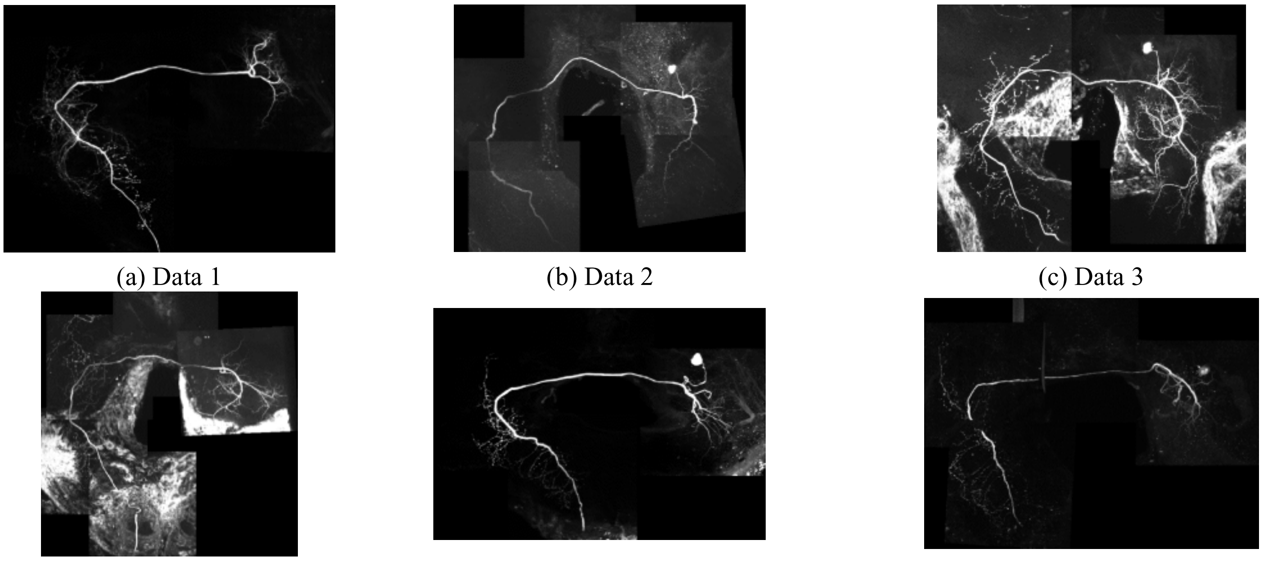

(a) Data 1 (b) Data 2 (c) Data 3

(d) Data 4. (e) Data 5. (f) Data 6.

Fig. 18. CLSM cross-sectional image series of premotor neurons of silkworm moths (projection image).

a line passing from the median point of main branch to the origin and to a point which is on a main branch and length of these lines are calculated as indicated Fig. 14. In Fig. 14, O is the origin and G is the median point of main branch, and P_t is a point on a main branch, and t is (0, 1, . . ., n_{right}): n_{right} is number of voxel on the main branch of right side, and P_0 is the origin. Therein, median point is obtained by averaging out coordinate values of a main branch. A correlation coefficient of these angles and lengths is set as Feature 2. This correlation coefficient is obtained with Eqs. (2)–(6).

$$f_2 = r = \frac{\sum_{t=0}^{n_{\text{right}}}(\theta_t - \bar{\theta})(l_t - \bar{l})}{\sqrt{\sum_{t=0}^{n_{\text{right}}}(\theta_t - \bar{\theta})^2}\sqrt{\sum_{t=0}^{n_{\text{right}}}(l_t - \bar{l})^2}}. \tag{2}$$

Where

$$\theta_t = \cos^{-1}\left(\frac{\overrightarrow{\mathrm{GP}_t} \cdot \overrightarrow{\mathrm{GO}}}{\left||\overrightarrow{\mathrm{GP}_t}|\right| \left||\overrightarrow{\mathrm{GO}}|\right|}\right) \tag{3}$$

$$\begin{aligned} l_t &= \left||\overrightarrow{\mathrm{GP}_t}|\right| \\ &= \sqrt{(x_g - x_t)^2 + (y_g - y_t)^2 + (z_g - z_t)^2} \end{aligned} \tag{4}$$

$$\bar{\theta} = \frac{1}{n_{\text{right}}} \sum_{t}^{n_{\text{right}}} \theta_t \tag{5}$$

$$\bar{l} = \frac{1}{n_{\text{right}}} \sum_{t}^{n_{\text{right}}} l_t. \tag{6}$$

Figure 15 shows the relationship between the angle and length. It is possible to replace a shape of main branch with an oval sphere in which a median point is the origin. If a main branch extends in crosswise direction, the coefficient correlation nears 1 and this branch has been positively correlated. In addition, if a main branch extends in downward direction, the coefficient correlation nears -1: negatively correlated. This feature expresses a shape of main branch of right side.

[Feature 3]

Each type has the characteristics in location which nerve fibers extend to. In Type A, nerve fibers spread to the whole LAL. This means many branching points are in near the origin. In addition, in Type B, because nerve fibers extend to the LAL and the VPC, branching points can be anywhere (Fig. 16). By the same token, in Type C, branching points are removed from the origin because nerve fibers of Type C extend to the VPC. Therefore second-order moment and the mean coordinates of the branching points at the origin is set as Feature 3 in order to calculate relationship between the origin and branching points on the main branch. This feature is based on Key point 2 and obtained with Eqs. (7), (8), and (9); $\mathrm{E}(l^2)$ and $\mathrm{E}(l)$ are second-order moment and a mean distance from origin to a branching point, respectively, and m is the number of sub-branches. Distance from the origin to a branching point is the Euclidean distance obtained using Eq. (9).

$$f_{3-1} = \mathrm{E}(l) = \frac{1}{m}\sum_{i=1}^{m} l_i \tag{7}$$

$$f_{3-2} = \mathrm{E}(l^2) = \frac{1}{m}\sum_{i=1}^{m} l_i^2 \tag{8}$$

where

$$l_i = \sqrt{(x_i - x_0)^2 + (y_i - y_0)^2 + (z_i - z_0)^2}. \tag{9}$$

[Feature 4]

Biologists focus attention on whether nerve fibers spread in the LAL or not and how they spread. Then breadths of the distribution of the coordinate values which are the near origin are set as Feature 4. This means the difference of distribution of nerve fibers in the LAL. This feature is obtained with an eigenvalue of Eq. (10). Equation (10) indicates a variance-covariance matrix of coordinate values