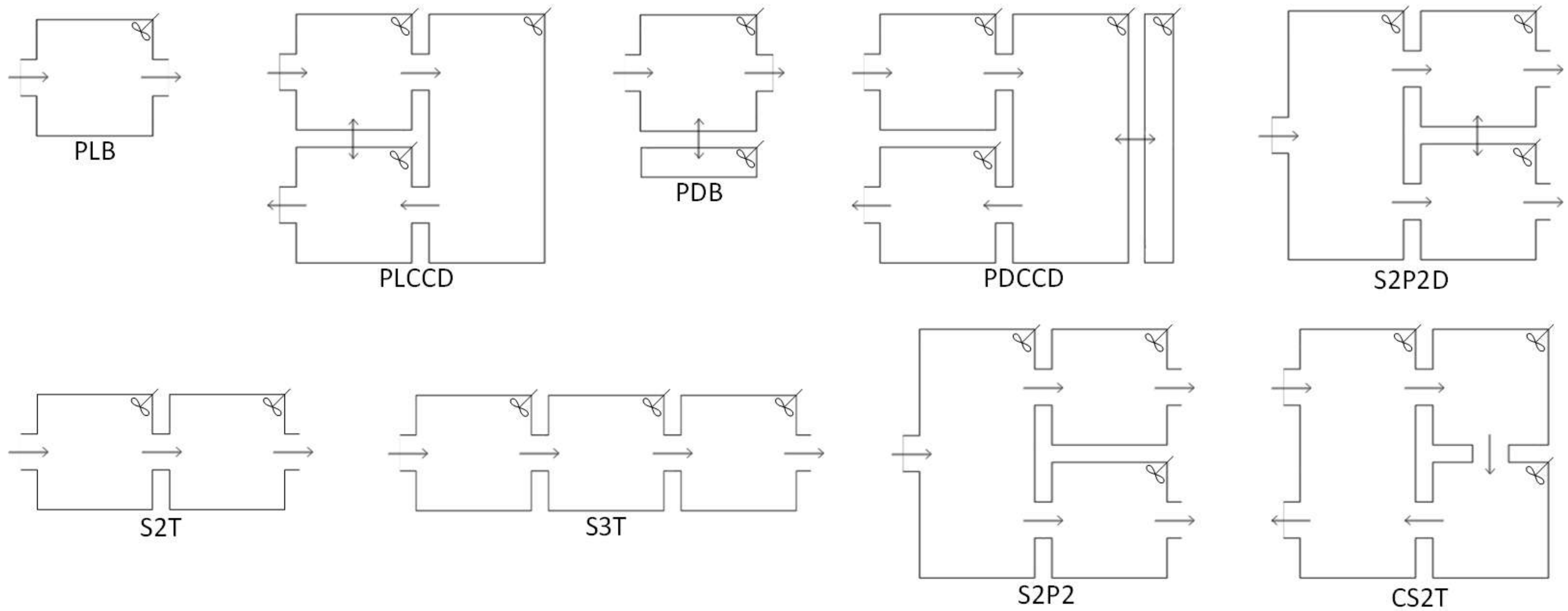

Figure 1: Conceptual Model Forms

Methods

Upon rederiving the original six models proposed by Doolette et al, using the principal of conservation of mass and assuming diffusion to be isotropic, we arrived at four distinct models: Perfusion-Limited Base (PLB), Perfusion-Limited Countercurrent Diffusion (PLCCD), Perfusion-Diffusion Base (PDB), and Perfusion-Diffusion Countercurrent Diffusion (PDCCD). In addition to these four models we investigated five other model structures designed to provide the delayed risk accumulation associated with decompression sickness from hyperbaric exposures: Serial Two Tissue (S2T), Serial Three Tissue (S3T), Serial Two Parallel Two (S2P2), Serial Two Parallel Two Diffusion (S2P2D), and Central Serial Two Tissue (CS2T). Conceptual drawings of the nine model structures are shown in Figure 1. The models were programmed in C# and C++ and fitted against the p97 data set described by Parker [3]. This is data set contains 1,349 distinct dive profiles and 223 cases of DCS.

Marginal DCS events have been shown not to contribute significantly to the quality of model fit and were ignored [4]. Model fitting was performed using the Nelder-Mead algorithm. Each model included at least one gain parameter which were calculated exactly instead of by fitting [5]. Resources used to fit the models to the data included both local resources at Duke University and a Blue Gene/Q computer located at Argonne National Laboratory's Leadership Computing Facility.

Preliminary Results

Our initial findings are summarized in Table 1. Thus far, several of the models (PDB, PDCCD, S2LPD, S2LP, and S3T) have generated few or no converged solutions. Fitting is considered to be complete when 256 solutions have been obtained. Currently, the CS2T model has found the largest log likelihood (-1366.75). Since few of the models are nested, the log likelihood difference test cannot be used to select the "best" model. Therefore, we assess model quality using Akaike Information Criterion (AIC).

The results of the AIC scoring show that the CS2T model provides the best fit to the dive data set.

Model	Solutions	Best Log Likelihood	AIC
CS2T	18	-1366.75	0.999992
PDB	0	N/A	0
PDCCD	0	N/A	0
PLB	256	-1387.17	4.19E-08
PLCCD	140	-1379.98	7.48E-06
S2LPD	1	-1482.98	3.1E-56
S2LP	2	-1388.39	6.11E-10
S2T	190	-1388.39	4.54E-09
S3T	2	-1400.15	4.77E-15

Table 1: Preliminary Results

References

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[4] Howle LE et al, J. of Appl. Physiol. 2009; 107:1539-1547
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Acknowledgements

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