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Title: Does the model of parallel connected bronchi in each generation functionally correspond to the true dichotomy structure of the bronchial tree?

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Body: Background: The structure of the bronchial tree is described in Weibel's model as a dichotomy pattern of the airways branching. The classic calculation of airways resistance (R_{aw}) is, however, based on the assumption of parallel connected bronchi in each generation. We investigated the conditions, under which this assumption correctly represents the dichotomy. Methods: We calculated R_{aw} by a classical model (parallel connected bronchi (PM)) und compared it with R_{aw} obtained by a dichotomous model (DM). In the latter, R_{aw} was calculated consecutively by pairs of branching in 23 generations. We simulated an obstruction of 50% of the bronchi to 0.5 (half) of their radius. Results: In case of normal structure (all bronchi of each generation have ideal radius) provided both models identical R_{aw}. Further analysis showed that PM is not sensitive for the spatial distribution of obstructive bronchi. It operates only with their number in each generation regardless whether the obstruction occurs in the same or in different segments. DM is sensible to the heterogeneity of obstruction. The simulations of random distributed obstruction showed that DM leads to a 2.1fold higher R_{aw} compared to PM. Primarily vertical bronchial heterogeneity plays an essential role. By simulation of different patterns of topographical heterogenous obstruction, estimated R_{aw} is in DM on the average 4.3fold higher than in PM. Conclusions: The classical model of parallel connected bronchi of each generation disregards the topography of obstruction that leads to falsely decreased R_{aw} estimation. Spatial heterogeneity of the obstruction is an important factor of R_{aw} increase.