Computational Cardiology Lecture 11

Image coordinates, pixel-cell meshes and geometric sensitivity

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An intensity array and a geometric image

$$I_{r,c} \in [0,1], \qquad x_{r,c} \in \mathbb{R}^2.$$

Intensities do not have length units. Spatial metadata determines physical positions.

Thresholding defines a set

$$M_t = \{(r, c) : I_{r,c} \geq t\}.$$

A binary mask defines selected indices before any area is measured.

The physical coordinate map

$$x = o + D\,\mathrm{diag}(s_x, s_y)\begin{pmatrix} c \\ r \end{pmatrix}.$$

Array indexing is row–column; the geometric vector is column–row.

Matrix order matters

$$D\,\mathrm{diag}(s_x, s_y) \neq \mathrm{diag}(s_x, s_y)D$$

for unequal spacings and a general rotation.

Pixel centers and corners

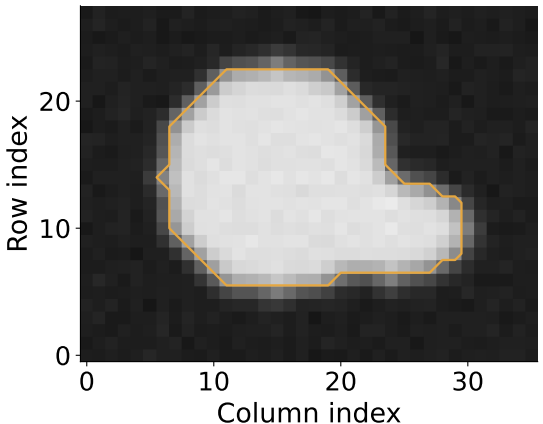
The origin locates the center of pixel zero. Corners use $(c \pm \frac{1}{2}, r \pm \frac{1}{2})$ before the physical transformation.

Area scaling

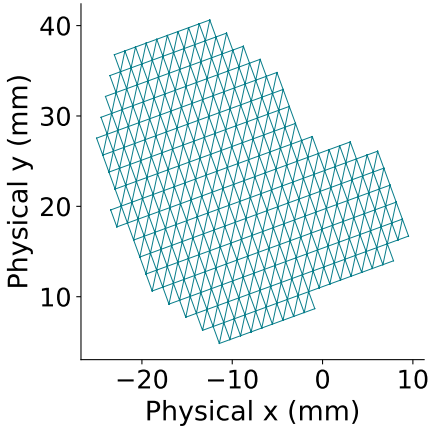
$$\det(D\,\mathrm{diag}(s_x, s_y)) = s_x s_y$$

when D is a proper rotation. Translation does not change area.

Image + threshold mask



Two triangles per cell



Triangulating the selected cells

Each foreground rectangle becomes two consistently oriented triangles with shared vertex indices. This is a mesh of the pixel-cell union.

Signed triangle area

$$A_T = \frac{1}{2} \det \begin{pmatrix} x_2 - x_1 & x_3 - x_1 \\ y_2 - y_1 & y_3 - y_1 \end{pmatrix}.$$

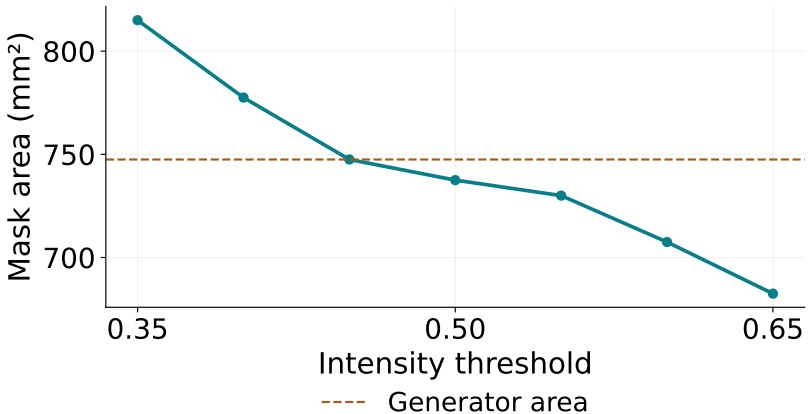
A sign reversal detects reversed vertex ordering.

Mask area and mesh area

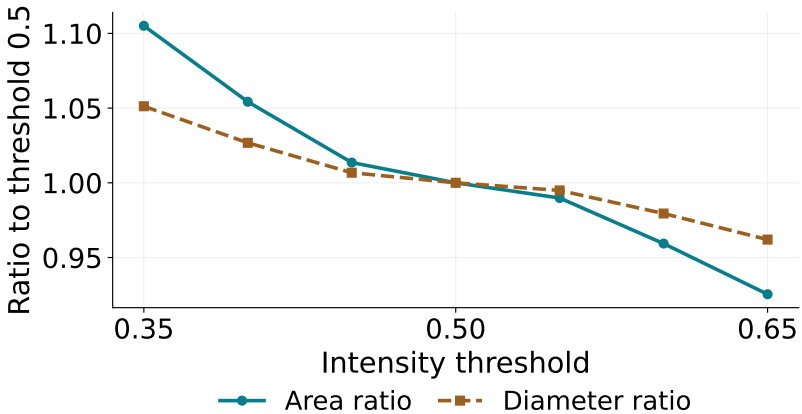
$$A_M = N_f s_x s_y = \sum_T A_T.$$

The default 295 selected pixels give 590 triangles, each of area 1.25 mm^2.

Segmentation sensitivity



Equivalent-circle summary



Threshold sets are nested

$$t_2 > t_1 \quad \Longrightarrow \quad M_{t_2} \subseteq M_{t_1}.$$

Area cannot increase, but component count need not be monotone.

Equivalent-circle diameter

$$d_{eq} = 2\sqrt{A_M/\pi}.$$

This is an area summary, not an estimate of every anatomical diameter.

Relative sensitivity

$$\frac{\delta d_{eq}}{d_{eq}} \simeq \frac{1}{2}\frac{\delta A}{A}.$$

A threshold range is not a confidence interval without a probability model.

Scale and location have different signatures

Doubling both spacings quadruples area. Translating the origin changes all positions while preserving every triangle area.

Refining the mesh does not refine the image

Subdividing triangles inside the same selected cells leaves the represented boundary unchanged. Resolving a finer boundary requires additional image information or a new geometric assumption.

Label resampling

Nearest-neighbor resampling preserves the set of label values. It need not preserve thin connections, area or boundary position on a new target grid.