

InterNational Committee for Information Technology Standards
INCITS Secretariat, Information Technology Industry Council (ITI)
1250 Eye St. NW, Room 200, Washington, DC 20005
Telephone 202-737-8888; Fax 202-638-4922
email: incits@itic.org

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Reply to: Cathy Tilton

Phone: 703-984-4080

email: cathy.tilton@daon.com

Daon Contribution to M1.2 on Common Transform Definitions

PURPOSE:

This preliminary proposal is for discussion purposes only at the June 6/7 meeting of M1.2. If favorably received, further steps can be defined at that meeting.

BACKGROUND:

Both BIAS and BioAPI 2.1 (19784-1, Amd 1) include “transform” operations, in which the particular transform operation to be performed is indicated by a parameter, the values and association of which is not defined in the standard. This preliminary proposal is to define a set of commonly used transform operations that can be utilized within each of these standards and thus enhance interoperability thereof.

BioAPI Transform Function:

8.1.13 BioAPI_Transform (BioAPI 2.1)

This subclause applies only when the BioAPI version number in use is 2.1.

BioAPI_RETURN BioAPI BioAPI_Transform

```
(BioAPI_HANDLE BSPHandle,  
const BioAPI_UUID *OperationUUID,  
const BioAPI_INPUT_BIR *InputBIRs,  
uint32_t NumberOfInputBIRs,  
BioAPI_BIR_HANDLE **OutputBIRs,  
uint32_t *NumberOfOutputBIRs);
```

8.1.13.1 Description

This function transforms one or more BIRs provided as input into one or more output BIRs. The transformation to be performed is identified by the OperationUUID parameter.

This International Standard does not specify any standard values for the OperationUUID parameter and does not specify any particular transformations. It is assumed that OperationUUID values and their semantics will be specified either by the provider of a particular BSP or by additional specifications (such as an application profile).

The function performs the following actions (in order):

- a) performs the transformation specified by the OperationUUID parameter using the BIR(s) provided as input and creating one or more output BIRs as required by the particular transformation;
- b) allocates a memory block large enough to contain an array of elements of type BioAPI_BIR_HANDLE with as many elements as the number of output BIRs created in (a);
- c) fills the array with the BIR handles of the output BIRs created in (a); and
- d) returns the address of the array in the OutputBIRs parameter and the size of the array in the NumberOfOutputBIRs parameter.

The memory block returned by the BioAPI function call shall be freed by the application using BioAPI_Free (see clause 8.7.2), and all the BIR handles present in the OutputBIRs array shall be destroyed using BioAPI_FreeBIRHandle.

8.1.13.2 Parameters

BSPHandle (input) – The handle of the attached biometric service provider.

OperationUUID (input) – A UUID that identifies the transformation to be performed by the BSP.

InputBIRs (input) - An array of BIRs (containing one or more BIRs) provided as input to the transformation.

NumberOfInputBIRs (input) - The number of BIRs in the array InputBIRs.

OutputBIRs (output) - A pointer to the address of an array of elements of type BioAPI_BIR_HANDLE containing the handles of the output BIRs created by the transformation.

NumberOfOutputBIRs (output) - A pointer to the number of elements of the array OutputBIRs.

8.1.13.3 Return Value

A BioAPI_RETURN value indicating success or specifying a particular error condition. The value BioAPI_OK indicates success. All other values represent an error condition.

8.1.13.4 Errors

BioAPIERR_BIOAPI_UNIT_NOT_INSERTED
BioAPIERR_UNIT_IN_USE
BioAPIERR_TRANSFORMATION_NOT_SUPPORTED
BioAPIERR_INVALID_BSP_HANDLE

See also **BioAPI Error Handling** (clause 11).

BIAS Transform Service

7.2.19 Transform Biometric Data

```
<interface name="TransformBiometricData">  
  <parameter name="InputBIR" type="CBEFF_BIR_Type" direction="in" />  
  <parameter name="TransformOperation"
```

```

    type="xs:unsignedLong" direction="in" />
    <parameter name="Return" type="xs:unsignedLong" direction="out" />
    <parameter name="OutputBIR" type="CBEFF_BIR_Type" direction="out" />
</interface>

```

7.2.19.1 Description

The Transform Biometric Data service shall transform or process a given biometric in one format into a new target format. Examples of transformations include:

- Feature Extraction
- Centering or cropping biometric images
- Standard biometric data format conversion

7.2.19.2 Parameters

Input BIR (input) – data structure containing the biometric information to be Transformed

Transform Operation (input) – value indicating the type of transformation to perform

Return (output) – return value indicating success or specifying a particular error Condition

Output BIR (output) – data structure containing the new, transformed biometric information

TRANSFORMS

The table below provides a preliminary list of transforms that are candidates for standardization.

Transform Name	Description
<i>Format Translation Transforms</i>	
Convert CBEFF Patron Format	Converts a BIR from one patron format to another (e.g., from a BioAPI to a PIV format). The BDB would remain unchanged.
Convert biometric data format	Converts a BDB from one format to another (e.g., from a Type-14 to INCITS 381 format).
Extract Data from Format	Extracts raw biometric data from within a data format structure (e.g., a JPEG image from an INCITS 385 record).
Base 64 encode/decode	Converts binary data to Base-64 encoded data or decodes base-64 to binary.

<i>Image Processing Transforms</i>	
Center/Crop Image	Either centers, crops, or both an input image.
Upsample/Downsample Image	Resamples an image to either increase or decrease its resolution.
Sharpen Image	Applies techniques to sharpen an input image.
<i>Compression Transforms</i>	
Compress Image	Compresses a raw data image (specify algorithm + compression ratio or target image size, ROI)
Decompress Image	Decompresses a compressed image
<i>Fingerprint Specific Transforms</i>	
Classify Fingerprint	Returns the Henry classification for an input fingerprint image
Segment Slap	Accepts a multi-finger slap fingerprint input image and returns either bounding box coordinates or separated individual fingerprint images.
<i>Other Transforms</i>	
Feature Extraction	Performs feature extraction from an input raw data sample (e.g., creates a minutiae template from a fingerprint image). AKA, template generation.
Quality Assessment	Returns a quality score for an input raw data sample (e.g., NFIQ score for a fingerprint image) based on a specified algorithm OR algorithm can be a return value.

APPROACH

Detailed specifications for each format will be required and would be performed under an approved project.

Since BioAPI uses a UUID and BIAS uses an unsigned long to indicate transform ID, both will need to be specified for each defined transform; however, the functionality should be the same.

In some cases, there are specific functions already available within the BioAPI or BIAS standards to perform a transform. In those cases, the user/application has a choice on which to use.

A given implementation may choose to implement 0, some, or all of the standard transforms. In the future, the discovery mechanisms may need to be extended to return information on which are supported, but initially this will be via product documentation.

It is NOT the intent to define every possible transform that will ever be used, only a set of commonly used transforms.

First thoughts are that this can be a separate standard in itself, though normatively referencing BIAS an BioAPI; however, there may be better ideas.

****Issue* – since there are no parameters for “transform properties”, transform IDs will be required for each specific transform operation.

2nd *issue* – BioAPI outputs must be in BIR format, so this may defeat the purpose of some of the operations.

EXAMPLE:

Transform ID: <assigned UUID or uint32>

Class/category: Format Translation/Extract Data from Format

Specific Transform: Extract JPEG image from INCITS 385 record.

Inputs:

Input BIR – INCITS 385 record (binary)

input BIRs - 1

Transform ID – as assigned

Outputs:

Output BIR – plain JPEG image record (JPEG format)

output BIRs - 1