Vessel Coordinate Parameter Information

Patient identification number is encoded in filename as R01-XXX. This can be used to connect tumor coordinates with vessel coordinates and tumor metabolic scaling in tumor\_vessel\_scaling.xlsx.

x,y,z Right-handed coordinates of vessel voxel (units of mm).

ID Identification for vessel, equivalent to ceiling value of nodeid. Do not use.

nodeid Identification for vessel using canonical generation labeling, unique within a

given patient

treeid Identification for vascular tree that nodeid is a member of, unique within a given

patient and tumor\_half

radius Radius of vessel determined as average of all spherical growth radii comprising

vessel (mm)

radius\_obs Radius of vessel determined from assuming cylindrical shape of vessel and

extracting from volume of cylinder (mm)

length Length of vessel as determined by Canonical Generation labeling (mm)

volume Volume of vessel as determined by Canonical Generation labeling (cubic mm)

n Number of vessels that reference this vessel as parent using canonical

generation labeling. NA indicates that this vessel is a terminal vessel

tumor\_half Binary indicating whether this vessel occurs in the hemilung with the tumor. (0 =

no tumor, 1 = tumor)

cen\_dist Distance from voxel to centroid of hemilung. Used to identify root within tree

parent Identification for vessel parent using canonical generation labeling, unique

within a given patient

generation Branching generation as determined by Horton-Strahler labeling

gen\_diff Difference in Horton-Strahler generation value between this vessel and its

parent

hs\_nodeid Identification for vessel using Horton-Strahler labeling, unique within a given

patient

hs\_parent Identification for vessel parent using Horton-Strahler labeling, unique within a

given patient

hs\_length Length of vessel as determined by Horton-Strahler labeling (mm)

beta.ave Average radial scale factor as determined by Canonical Generation labeling. NA

indicates a terminal branch with no child branches for calculation

gamma.ave Average length scale factor as determined by Canonical Generation labeling. NA

indicates a terminal branch with no child branches for calculation

beta.diff Difference radial scale factor as determined by Canonical Generation labeling.

NA indicates a terminal branch with no child branches for calculation

gamma.diff Difference length scale factor as determined by Canonical Generation labeling.

NA indicates a terminal branch with no child branches for calculation

asymmetry Asymmetry type as determined by Canonical Generation labeling. True indicates

positive asymmetry, False indicates negative asymmetry. NA indicates a terminal branch with no child branches for calculation