Three-dimensional reconstruction and NURBS-based structured meshing of coronary arteries from the conventional X-ray angiography projection images

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Appendix S1: Nomenclature

Nomenclature legend

$\mathbf{x}$	– Data vector-array,	(bold lowercase)
$\mathbf{X}$	– Matrix,	(bold uppercase)
$\vec{\mathbf{x}}$	– Point in 2D space (at X-ray plane detector),	(bold lowercase with vector-arrow)
$\vec{\mathbf{X}}$	– Point in 3D space,	(bold uppercase with vector-arrow)
x	– Constant variable,	(regular lowercase)
x	– Scalar variable,	(italic lowercase)
X()	– Scalar function, result is scalar variable (x),	(regular uppercase)
$\vec{\mathrm{x}}()$	– Vector function, result is point in 2D ($\vec{\mathbf{x}}$),	(regular lowercase with vector-arrow)
$\vec{\mathrm{X}}()$	– Vector function, result is point in 3D space ($\vec{\mathbf{X}}$);	(regular uppercase with vector-arrow)

Notes:

- **Bold** indicates data structure; regular style indicates variable or function.
- UPPERCASE indicates that data or computation is in 3D; lowercase indicates that data is in 2D DICOM plane.
- Vector-arrow indicates that type of function or data is point (2D lowercase or 3D UPPERCASE).

At the implementation level these should be different classes (data types).

Nomenclature

n –Number of point samples used for the device calibration

s –Number of vessel centreline samples

$2s$ –Number of vessel borders samples

m –Number of frames acquired from primary view

p –Number of frames acquired from secondary view

$\vec{\mathbf{q}}_{i,j}^{k}\left\{i=1,2;\ j=1,n;k=1,\frac{m\ \ for\ i=1}{p\ \ for\ i=2}\right\}$ –Point samples used for calibration

$\vec{\mathrm{c}}_{i,j}^{k}\left\{i=1,2;\ j=1,s;k=1,\frac{m\ \ for\ i=1}{p\ \ for\ i=2}\right\}$ –Parameterized vessels centrelines

$\vec{\mathrm{b}}_{i,j}^{k}\left\{i=1,2;\ j=1,2s;k=1,\frac{m\ \ for\ i=1}{p\ \ for\ i=2}\right\}$ –Parameterized vessels borders (two for each centreline)

κ –Pixel spacing at 2D X-ray plane detector

α –Primary angle: Right Anterior Oblique (RAO) / Left Anterior Oblique (LAO)

β –Secondary angle: Cranial (CRA) / Caudal (CAU)

d_{SOD} –Distance from patient to X-ray source

d_{SID} –Distance from X-ray source to intensifier plane

$\mathbf{M}$ –C-arm rotation matrix

$\vec{\mathbf{F}}$ –Position of X-ray source in 3D

$\vec{\mathbf{O}}$ –Position of intensifier plane origin in 3D

$\vec{\mathbf{p}}$ –Coordinates of an arbitrary vessel centreline point in the intensifier (DICOM) 2D plane

$\vec{\mathbf{P}}$ –Coordinates of an arbitrary vessel centreline point in the 3D

$\vec{\mathbf{p}}_i\left(\vec{\mathbf{P}}\right)$ –Projection of $\vec{\mathbf{P}}$ back on the intensifier plane for i -th view

$\boldsymbol{\Delta\theta}$ –Intensifier 3D rotation around its origin $\vec{\mathbf{O}}$

$\mathbf{R}_{\boldsymbol{\Delta\theta}}$ –Rotation matrix computed from three components in rotation vector $\boldsymbol{\Delta}\vec{\mathbf{O}} = \begin{bmatrix} \Delta o_x & \Delta o_y & \Delta o_z & 1 \end{bmatrix}^{\mathrm{T}}$

$\boldsymbol{\Delta}\vec{\mathbf{O}} = \begin{bmatrix} \Delta o_x & \Delta o_y & \Delta o_z & 1 \end{bmatrix}^{\mathrm{T}}$ –Intensifier 3D translation from its origin $\vec{\mathbf{O}}$

$\vec{\mathbf{I}}_1$ –Isocenter of primary view

$\vec{\mathbf{I}}_2$ –Isocenter of secondary view

$\boldsymbol{\Delta}\mathbf{i}$ –Translation of the secondary view isocenter $\vec{\mathbf{I}}_2$ from the global origin

$\overset{*}{\mathbf{X}}\mathbf{A}\left\{ \alpha_2, \beta_2, \boldsymbol{\Delta\theta}, \boldsymbol{\Delta}\vec{\mathbf{O}}, \boldsymbol{\Delta}\vec{\mathbf{i}} \right\}$ –List of device parameters optimized during calibration

F –Cost-function used during the calibration of device parameters $\overset{*}{\mathbf{X}}\mathbf{A}$

$\mathbf{D}$ –Cost-matrix for finding correspondence between two series

ξ –Function for calculating values in the cost-matrix

δ –Cost-value for skipping elements from two matching series

$\overset{*}{\varepsilon}_{\min}$ –Calibration error

$\overset{*}{\mathbf{C}}\mathbf{F}$ –List of corresponding frames

$\vec{\mathrm{C}}(t)$ –Length-parameterized vessel centreline, $t \in \{0,1\}$

$\vec{\mathbf{C}}(t)$ –Arbitrary 3D point along the parameterized vessel centreline $\vec{\mathrm{C}}(t)$, $t \in \{0,1\}$

$\vec{T}(t)$ –Tangent of the centreline $\vec{\mathrm{C}}(t)$ at point $\vec{\mathbf{C}}(t)$, $t \in \{0,1\}$

$\vec{N}(t)$ –Normal of the centreline $\vec{\mathrm{C}}(t)$ at point $\vec{\mathbf{C}}(t)$, $t \in \{0,1\}$

$\vec{B}(t)$ –Binormal of the centreline $\vec{\mathrm{C}}(t)$ at point $\vec{\mathbf{C}}(t)$, $t \in \{0,1\}$

$\vec{\mathrm{c}}_i(t_i)$ –Parameterized vessel centreline on i -th projection, $t_i \in \{0,1\}$ (note that $t \neq t_i$)

$\vec{\mathbf{c}}_i(t_i)$ –Arbitrary point along the parameterized vessel centreline $\vec{\mathrm{c}}_i(t_i)$ on i -th projection, $t_i \in \{0,1\}$ $(t \neq t_i)$

$\vec{\mathrm{t}}_i(t_i)$ –Tangent of the centreline $\vec{\mathrm{c}}_i(t_i)$ at the point $\vec{\mathbf{c}}_i(t_i)$, $t_i \in \{0,1\}$ $(t \neq t_i)$

$\vec{\mathrm{n}}_i(t_i)$ –Normal of the centreline $\vec{\mathrm{c}}_i(t_i)$ at the point $\vec{\mathbf{c}}_i(t_i)$, $t \in \{0,1\}$ $(t \neq t_i)$

$\vec{\mathbf{b}}_{i,1}, \vec{\mathbf{b}}_{i,2}$ –Intersections of centreline normal $\vec{n}_i(t_i)$ with vessel borders on i -th projection

$\vec{\mathbf{P}}_{a,i}, \vec{\mathbf{P}}_{b,i}$ –Points $\vec{\mathbf{b}}_{i,1}, \vec{\mathbf{b}}_{i,2}$ positioned in 3D

$\vec{L}_1(\vec{F}_i, \vec{\mathbf{P}}_{a_i}), \vec{L}_2(\vec{\mathbf{C}}(t), \vec{T}(t))$ – lines (X-rays) – $\vec{L}_1(\vec{F}_i, \vec{\mathbf{P}}_{a_i})$ is defined by the X-ray source point $\vec{F}_i$ and point $\vec{\mathbf{P}}_{a_i}$ and the second line $\vec{L}_2(\vec{\mathbf{C}}(t), \vec{T}(t))$ was defined by the point $\vec{\mathbf{C}}(t)$ and direction vector $\vec{T}(t)$. $t \in \{0,1\}$

$\vec{\mathbf{A}}_i(s_u, t), \vec{\mathbf{B}}_i(s_u, t)$–Points that belong to both rays $L_{1/2}$ and vessel lumen (3D surface) for i -th projection, $t \in \{0,1\}$

$\vec{S}_j(u, v)$–Parameterized NURBS surface of j -th vessel branch lumen defined by centreline $\vec{P}_j(t)$ and patches obtained along the centreline, $u, v \in \{0,1\}$

$\mathbf{B}$ –Bifurcation list that describes connectivity of considered vessel branches

Appendix S2: Pseudo-code

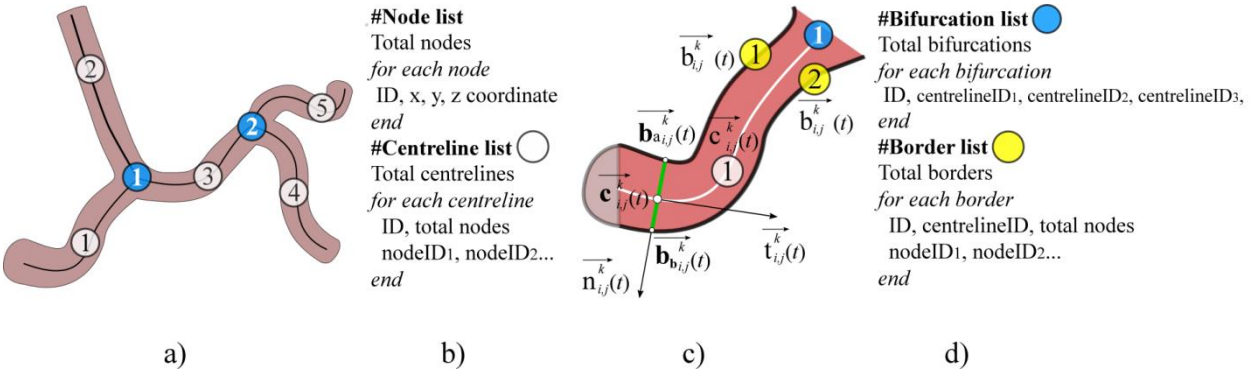
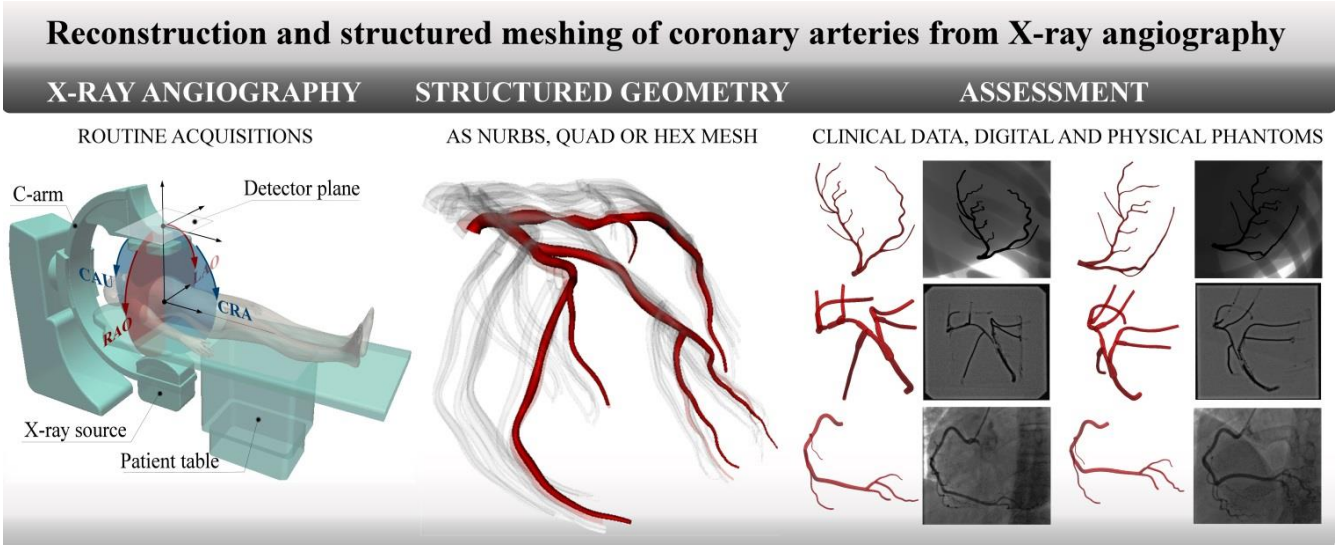


Figure A1. Pre-processing steps and inputs. (a, c) Schematic illustration of the data to be extracted from X-ray angiography (XRA) images; (b, d) Description of input data structures.

The procedure requires two sequences of XRA images acquired from different viewpoints (overall Algorithm 1). After picking the pair of end-diastole frames, a couple (n) of corresponding points $\vec{\mathbf{q}}_{i,j}^{k}\{i=1,2;\ j=1,n;\ k=\text{end-diastole}\}$ were extracted for the purpose of calibration (Algorithm 2) and frames-pairing (Algorithm 3). For the purposes of CA centerlines (Algorithm 4) and surface (Algorithms 5 and 6) reconstruction, the total s vessel centerlines $\vec{\mathrm{c}}_{i,j}^{k}\left\{i=1,2;\ j=1,s;\ k=1,\frac{m\ for\ i=1}{p\ for\ i=2}\right\}$ and its corresponding borders $\vec{\mathrm{b}}_{i,j}^{k}\left\{i=1,2;\ j=1,2s;\ k=1,\frac{m\ for\ i=1}{p\ for\ i=2}\right\}$ were extracted for each vessel branch; where index i indicates the XRA view, j indicates the point or centerline number, and k indicates the index of the XRA frame in the sequence. Both centerlines $\vec{\mathrm{c}}_{i,j}^{k}$ and borders $\vec{\mathrm{b}}_{i,j}^{k}$ were defined as parametric curves, so the computation of intersections between the centerline's normal and borders (required for the surface reconstruction) was performed automatically (Fig. A1).



Algorithm 1 Three-dimensional reconstruction of coronary arterial trees from uncalibrated angiographic X-ray projections (overall algorithm)

Input:	Total n point samples from two XRA views tracked over m frames from primary view and p frames from secondary view $\vec{\mathbf{q}}_{i,j}^{k}\{i=1,2;\ j=1,n;\ k=\text{end-diastole}\}$.
Input:	Total s vessel centrelines $\vec{\mathrm{c}}_{i,j}^{k}\left\{i=1,2;\ j=1,s;\ k=1,\frac{m\ for\ i=1}{p\ for\ i=2}\right\}$ tracked over the XRA frames.
Input:	Total $2s$ borders (two for each centreline) $\vec{\mathrm{b}}_{i,j}^{k}\left\{i=1,2;\ j=1,2s;\ k=1,\frac{m\ for\ i=1}{p\ for\ i=2}\right\}$.
Output:	Structured 3D+t mesh of CA tree.
Output:	Calibrated XRA device parameters $\overset{*}{\mathbf{XA}}$.

1	Find optimal device parameters $\overset{*}{\mathbf{XA}}$ and correspondence $\overset{*}{\mathbf{CP}}$ between the acquired frames (see Algorithm 3)
2	**for** k=1 **to** number of corresponding pairs in the list $\overset{*}{\mathbf{CP}}$ **do**
3	By using $\overset{*}{\mathbf{XA}}$ and the input data for k-th corresponding pair of frames generate a structured 3D mesh of CA tree (see later Algorithm 6)
4	**end for**

Algorithm 2 XRA device calibration using the mathematical model from Section 2.3 and two end-diastole frames (Section 2.4)

Input:	Total of n 2D corresponding points from two end-diastole XRA views $\vec{\mathbf{q}}_{i,j}\{i=1,2;\ j=1,n\}$.
Input:	Initial XRA parameters: $\mathbf{XA}\{\alpha_2, \beta_2, d_{SOD_{12}}, d_{SID_{12}}, \mathbf{\Delta\theta}=[0,0,0], \mathbf{\Delta\vec{O}}=[0,0,0], \mathbf{\Delta i}=[0,0,0]\}$.
Input:	Number of GA generations N (in this study $N=100$).
Input:	Size of GA population M (in this study $M=30$).
Output:	Optimized parameters $\overset{*}{\mathbf{XA}}\{\alpha_2, \beta_2, \mathbf{\Delta\theta}, \mathbf{\Delta\vec{O}}, \mathbf{\Delta\vec{i}}\}$.
Output:	Calibration error $\overset{*}{\varepsilon}_{\min}$.

1	Select an initial population of genomes $g_1^{(l)}, l \in \{1...M\}$		
2	Set $\varepsilon_{\min}$ to ∞		
3	**for** t=1 to N **do**		
4		**for all** $g_t^{(l)}$ **do**	
5			Set current genome as XRA parameters $g_t^{(l)} \rightarrow \mathbf{XA}$
6			Reconstruct points $\vec{\mathbf{Q}}_j\{j=1,n\}$ from $\vec{\mathbf{q}}_{i,j}\{i=1,2;\ j=1,n\}$ according to Equations 1–5
7			Compute error $\varepsilon = \dfrac{\sum_{i=1}^{2}\sum_{j=1}^{n}\left\|\vec{\mathbf{q}}_{i,j} - \vec{\mathbf{q}}_{i,j}\left(\vec{\mathbf{Q}}_j\right)\right\|^2}{n}$ according to Equation 6
8			**if** $\varepsilon < \varepsilon_{\min}$ **then**
9			$\overset{*}{\varepsilon}_{\min} = \varepsilon_{\min}$, $\overset{*}{\mathbf{XA}} = \mathbf{XA}$
10			**end if**
11		**end for**	
12	Reproduce genomes with the lowest training error in the population to form new genomes through crossover and mutation		
13	Replace the worst genomes in the population with the best new genomes		
14	**end for**		

Algorithm 3 Partial matching of XRA frame series acquired from two views (Section 2.5)

Input:	Total n 2D bifurcation points sampled from two XRA views over m frames from primary view and p frames from secondary view $\vec{\mathbf{q}}_{i,j}^{k}\left\{i=1,2;\ j=1,n;k=1,\frac{m \text{ for } i=1}{p \text{ for } i=2}\right\}$.
Input:	Optimized device parameters $\overset{*}{\mathbf{XA}}$. Computed following Algorithm 2.
Output:	Optimal correspondence $\overset{*}{\mathbf{CF}}$ between the acquired frames.

1	Compute jump-cost C according to Equation 12
2	Use referent corresponding end-diastole pair
3	Compute jump cost $\xi(\mathbf{a},\mathbf{b})$ according to Equation 8
4	Compute cost matrix $\mathbf{D}$ according to Equations 8 and 9
5	Find corresponding frames $\overset{*}{\mathbf{CF}}=\mathrm{OSB}(\mathbf{D},\delta)$ according to Equation 7

Algorithm 4 Reconstruction of vessel centreline from its two corresponding projections (Section 2.6)

Input:	Calibrated device parameters $\overset{*}{\mathbf{XA}}$.
Input:	Centreline point samples from two corresponding frames $\vec{\mathbf{c}}_{i,j}\left\{i = 1,2;\ j = 1,\begin{matrix} m\ \ for\ i = 1 \\ p\ \ for\ i = 2 \end{matrix}\right\}$, where m and p indicates number of points sampled from primary view and secondary view.
Output:	Parameterized vessel centreline in 3D $\vec{\mathrm{C}}(t)$.

1	Compute jump cost $\xi(\mathbf{a},\mathbf{b})$ according to Equation 10
2	Compute cost matrix $\mathbf{D}$ according to Equations 10 and 11
3	Find correspondences between candidate points $\mathbf{a} = \vec{\mathbf{c}}_{i,j}\{i = 1;\ j = 1...g\}$ and $\mathbf{b} = \vec{\mathbf{c}}_{i,j}\{i = 2;\ j = 1...h\}$ as $\overset{*}{\mathbf{CP}} = \mathrm{OSB}(\mathbf{D},\delta)$ according to Equation 7
4	Define parameterized curve $\vec{\mathrm{C}}(t)$ from obtained q corresponding points $\overset{*}{\mathbf{CP}}$

Algorithm 5 Reconstruction of vessel branch 3D surface $\vec{S}(u,v)$ from its two projections (Section 2.7)

Input:	Calibrated device parameters $\overset{*}{\mathbf{XA}}$ obtained following Algorithm 3.
Input:	Parameterized vessel centreline $\vec{C}(t)$ following Algorithm 4.
Input:	Parameters $\mathbf{t} = \{t_1, t_2, ...\}$ that define positions of patches along the centreline $\vec{P}(t)$.
Input:	Parameters vessel centrelines $\vec{c}_i \{i = 1,2\}$ and their corresponding borders $\vec{b}_{i,j} \{i = 1,2; j = 1,2\}$ from two corresponding XRA views.
Output:	Parameterized 3D NURBS surface $\vec{S}(u,v)$ of the vessel.

1	**for each** t **in** vector **t do**
2	At point $\vec{\mathbf{C}}(t)$ define a trihedron by the curve's tangent $\vec{T}(t)$, normal $\vec{N}(t)$ and binormal $\vec{B}(t)$
3	**for** i = 1 **to** 2 (or more XRA views available) **do**
4	Consider centreline point $\vec{\mathbf{C}}(t)$ and its corresponding 2D point $\vec{\mathbf{c}}_i(t_i)$ on the i-th view
5	Calculate normal $\vec{n}_i(t_i)$ of centreline curve at point $\vec{\mathbf{c}}_i(t_i)$
6	Calculate points $\vec{\mathbf{p}}_{\mathbf{a}_i}(t_i)$ and $\vec{\mathbf{p}}_{\mathbf{b}_i}(t_i)$ as intersection of normal $\vec{n}_i(t_i)$ with borders $\vec{b}_{i,j}$
7	Calculate $\vec{\mathbf{P}}_{\mathrm{a,i}}(t)$ from $\vec{\mathbf{p}}_{\mathrm{a}_i}(t_i)$ according to Equation 3
8	Define line $\vec{L}_1(\vec{F}_i, \vec{\mathbf{P}}_{\mathbf{a}_i})$ using X-ray source point $\vec{\mathbf{F}}_{\mathbf{i}}$ and point $\vec{\mathbf{P}}_{\mathbf{a}_i}(t)$
9	Define second line $\vec{L}_2(\vec{\mathbf{C}}(t), \vec{T}(t))$ with point $\vec{\mathbf{P}}(\mathbf{t})$ and direction vector $\vec{T}(t)$
10	Find $\vec{\mathbf{A}}_i(s_u, t)$ by solving Equations 1–5for lines L_1 and L_2
11	Find $\vec{\mathbf{B}}_i(s_u, t)$ by repeating steps 8–11 for $\vec{\mathbf{p}}_{\mathbf{b}_i}(t_i) \rightarrow \vec{\mathbf{P}}_{\mathbf{b}_i}(t)$
12	Project $\vec{\mathbf{A}}_i(s_u, t)$ and $\vec{\mathbf{B}}_i(s_u, t)$ to normal–binormal plane of the trihedron
13	**end for**
14	Depending on the available projection numbers, fit either a circle, ellipse, or polygonal t-th patch on the points in the normal–binormal plane of the trihedron
15	**end for**
16	Interpolate each of q patches with w points, and use them to construct NURBS surface $\vec{S}(u,v)$ according to Equation 18

Algorithm 6 Reconstruction of CA tree mesh from its two corresponding projections (Section 2.9)

Input:	Device parameters $\overset{*}{\mathbf{XA}}$ calibrated following Algorithm 3.
Input:	Total s vessel centrelines parameterized with B-splines $\vec{\mathrm{C}}_j(t)\{j=1,s\}$ following Algorithm 4.
Input:	Bifurcations list describing the connectivity between the CA trees' branches (centrelines). Example: For CA tree composed of tree branches $\vec{\mathrm{C}}_1$ (inlet), $\vec{\mathrm{C}}_2$ (outlet), $\vec{\mathrm{C}}_3$ (outlet), and one bifurcation, the bifurcation list is $\mathbf{B}=[1 \quad 2 \quad 3]$.
Output:	Reconstructed CA tree.

1	**for** t = 1 **to** the total number of bifurcations in **B do**
2	Direct trihedrons orientation of the output branches $\vec{\mathrm{C}}_{\mathbf{B}_t(2)}$ and $\vec{\mathrm{C}}_{\mathbf{B}_t(3)}$ according to the end-trihedron of the input branch $\vec{\mathrm{C}}_{\mathbf{B}_t(1)}$ (see Figure 7 c)
3	**end for**
4	**for** j = 1 **to** the total number of branches s **do**
5	Reconstruct vessel surface $\vec{\mathrm{S}}_j(u,v)$ from its two corresponding projections following Algorithm 5 (see Figure 7 d)
6	**end for**
7	**for** t = 1 to the total number of bifurcations in **B do**
8	Trim outlet-side of the input branch $\vec{\mathrm{S}}_{\mathbf{B}_t(1)}$ and inlet-side of the output branches $\vec{\mathrm{S}}_{\mathbf{B}_t(2)}$ and $\vec{\mathrm{S}}_{\mathbf{B}_t(3)}$ following the pattern in Figure 7 e and f
9	**end for**