

Name	Description	Parameter	Return
<b>Manage instances of the reader/writer modules</b>			
AddJointReader	In this method an instance of the joint reader is added to the interface.	<b>name:</b> Name for the joint reader instance, later used to identify it. ( <i>string</i> )	-
AddJointWriter	In this method an instance of the joint writer is added to the interface.	<b>name:</b> Name for the joint writer instance, later used to identify it. ( <i>string</i> )	-
AddSkinReader	In this method an instance of the skin reader is added to the interface.	<b>name:</b> Name for the skin reader instance, later used to identify it. ( <i>string</i> )	-
AddVisualReader	In this method the instance of the visual reader is added to the interface.	-	-
RemoveVisualReader	In this method the instance of the visual reader is removed from the interface.	-	-
<b>Joint reader member functions</b>			
JointRInit	This method initializes the joint reader instance with the given parameters.	<b>name:</b> Name of the joint reader instance to identify it. ( <i>string</i> ) <b>part:</b> iCub part which should be controlled with this instance. ( <i>string</i> ) <b>sigma:</b> Standard deviation of the Gaussian encoding for the population coded joint angles. ( <i>double</i> ) <b>n_pop:</b> Set the Population size for the joint angle population coding. ( <i>int</i> ) <b>degr_per_neuron:</b> neuron degree resolution for the population coding; default value 0.0: if non-zero the population size for each joint is computed with the given resolution and the joint angle range. ( <i>double</i> )	A failure indication value, being true for a successful execution. ( <i>bool</i> )
JointRClose	This method closes the joint reader with a cleanup.	<b>name:</b> Name of the joint reader instance to identify it. ( <i>string</i> )	-
JointRGetJointCount	This method returns the number of	<b>name:</b> Name of the joint reader instance to identify it.	Amount of joints associated to the

Name	Description	Parameter	Return
	joints controlled by the joint reader.	( <i>string</i> )	joint reader ( <i>int</i> )
JointRGetJointsDegRes	This method returns the resolution of the populations encoding the joint angles.	<b>name:</b> Name of the joint reader instance to identify it. ( <i>string</i> )	Resolution of the joints in degree. ( <i>vector[double]</i> )
JointRGetNeuronsPerJoint	This method returns the size of the populations encoding the joint angles	<b>name:</b> Name of the joint reader instance to identify it. ( <i>string</i> )	Neurons in the populations per associated joint. ( <i>vector[int]</i> )
JointRReadDouble	This method reads the angle of one joint and return the joint angle directly as a double value.	<b>name:</b> Name of the joint reader instance to identify it. ( <i>string</i> ) <b>joint:</b> number of the selected joint ( <i>int</i> )	Joint angle in degree. ( <i>double</i> )
JointRReadPopAll	This method reads the angles of all joints and returns the joint angles encoded in vectors.	<b>name:</b> Name of the joint reader instance to identify it. ( <i>string</i> )	The joint angles of all joints encoded in populations. ( <i>vector[vector[double]]</i> )
JointRReadPopOne	This method reads the angle of one joint and return the joint angle encoded in a vector	<b>name:</b> Name of the joint reader instance to identify it. ( <i>string</i> ) <b>joint:</b> number of the selected joint ( <i>int</i> )	The joint angles of the selected joint encoded in populations. ( <i>vector[double]</i> )
<b>Joint writer member functions</b>			
JointWInit	This method initializes the joint writer with the given parameters.	<b>name:</b> Name of the joint writer instance to identify it. ( <i>string</i> ) <b>part:</b> iCub part which should be controlled with this instance. ( <i>string</i> ) <b>n_pop:</b> Set the Population size for the joint angle population coding. ( <i>int</i> ) <b>degr_per_neuron:</b> neuron degree resolution for the population coding; default value 0.0; if non-zero the population size for each joint is computed with the given resolution and the joint angle range. ( <i>double</i> ) <b>speed:</b> Joint velocity value set for all joints. ( <i>double</i> )	A failure indication value, being true for a successful execution. ( <i>bool</i> )

Name	Description	Parameter	Return
JointWClose	This method closes the joint writer with a cleanup.	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i>	-
JointWGetJointCount	This method returns the number of joints controlled by the joint writer.	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i>	Amount of joints associated to the joint writer. <i>(int)</i>
JointWGetJointsDegRes	This method returns the resolution of the populations encoding the joint angles.	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i>	Resolution of the joints in degree <i>(vector[double])</i>
JointWGetNeuronsPerJoint	This method returns the size of the populations encoding the joint angles	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i>	Neurons in the populations per associated joint. <i>(vector[int])</i>
JointWSetJointVelocity	In this method the joint velocity is set. Two modes are possible, set the velocity for one selected joint or set the velocity for all joints.	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i> <b>speed:</b> The velocity value which should be set. <i>(double)</i> <b>joint:</b> number of the selected joint, -1 to set all joints <i>(int)</i>	A failure indication value, being true for a successful execution. <i>(bool)</i>
JointWWriteDoubleAll	This method write all joints with double values. The joint motion can be executed in a non-blocking or a blocking mode.	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i> <b>position:</b> joint angle values for all joints <i>(vector[double])</i> <b>blocking:</b> Control the blocking execution of the joint movement. Default value is true. <i>(bool)</i>	A failure indication value, being true for a successful execution. <i>(bool)</i>
JointWWriteDouble	This method write one joint with a double value. The joint motion can be executed in a non-blocking or a blocking mode.	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i> <b>position:</b> joint angle value for the selected joint <i>(double)</i> <b>joint:</b> number of the selected joint <i>(int)</i> <b>blocking:</b> Control the blocking execution of the joint movement. Default value is true. <i>(bool)</i>	A failure indication value, being true for a successful execution. <i>(bool)</i>
JointWWritePopAll	This method write all joints with joint angles encoded in populations.	<b>name:</b> Name of the joint writer instance to identify it. <i>(string)</i>	A failure indication value, being true for a successful execution. <i>(bool)</i>

Name	Description	Parameter	Return
		<b><i>position_pops</i></b> : The joint angles for all joints encoded in populations. ( <i>vector[vector[double]]</i> ) <b><i>blocking</i></b> : Control the blocking execution of the joint movement. Default value is true. ( <i>bool</i> )	
JointWWritePopOne	This method write one selected joint with the joint angle encoded in a population.	<b><i>name</i></b> : Name of the joint writer instance to identify it. ( <i>string</i> ) <b><i>position_pop</i></b> : The joint angles for all joints encoded in populations. ( <i>vector[double]</i> ) <b><i>joint</i></b> : number of the selected joint ( <i>int</i> ) <b><i>blocking</i></b> : Control the blocking execution of the joint movement. Default value is true. ( <i>bool</i> )	A failure indication value, being true for a successful execution. ( <i>bool</i> )
<b>Skin reader member functions</b>			
SkinRInit	This method initialize the skin reader with the given parameters.	<b><i>name</i></b> : Name of the skin reader instance to identify it. ( <i>string</i> ) <b><i>arm</i></b> : A parameter selecting the skin side. Right 'R'/'r' or left 'L'/'l' is possible . ( <i>char</i> ) <b><i>norm</i></b> : A bool parameter to control if the tactile sensor data is returned normalized. The default value is true. ( <i>bool</i> )	A failure indication value, being true for a successful execution. ( <i>bool</i> )
SkinRClose	This method closes the skin reader and cleans up the module.	<b><i>name</i></b> : Name of the skin reader instance to identify it. ( <i>string</i> )	-
SkinRGetTactileArm	Returns the tactile data of the upper arm skin sensors.	<b><i>name</i></b> : Name of the skin reader instance to identify it. ( <i>string</i> )	Tactile data for the upper arm skin section, divided in steps (first dim: step, second dim: sensor data non-normalized: [0..255] or normalized: [0..1]). (C++: <i>vector[vector[double]]</i> ; Python: <i>numpy array</i> )
SkinRGetTactileForearm	Returns the tactile data of the forearm	<b><i>name</i></b> : Name of the skin reader instance to identify it.	Tactile data for the forearm skin

Name	Description	Parameter	Return
	skin sensors.	( <i>string</i> )	section, divided in steps (first dim: step, second dim: sensor data non-normalized: [0..255] or normalized: [0..1]). (C++: <i>vector[vector[double]]</i> ; Python: <i>numpy array</i> )
SkinRGetTactileHand	Returns the tactile data for hand skin sensors.	<b>name:</b> Name of the skin reader instance to identify it. ( <i>string</i> )	Tactile data for the hand skin section, divided in steps (first dim: step, second dim: sensor data non-normalized: [0..255] or normalized: [0..1]). (C++: <i>vector[vector[double]]</i> ; Python: <i>numpy array</i> )
SkinRGetTaxelPos	Returns the taxel positions, given by the simulator ini-files, for the selected skin section.	<b>name:</b> Name of the skin reader instance to identify it. ( <i>string</i> ) <b>skin_part:</b> Selection of the skin section. Possible are: arm, forearm and hand. ( <i>string</i> )	Taxel positions for the different skin sections in relation to the kinematic links. (C++: <i>vector[vector[double]]</i> ; Python: <i>numpy array</i> )
SkinRReadTactile	In this method the complete sensor data is read and splitted in the different skin sections: upper arm, forearm and hand.	<b>name:</b> Name of the skin reader instance to identify it. ( <i>string</i> )	A failure indication value, being true for a successful execution. ( <i>bool</i> )
<b>Visual reader member functions</b>			
VisualRInit	Initializes the visual reader with given parameters. Returns a failure indication flag.	<b>eye:</b> Select the associated eye for the visual reader, 'L'/'l' for the left eye and 'R'/'r' for the right eye. ( <i>char</i> ) <b>fov_width:</b> Choose the width of the output field of view (fov). The iCub fov width is 60°. The default value is the 60°. ( <i>double</i> ) <b>fov_height:</b> Choose the height of the output field of view (fov). The iCub fov height is 48°. The default value is the 48°. ( <i>double</i> )	A failure indication value, being true for a successful execution. ( <i>bool</i> )

Name	Description	Parameter	Return
		<p><b><i>img_width</i></b>: Select the out image width in pixel. The default simulator image output width is 320 px, therefore the default value is 320 px. (<i>int</i>)</p> <p><b><i>img_height</i></b>: Select the out image height in pixel. The default simulator image output height is 240 px, therefore the default value is 240 px. (<i>int</i>)</p> <p><b><i>fast_filter</i></b>: A flag to select the filter for the image up-scaling. In the case of true a faster filter is selected with a slightly worse quality (cv::INTER_LINEAR). If the flag is not set, a filter with a higher quality is used, which is slower (cv::INTER_CUBIC). The default value for this parameter is true. (<i>bool</i>)</p>	
VisualRReadFromBuf	This method returns an image vector from the image buffer and removes it from the buffer	-	The camera image of the selected eye. The image is normalized and flattened from 2-D to 1-D (C++: <i>vector&lt;double&gt;</i> ; Python: <i>numpy array</i> )
VisualRStart	This method starts YARP-RF-Module, which reads the images from the iCub, normalizes and flatten the images and finally stores them in a buffer.	-	-
VisualRStop	This stop the RF-Module, reading the images from the iCub and terminates it.	-	-