PVC Workgroup Validation Metrics

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1   Input Data:

To validate the inverse solutions, there are three types of data that need to be considered. Each one appears at a different step from the inverse solutions. These correspond to the reconstructed potentials on the heart, the activation times estimated on those and the site of first activation (or pacing site). Since each inverse method is different, the results reported in each contribution will contain all or a subset of these three types of data.
Multiple realizations of an inverse should be allowed. For example there could be multiple recordings of the same underlying phenomena or should be possible to test an algorithm under different noise realizations. For this reason it is also necessary to be able to accept multiple solutions (epochs) of the same experiment in order to calculate statistics on the methods and derive some measure of robustness.
The data involved in these experiments is multidimensional, for this reason, it is necessary to first define some convention:

- the spatial dimension uses the index m which is defined from 1 to M number of nodes on the heart.

- the temporal dimension uses the index t, defined from 1 to T temporal samples in an epoch.

- the epoch dimension uses the index r, defined from 1 to R epochs in an experiment

Here we describe the type of results needed for validation:

1. **Potentials (EGM):** These are the potential distributions obtained through the inverse solution (in mV). They consist on matrices of size M by T (size of nodes on the heart by time instances available).

2. **Activation times (ACTT):** This vector represents the time instant at which a node on the heart is considered to be activated defined in (ms). It consists on a vector of size M (number of nodes on the heart).

3. **Pacing Coordinates (pacXYZ):** These are the coordinates where the pacing site is localized (in mm). These do not need to be placed exactly on a specific node of the geometry. It consists on a vector of 3 coordinates (X, Y, Z).

2 Metrics:

The metrics defined here are referenced to a set of true solutions that need to be uploaded on the server a priori. The elements that form this ground truth are EGM_{ref} which corresponds to the true EGM solution, $ACTT_{ref}$ which is the activation times obtained from the ground truth and $pacXYZ_{ref}$ which is the location of the first activation site.

On top of the previous references, the program must have the 3D coordinates of each element of the heart, a mask mapping node of the heart to ventricle (left/right), a mask mapping from heart node to surface (endocardial/epicardial), a mask mapping from heart node to AHA segment and the corresponding graph defined by the AHA segments.

1. **Relative Error (RMSE):** This metric measures the relative mean squared error (RMSE) in space averaged across time. That is, the RMSE obtained per each time instance averaged. To define it we will use the following definitions:

$$
\begin{aligned}
x &= EGM_r \in \Re^{M,T} \\
y &= EGM_{ref,r} \in \Re^{M,T}
\end{aligned}
\tag{1}
$$

$$
\begin{aligned}
RMSEr &= \frac{1}{T} \sum_{t=1}^{T} \frac{\|x_t - y_t\|_2^2}{\|y_t\|_2^2} \\
&= \frac{1}{T} \sum_{t=1}^{T} \frac{\sum_{m=1}^{M}(x_{m,t} - y_{m,t})^2}{\sum_{m=1}^{M}(y_{m,t})^2}
\end{aligned}
\tag{2}
$$

After obtaining the relative error per each epoch $RMSE_r$, we will measure its mean and standard deviation.

$$
\begin{aligned}
\overline{RMSE} &= \frac{1}{R} \sum_{r=1}^{R} RMSEr \\
\sigma_{RMSE} &= \sqrt{\frac{1}{R} \sum_{r=1}^{R} (RMSEr - \overline{RMSE})^2}
\end{aligned}
\tag{3}
$$

2. **Correlation of EGM (corrEGM):** This metric is the average correlation in space between true and measured potentials.

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To define it we will use the following definitions:

$$x = EGM_r \in \Re^{M,T}$$
$$y = EGM_{ref,r} \in \Re^{M,T} \tag{4}$$

$$\overline{x}_t = \frac{1}{M}\sum_{m=1}^{M} x_{m,t}$$
$$\overline{y}_t = \frac{1}{M}\sum_{m=1}^{M} y_{m,t} \tag{5}$$

$$corr\,EGM_r = \frac{1}{T}\sum_{t=1}^{T} \frac{\sum_{m=1}^{M}(x_{m,t}-\overline{x}_t)*(y_{m,t}-\overline{y}_t)}{\sqrt{\sum_{m=1}^{M}(x_{m,t}-\overline{x}_t)^2}*\sqrt{\sum_{l=1}^{M}(y_{l,t}-\overline{y}_t)^2}} \tag{6}$$

As done with the RMSE measures, the mean and standard deviation of this metric need to be measured.

3. **Activation Times Correlation (ACTTCorr):** This metric measures the correlation between reconstructed and true activation times. It is defined similarly to the correlation in EGM, but this time the input vectors are defined as:

$$x = ACTT_r \in \Re^{M}$$
$$y = ACTT_{ref,r} \in \Re^{M} \tag{7}$$

$$\overline{x} = \frac{1}{M}\sum_{m=1}^{M} x_m$$
$$\overline{y} = \frac{1}{M}\sum_{m=1}^{M} y_m \tag{8}$$

$$ACTTCorr_r = \frac{\sum_{m=1}^{M}(x_m-\overline{x})*(y_m-\overline{y})}{\sqrt{\sum_{m=1}^{M}(x_m-\overline{x})^2 * \sum_{l=1}^{M}(y_l-\overline{y})^2}} \tag{9}$$

4. **Localization Error (locErr):** This metric measures the euclidean distance of the reconstructed location of the first activation versus the true.

$$x = pacXYZ(1); \quad x_{ref} = pacXYZ_{ref}(1);$$
$$y = pacXYZ(2); \quad y_{ref} = pacXYZ_{ref}(2);$$
$$z = pacXYZ(3); \quad z_{ref} = pacXYZ_{ref}(3); \tag{10}$$
$$locErr_r = \sqrt{(x-x_{ref})^2 + (y-y_{ref})^2 + (z-z_{ref})^2}$$

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As done with the RMSE measures, the mean and standard deviation of this metric need to be measured.

5. **Ventricle Location (ventLoc):** This is a boolean measure. It is true if the node on the heart that is closest to the reconstructed pacing site is placed on the correct ventricle. The algorithm to measure it is the following:

    (a) find closest node on the heart from true pacing site.

    (b) determine ventricle of node from that node from predetermined mask and store in ventTrue.

    (c) find closest node on the heart from reconstructed pacing site.

    (d) determine ventricle of node from that node from predetermined mask and store in ventRec.

    (e) ventLoc = (ventRec =? ventTrue)

As done with the RMSE measures, the mean and standard deviation of this metric need to be measured.

6. **AHA location (ahaLoc):** This metric measures the distance of the reconstructed pacing site from the true location on the graph created with the AHA segmentation of the heart. The algorithm to measure it is the following:

    (a) find closest node on the heart from true pacing site.

    (b) determine the AHA segment of node from that node from predetermined mask and store in ahaTrue.

    (c) find closest node on the heart from reconstructed pacing site.

    (d) determine the AHA segment of node from that node from predetermined mask and store in ahaRec.

    (e) ahaLoc = dist(ahaRec, ahaTrue)

Where the dist(,) is a function that calculates the shortest distance on the graph (it casn be precomputed in a lookup table).

As done with the RMSE measures, the mean and standard deviation of this metric need to be measured.

7. **Correct Selection of Endo/Epi-cardial side (endoEpiSel):** This is a boolean measure. It is true if the node on the heart that is closest to the reconstructed pacing site is placed on the correct side of the heart wall (endocardium or epicardium). The algorithm to measure it is the following:

    (a) find closest node on the heart from true pacing site.

    (b) determine surface of node from that node from predetermined mask and store in surfTrue.

(c) find closest node on the heart from reconstructed pacing site.

(d) determine surface of node from that node from predetermined mask and store in surfRec.

(e) endoEpiSel = (surfRec =? surfTrue)

As done with the RMSE measures, the mean and standard deviation of this metric need to be measured.