

Joint Velocity

The Joint Velocity model-based item is a vector that describes the relative angular velocity of one segment relative to another segment.

Compute Model Based Data

Data Name: Lt Knee Ang Vel

Folder: ORIGINAL

Result Folder will always be Original

Joint Angular Velocity (degrees/sec):

Segment and Reference Segment define the joint angular velocity.

Resolution coordinate system defines the velocity relative to the lab or a segment.

Model Based Item Properties

JOINT_VELOCITY

Use Negative

X ☐ Y ☐ Z ☐

Segment: Left Shank

Reference Segment: Left Thigh

Resolution Coordinate System: Left Thigh

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Relationship between the Joint Angular Velocity and the derivative of the Cardan Joint Angles

The Joint Velocity can be a bit troublesome to interpret unless you recognize that the signal is not the same as the derivative of the Joint Angle. It is possible that the some terms of the Joint Velocity are not consistent with the derivative of the Joint Angle. Euler angles are not vectors, so it isn't possible to compute joint angular velocity by taking the first derivative of the joint angles (e.g. Euler/Cardan angles).

With respect to the default Visual3D convention of an XYZ sequence for the Cardan angle, the joint angular velocity can be expressed in Euler angles using the following relationship.

The angular velocity in body coordinates $\omega = \begin{bmatrix} \omega_x \\ \omega_y \\ \omega_z \end{bmatrix}$

can be expressed in terms of

the derivatives of the Euler angles $\dot{\theta} = \begin{bmatrix} \dot{\theta}_x \\ \dot{\theta}_y \\ \dot{\theta}_z \end{bmatrix}$

as:

$$\begin{bmatrix} \omega_x \\ \omega_y \\ \omega_z \end{bmatrix} = \begin{bmatrix} \dot{\theta}_x \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 \\ 0 & c_x & -s_x \\ 0 & s_x & c_x \end{bmatrix} \begin{bmatrix} 0 \\ \dot{\theta}_y \\ 0 \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 \\ 0 & c_x & -s_x \\ 0 & s_x & c_x \end{bmatrix} \begin{bmatrix} c_y & 0 & s_y \\ 0 & 1 & 0 \\ -s_y & 0 & c_y \end{bmatrix} \begin{bmatrix} 0 \\ 0 \\ \dot{\theta}_z \end{bmatrix}$$

$$\begin{bmatrix} \omega_x \\ \omega_y \\ \omega_z \end{bmatrix} = \begin{bmatrix} \dot{\theta}_x \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 1 & 0 & 0 \\ 0 & c_x & -s_x \\ 0 & s_x & c_x \end{bmatrix} \begin{bmatrix} 0 \\ \dot{\theta}_y \\ 0 \end{bmatrix} + \begin{bmatrix} c_y & 0 & s_y \\ s_x s_y & c_x & -s_x c_y \\ -c_x s_y & s_x & c_x c_y \end{bmatrix} \begin{bmatrix} 0 \\ 0 \\ \dot{\theta}_z \end{bmatrix}$$

$$\begin{bmatrix} \omega_x \\ \omega_y \\ \omega_z \end{bmatrix} = \begin{bmatrix} \dot{\theta}_x \\ 0 \\ 0 \end{bmatrix} + \begin{bmatrix} 0 \\ c_x \dot{\theta}_y \\ s_x \dot{\theta}_y \end{bmatrix} + \begin{bmatrix} s_y \dot{\theta}_z \\ -s_x c_y \dot{\theta}_z \\ c_x c_y \dot{\theta}_z \end{bmatrix} = \begin{bmatrix} \dot{\theta}_x + s_y \dot{\theta}_z \\ c_x \dot{\theta}_y - s_x c_y \dot{\theta}_z \\ s_x \dot{\theta}_y + c_x c_y \dot{\theta}_z \end{bmatrix}$$

Where $s_i = \sin(\theta_i)$, $c_i = \cos(\theta_i)$ for $i = x, y, z$

Example - Comparing Joint Angle and Joint Angular Velocity

Joint Angles are typically represented in a Cardan sequence and Joint Velocities are typically represented as vectors. The consequence is that you cannot compare directly all 3 components of the Joint Angle with, what appear to be homologous, components of the Joint Velocity. For example, given the following definition of the Right Knee Angle:

Compute Model Based Data

Data Name

RKNEE_ANGLE

Folder

ORIGINAL

Result Folder will always be Original

Joint Angle (degrees):

Segment and Reference Segment define the angle desired.

Normalization is relative to standing posture.

The Cardan Sequence defines the order of rotations.

Warning!!! If you are using the anatomical axes (ML, AP, or AXIAL) the sign of the angle follows the Right Hand Rule about the actual corresponding segment coordinate system axes.

Create

Reset Dialog

Close

Model Based Item Properties

JOINT_ANGLE

Use Negative

☐ X
☐ Y
☐ Z

Normalization

Normalization Off

Segment

Right Shank

Reference Segment

Right Thigh

Cardan Sequence

X-Y-Z

and the following definition of the Right Knee Angular Velocity:

Compute Model Based Data

Data Name

RKNEE_VELOCITY1

Folder

ORIGINAL

Result Folder will always be Original

Joint Angular Velocity (degrees/sec):

Segment and Reference Segment define the joint angular velocity.

Resolution coordinate system defines the velocity relative to the lab or a segment.

Create

Reset Dialog

Close

Model Based Item Properties

JOINT_VELOCITY

Use Negative

☐ X
☐ Y
☐ Z

Segment

Right Shank

Reference Segment

Right Thigh

Resolution Coordinate System

Right Thigh

only the X-components of the two signals are related (i.e., these components relate to the segment's rotation about the same axis).

If a second Joint Velocity item is created as follows:

Compute Model Based Data

Data Name

RKNEE_VELOCITY2

Folder

ORIGINAL

Result Folder will always be Original

Joint Angular Velocity (degrees/sec):

Segment and Reference Segment define the joint angular velocity.

Resolution coordinate system defines the velocity relative to the lab or a segment.

Create

Reset Dialog

Close

Model Based Item Properties

JOINT_VELOCITY

Use Negative

☐ X

☐ Y

☐ Z

Segment

Right Thigh

Reference Segment

Right Shank

Resolution Coordinate System

Right Shank

then the Z-components of this second definition and the original joint angle definition can be compared.

If the Y-component (the 2nd component) of the knee angle is small it is often referred to as ab/adduction, but it is important to note that this rotation is technically isn't about either the y-axis of the thigh or shank segments. If this Joint Angle Y-component isn't small then it is not really possible to compare the Y-components between the Joint Angle and Joint Velocity items.

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