

Observation Identification Service API specifications

Notes on terminology

- Identification *model implementations* are published instead of models (a model implementation is a combination of one or more models and a configuration of how to use them)

API endpoints

The v1 API is the first stable version of the API. Updates to the v1 API will be backwards compatible with existing v1 applications.

- `<tag>` refers to a manually assigned name for a specific model implementation

Identify	<code>/v1/observation/identify</code>	Common endpoint for all model implementations
	<code>/v1/observation/identify/<tag></code>	Endpoint for specific implementation
	<code>/v1/observation/identify/<tag>/auth</code>	Endpoint for specific implementation with user authorization
Taxa	<code>/v1/observation/taxa/<tag></code>	Endpoint for taxa in implementation
	<code>/v1/observation/taxa/<tag>?id=<id></code>	Endpoint for taxa in implementation filtered by taxon id
Documentation	<code>/v1/observation/documentation/<tag></code>	Endpoint for documentation of implementation (description, release notes, etc.)
Endpoints	<code>/v1/observation/endpoints/<tag></code>	Endpoint that lists all the endpoints for a specific tag
	<code>/v1/observation/endpoints</code>	Endpoint that lists all the endpoints

Detailed specifications

Identify

title:	Observation Identification Service - Identify										
description:	provides species identification implementations based on images										
endpoint:	<code>/v1/observation/identify</code> <code>/v1/observation/identify/<tag></code>										
method:	POST										
parameters:	<p><u>POST</u> image: binary image data</p> <p><u>URL (path)</u> tag: [optional] name of implementation to be used, if no tag is specified the Dutch/Belgium model will be used</p>										
response (successful):	<p>HTTP code: 200</p> <p>JSON-structure, containing the following elements:</p> <ul style="list-style-type: none">• identification<ul style="list-style-type: none">◦ image<ul style="list-style-type: none">■ confidence• predictions[...]<ul style="list-style-type: none">◦ probability◦ taxon<ul style="list-style-type: none">■ id■ name• model_implementation<ul style="list-style-type: none">◦ version• links<ul style="list-style-type: none">◦ taxa<ul style="list-style-type: none">■ url◦ taxa_with_filter<ul style="list-style-type: none">■ url <table><tr><th><i>JSON field</i></th><th><i>data-type</i></th><th><i>values</i></th><th><i>description</i></th></tr><tr><td>identification.image.confidence</td><td>string</td><td>"confident" (most likely prediction has a probability > 0.9) "uncertain" (most likely prediction has a probability > 0.2). "unknown" (otherwise)</td><td>indicates verbally the confidence of the image based species identification</td></tr></table>			<i>JSON field</i>	<i>data-type</i>	<i>values</i>	<i>description</i>	identification.image.confidence	string	"confident" (most likely prediction has a probability > 0.9) "uncertain" (most likely prediction has a probability > 0.2). "unknown" (otherwise)	indicates verbally the confidence of the image based species identification
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	predictions	array	top 10 predictions, ordered on probability, highest first.	most likely predictions
	predictions[...].probability	float	[0.0, 1.0]	probability of match for taxon
	predictions[...].taxon.id	string	unique taxon identifier in format {id_at_source}@{source_identifier}	identifies taxa in and across sources NB source_identifier = "WRN" for waarneming.nl
	predictions[...].taxon.name	string	scientific name of the taxon	accepted scientific name for taxon
	model_implementation.version	string	unique model implementation identifier	see values
	links.taxa.url	string	valid URL	points to the endpoint for retrieving the taxa
	links.taxa_with_filter.url	string	valid URL	points to the endpoint for retrieving the taxa based on a filter
response (error):	<p>HTTP code: 400</p> <pre>{ "error": { "code": "model_implementation_not_found", "message": "The model implementation with the requested tag does not exist" } }</pre> <p>HTTP code: 400</p> <pre>{ "error": { "code": "received_no_files", "message": "Did not receive any files" } }</pre> <p>HTTP code: 405</p> <pre>{ "error": { "code": "method_not_allowed", "message": "Method not allowed (only supports POST)" } }</pre> <p>HTTP code: 415</p> <pre>{</pre>			

	<pre> "error": { "code": "unsupported_media_type", "message": "Unsupported media type" } } HTTP code: 500 { "error": { "code": "general_server_error", "message": "General server error" } } </pre>
example request:	<pre> curl -X POST -F "image=@sperwer_1.jpg" -F "image=@sperwer_2.jpg" \ https://identify.biodiversityanalysis.nl/v1/observation/identify </pre>
example response:	<pre> { "identification": { "image": { "confidence": "confident" }, }, "predictions": [{ "probability": 0.9970064163208008, "taxon": { "id": "178@WRN", "name": "Accipiter nisus" } }, { "probability": 0.0029197214171290398, "taxon": { "id": "117@WRN", "name": "Accipiter gentilis" } }, "...", { "probability": 2.6637922090344546e-08, "taxon": { "id": "326@WRN", "name": "Falco columbarius" } }], "links": { "taxa": { "url": "/v1/observation/taxa/benlall" } } } </pre>

	<pre> }, "taxa_with_filter": { "url": "/v1/observation/taxa/benlall?id={taxon_id}" } }, "model_implementation": { "version": "1fd68f8c8cb93ec4e45049fcf9a056628e9599aa815790a2a7b568aa" } } </pre>
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Taxa

title:	Observation Identification Service - Taxa														
description:	lists the taxa that are included in an identification implementation														
endpoint:	/v1/observation/taxa/<tag>														
method:	GET														
parameters:	URL (query) id: [optional] query field for taxon id, filters the output list														
response (successful):	HTTP code: 200 JSON-structure, containing the following elements: <ul style="list-style-type: none"> • taxa[...] <ul style="list-style-type: none"> ○ id ○ name ○ vernacular_names ○ alternate_ids • model_implementation <ul style="list-style-type: none"> ○ version <table border="1"> <thead> <tr> <th><i>JSON field</i></th><th><i>data-type</i></th><th><i>values</i></th><th><i>description</i></th></tr> </thead> <tbody> <tr> <td>taxa</td><td>array</td><td>list of records of taxa included in implementation</td><td>see values</td></tr> <tr> <td>taxa[...].id</td><td>string</td><td>unique taxon identifier in format {id_at_source}@{source_identifier}</td><td>identifies taxa in and across sources NB source_identifier = "WRN" for waarneming.nl</td></tr> </tbody> </table>			<i>JSON field</i>	<i>data-type</i>	<i>values</i>	<i>description</i>	taxa	array	list of records of taxa included in implementation	see values	taxa[...].id	string	unique taxon identifier in format {id_at_source}@{source_identifier}	identifies taxa in and across sources NB source_identifier = "WRN" for waarneming.nl
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	taxa[...].name	string	scientific name of the taxon	accepted scientific name for taxon
	taxa[...].alternate_ids	list	list of qualified taxon ids, see .id	IDs of the taxon in other sources such as soortenregister.nl, can be empty
	taxa[...].vernacular_names	map	<i>key</i> : language code <i>value</i> : vernacular name	vernacular names for taxon, can be empty
	model_implementation.version	string	unique implementation identifier	see values
response (error):	HTTP code: 400 <pre>{ "error": { "code": "model_implementation_not_found", "message": "The model implementation with the requested tag does not exist" } }</pre>			
example request:	<pre>curl https://identify.biodiversityanalysis.nl/v1/observation/taxa/benla11 curl https://identify.biodiversityanalysis.nl/v1/observation/taxa/benla11?id=20796@WRN</pre>			
example response:	<pre>{ "taxa": [{ "id": "20796@WRN", "name": "Abax parallelepipedus", "vernacular_names": { "nl": "Bosbulldozer" }, "alternate_ids": [] }, { "id": "153533@WRN", "name": "Abia aenea", "vernacular_names": {}, "alternate_ids": [] }], }</pre>			

	<pre> "model_implementation": { "version": "1fd68f8c8cb93ec4e45049fcf9a056628e9599aa815790a2a7b568aa" } } </pre>
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Documentation

title:	Observation Identification Service - Documentation														
description:	provides structured documentation for model														
endpoint:	/v1/observation/documentation/<tag>														
method:	GET														
parameters:	None														
response (successful):	<p>HTTP code: 200</p> <p>JSON-structure, containing the following elements:</p> <ul style="list-style-type: none"> • release_notes • description • use_policy <ul style="list-style-type: none"> ○ unauthorized <ul style="list-style-type: none"> ■ max_per_day ○ authorized <ul style="list-style-type: none"> ■ max_per_day ■ url ■ authentication • model_implementation: <ul style="list-style-type: none"> ○ class_count ○ version <table border="1"> <thead> <tr> <th><i>JSON field</i></th><th><i>data-type</i></th><th><i>values</i></th><th><i>description</i></th></tr> </thead> <tbody> <tr> <td>release_notes</td><td>map</td><td>key: language code value: JSON escaped HTML</td><td>Release notes indicate changes a.o. changes w.r.t. to previous models</td></tr> <tr> <td>description</td><td>map</td><td>key: language code value: JSON escaped HTML</td><td>The description is a natural language description of what the model caurl https://identify.biodiversityanalysis.nl/v1/observation/docume ntation/benlalln do</td></tr> </tbody> </table>			<i>JSON field</i>	<i>data-type</i>	<i>values</i>	<i>description</i>	release_notes	map	key: language code value: JSON escaped HTML	Release notes indicate changes a.o. changes w.r.t. to previous models	description	map	key: language code value: JSON escaped HTML	The description is a natural language description of what the model caurl https://identify.biodiversityanalysis.nl/v1/observation/docume ntation/benlalln do
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				(and can't)
	use_policy.unauthorized.max_per_day	int	[0, 2 ³² - 1]	Maximum number of identifications per day without authentication
	use_policy.authorized.max_per_day	string	"fair use"	Indicates the conditions of use of the API when authorized
	use_policy.authorized.url	string	valid URL	URL to the authorized version of the service
	use_policy.authorized.authentication	string	"https://tools.ietf.org/html/rfc7617"	describes the type of authentication used
	model_implementation.version	string	unique implementation identifier	see values
	model_implementation.class_count	int	[2, 2 ³² - 1]	Number of classes (taxa) in implementation
response (error):	HTTP code: 400 <pre>{ "error": { "code": "model_implementation_not_found", "message": "The model implementation with the requested tag does not exist" } }</pre> url https://identify.biodiversityanalysis.nl/v1/observation/documentation/benlall			
example request:	curl https://identify.biodiversityanalysis.nl/v1/observation/documentation/benlall			
example response:	<pre>{ "description": { "en": "The webservice identifies species of plants, animals and fungi that naturally occur in The Netherlands and Belgium,\nbased on photos of observations. The underlying recognition model has been trained using photos from Waarneming.nl. The model contains\n 16148 taxa: 13767 species, 1530 species-groups, 734 subspecies and 117 hybrid species. Identifications can benefit from multiple photos\n from the same observation. Provide up to four photos in a single request to improve identification results." } }</pre>			

	<pre> }, "model_implementation": { "class_count": 16148, "version": "0ff1954435b340fbef20e27e9d892d95f38f53754d576c529b6e54ac" }, "release_notes": { "en": "release candidate for public release" }, "use_policy": { "authorized": { "authentication": "https://tools.ietf.org/html/rfc7617", "max_per_day": "fair use", "url": "https://identify.biodiversityanalysis.nl/v1/observation/identify/ benlall/auth" }, "unauthorized": { "max_per_day": 10 } } } } </pre>
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Endpoints

title:	Observation Identification Service - Endpoints
description:	provides a list of endpoints
endpoint:	/v1/observation/endpoints /v1/observation/endpoints/<tag>
method:	GET
parameters:	None
response (successful):	<p>HTTP code: 200</p> <p>JSON-structure, containing the following elements:</p> <ul style="list-style-type: none"> • endpoints <ul style="list-style-type: none"> ○ documentation <ul style="list-style-type: none"> ■ url ○ endpoints <ul style="list-style-type: none"> ■ url ○ identify <ul style="list-style-type: none"> ■ url ○ identify_base

	<ul style="list-style-type: none">■ url○ taxa<ul style="list-style-type: none">■ url○ taxa_with_filter<ul style="list-style-type: none">■ url <table><tr><th>JSON field</th><th>data-type</th><th>values</th><th>description</th></tr><tr><td>endpoints.documentation.url</td><td>string</td><td>valid URL</td><td>points to the endpoint for documentation</td></tr><tr><td>endpoints.endpoints.url</td><td>string</td><td>valid URL</td><td>points to the endpoint for the endpoints</td></tr><tr><td>endpoints.identify.url</td><td>string</td><td>valid URL</td><td>points to the endpoint for a specific species identification implementation</td></tr><tr><td>endpoints.identify_base.url</td><td>string</td><td>valid URL</td><td>points to the general endpoint for species identification</td></tr><tr><td>endpoints.taxa.url</td><td>string</td><td>valid URL</td><td>points to the endpoint for retrieving the taxa</td></tr><tr><td>endpoints.taxa_with_filter.url</td><td>string</td><td>valid URL</td><td>points to the endpoint for retrieving the taxa based on a filter</td></tr></table>	JSON field	data-type	values	description	endpoints.documentation.url	string	valid URL	points to the endpoint for documentation	endpoints.endpoints.url	string	valid URL	points to the endpoint for the endpoints	endpoints.identify.url	string	valid URL	points to the endpoint for a specific species identification implementation	endpoints.identify_base.url	string	valid URL	points to the general endpoint for species identification	endpoints.taxa.url	string	valid URL	points to the endpoint for retrieving the taxa	endpoints.taxa_with_filter.url	string	valid URL	points to the endpoint for retrieving the taxa based on a filter
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	<pre> "url": "/v1/observation/taxa/{tag}" }, "endpoints": { "url": "/v1/observation/endpoints/{tag}" }, "identify": { "url": "/v1/observation/identify/{tag}" }, "identify_base": { "url": "/v1/observation/identify" }, "taxa": { "url": "/v1/observation/taxa/{tag}" }, "taxa_with_filter": { "url": "/v1/observation/taxa/{tag}?id={taxon_id}" } }</pre>
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