Computational Cardiology Lecture 11

Image coordinates, pixel-cell meshes and geometric sensitivity

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An intensity array and a geometric image

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

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

Thresholding defines a set

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

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

The physical coordinate map

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

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

Matrix order matters

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for unequal spacings and a general rotation.

Pixel centers and corners

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Area scaling

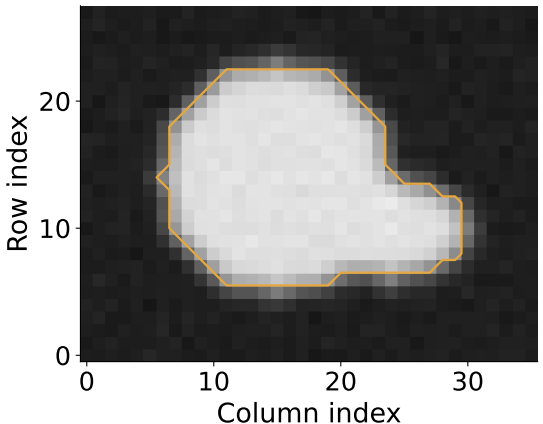
$$\det(D\,\mathrm{diag}(s_x, s_y)) = s_x s_y$$

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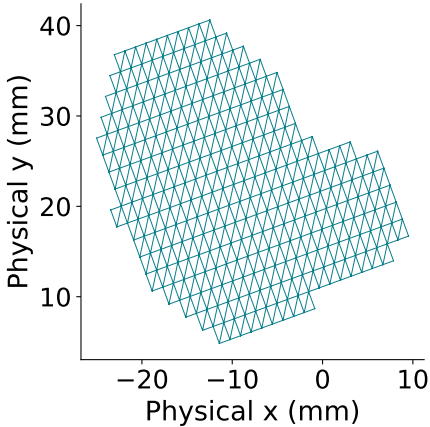
$$\det(D\,\mathrm{diag}(s_x, s_y)) = s_x s_y$$

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.

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

Signed triangle area

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

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A sign reversal detects reversed vertex ordering.

Mask area and mesh area

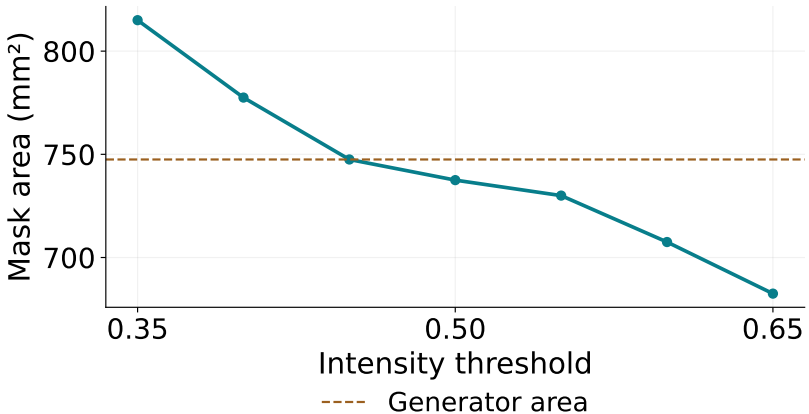
$$A_M = N_f s_x s_y = \sum_T A_T.$$

Mask area and mesh area

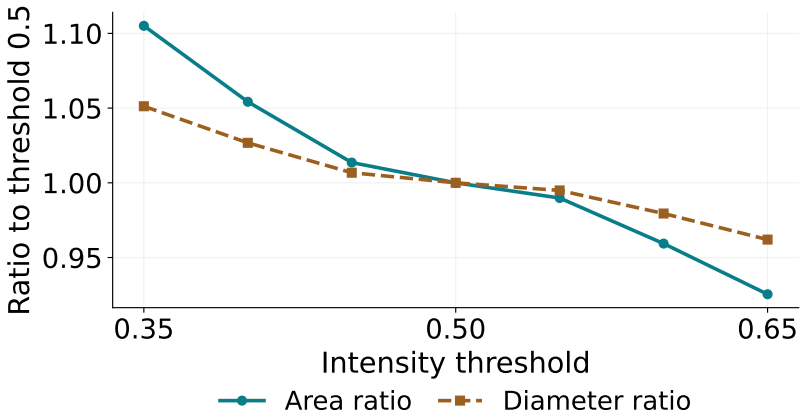
$$A_M = N_f s_x s_y = \sum_T A_T.$$

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

Segmentation sensitivity



Equivalent-circle summary



Threshold sets are nested

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

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

Equivalent-circle diameter

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

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

Relative sensitivity

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

Scale and location have different signatures

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

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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.

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