

TraIT BMIA security description

General information about BMIA and its tools

The TraIT BioMedical Image Archive (BMIA) offers services for handling medical imaging data for clinical trials. BMIA consists of a suite of software tools (currently NBIA, XNAT, CTP and Keosys) designed to de-identify, upload, archive, view, analyse, query and download medical imaging study data:

National Biomedical Imaging Archive (NBIA)

Submitting sites (e.g. hospital, general practitioner, university) can store (clinical) images - after local de-identification - in NBIA. Authenticated and authorized parties can retrieve images using a 'webshop' functionality. This is the more user-friendly image archive, originally developed by the National Cancer Institute (NCI). It has basic image viewing capabilities through its native web-based interface and (in future releases) integration with other web-based DICOM viewers. NBIA will be extended in 2015 with basic workflow capabilities, meaning that NBIA can be configured to send emails if images are submitted and ready for review/download. This is especially relevant in trials where fast central review of images is required.



Figure 1: TraIT-NBIA frontend (dcm.bmia.nl)

XNAT (Extensible Neuroimaging Archive Toolkit)

XNAT is similar to NBIA. It enables data access via a website (manual upload and download), via the DICOM protocol and via an application programming interface (API), which makes it flexible. Furthermore, XNAT stores not only the images, but also image-derived information, such as annotations and processed versions of the images. It is therefore of interest for the more advanced, technically oriented researchers, and for large studies which require automated image analysis. A short introduction on its use is given on <http://xnat.bigr.nl>. Using the XNAT DICOM Gateway (built on top of the XNAT API), many image viewing applications can interface with XNAT. These include popular viewers such as Osirix and 3D Slicer. For more information on these capabilities see <http://xnat.bigr.nl/index.php/Xnat:Viewing>

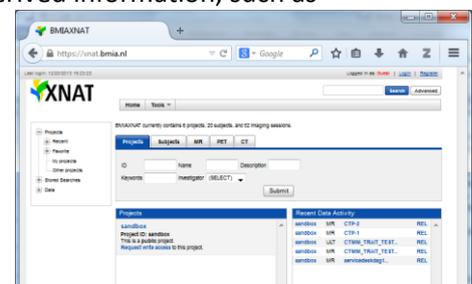


Figure 2: TraIT-XNAT frontend (xnat.bmia.nl)

Clinical Trial Processor (CTP)

CTP is a stand-alone Java client program for de-identification and submission of imaging data to a central archive. CTP has the following key features:

- Single-click installation.
- Support for multiple image upload pipelines.
- Image processing pipelines supporting multiple configurable stages such as audit trails, anonymization, filtering to exclude undesired data elements etc.
- Support for multiple quarantines for data objects which are rejected during processing.
- Pre-defined implementations for key components:
 - HTTP / DICOM Import
 - DICOM Anonymizer

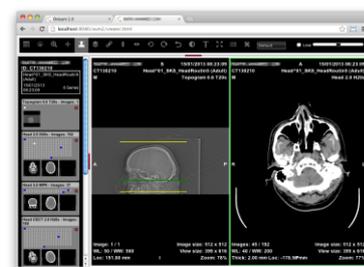


Figure 3: Oviyam viewer

- HTTP(s) / DICOM / FTP(s) Export
- Web-based monitoring of the application's status, including configuration, logs, quarantines. More information is available from RSNA: http://mircwiki.rsna.org/index.php?title=CTP_Articles.

Imagys

A proprietary Imagys viewer from TraIT Partner Keosys (<http://www.keosys.com/>) which allows the user to view and analyze images he/she is authorized to. Keosys specializes in image diagnostic and image management solutions for radiology and nuclear medicine with a focus on clinical trials. The Imagys viewer is offered as Software-as-a-Service via TraIT and can be launched directly from the NBIA archive.

DICOM

All tools adhere to the DICOM standard (Digital Imaging and Communications in Medicine) which is the medical imaging standard used in all hospitals worldwide for exchanging and organizing clinical imaging data. Additionally XNAT enables the storage of data or files associated with an image series, a patient scan study, a patient, or a whole project (collection).

License model, support and continued development

XNAT, NBIA and CTP are open-source applications, while Imagys is a closed-source solution as no good open-source solution is available at this time. The advantage of the open-source model compared to a proprietary model, is that multiple independent contributors can review the source code. Any enhancements made are then added to the version available to the entire community. This external review possibility increases the quality of the software and is called the 'many-eyes' principle.

All tools are supported by large communities and/or organizations guaranteeing their continued development. Specifically NBIA is maintained by the United States National Cancer Institute (NCI), XNAT by the Washington University School of Medicine, CTP by the Radiological Society of North America (RSNA), and Imagys by Keosys. User forums and/or direct contact with developing organizations are available for all tools where users can ask questions, submit suggestions for new features, and report issues. TraIT has reported on and contributed to a number of enhancements and bug fixes through these channels.

Uptake

Since its initial release as a tool for the neuroimaging community, XNAT is now used to support biomedical imaging research in institutions around the world. Examples ranging from neuroscience to cancer to cardiology to ophthalmology, see <http://xnat.org/about/xnat-implementations.php>. NBIA was developed as part of the NCI's cancer Biomedical Informatics Grid program and is the backbone for TCIA, the largest public cancer imaging archive (<http://www.cancerimagingarchive.net/>) containing images of more than 25,000 patients. CTP is the client used by RSNA for conducting clinical trials. RSNA is the largest professional organization in radiology. It is also NCI's preferred tool for image de-identification.

Process to upload

The steps to submit images to NBIA / XNAT are as follows:

- the data-manager selects the images in the PACS workstation;
- the data-manager sends the images to the CTP-client;
- the CTP-client de-identifies the images;
- the CTP-client sends the images through a secure HTTPS connection to NBIA / XNAT.

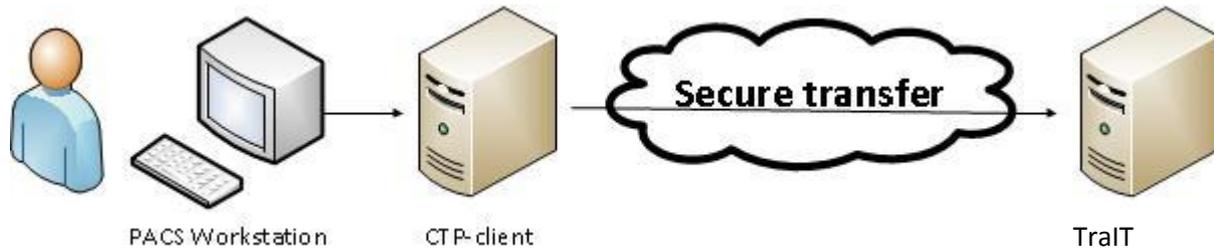


Figure 4: Flow from hospital PACS to TraIT using the CTP client

Why TraIT BMIA?

TraIT hosts and supports NBIA, XNAT and Imagys and supports hospitals with the installation and maintenance of local CTP clients.

The advantages of using TraIT BMIA:

- Free of charge, at least until January 2016 (a fair-use policy applies, see also Pricing Model)
- Secure deployment by professional hosting party
- High-quality user support via TraIT servicedesk
- Study/Principal Investigator (PI) are the only controller of the data
- Links to other data storage and analysis tools within the TraIT platform, allowing researchers to integrate and analyse case-report data, imaging data, experimental data and bio banking information.
- Possibility to integrate with a Trusted Third Party which allows to securely use identifiable data within BMIA

TraIT BMIA features and services

Please find below some features of TraIT BMIA and description of the TraIT BMIA services .

Links to other data storage and analysis tools

The CTMM Translational Research IT (TraIT) project is developing a long-lasting IT infrastructure for the Netherlands that facilitates the collection, storage, analysis, archiving and securing of the data generated in investigator-driven biomedical research projects.

The TraIT services go well beyond the basic hosting of a set of tools. The project is creating an integrated IT platform that will help to accelerate translational research: link results of basic biomedical research to (the variation in) patient's symptoms or clinical outcome to enable development of new diagnostic methods or therapies to be used in clinical care.

One of the pivotal TraIT solutions is the central data warehouse tranSMART, which is also an open-source solution. A user-friendly interface ensures that researchers can query the data collection using the tools of their choice allowing to integrate and analyse case report data, imaging data, experimental data and biobanking information.

TraIT also aims to develop data registration links with important data sources, such as hospital systems and large registries. For clinical images the Clinical Trial Processor (CTP) is used to provide this link. After CTP is installed and configured correctly clinical images can be uploaded from the hospital PACS to BMIA in a one click manner. Moreover, once configured and functioning it can easily be re-used for other translational research projects by defining additional de-identification and export procedures. This system has been implemented in many hospitals in the Netherlands and internationally. TraIT offers services to support installation and configuration of CTP by local hospital staff.

Security

TraIT BMIA has taken a number of security measures. We use standardized TraIT procedures (SOPs) for creating new user accounts in order to comply to the data owner's data access policies and to prevent unauthorized access to study data. The TraIT BMIA environments are hosted by Vancis (www.vancis.nl). Vancis meets the ISO 27001 standard for information security management. The network communication with the TraIT BMIA web-applications (incl. the upload process) is secured via the HTTPS protocol, meaning that hospitals do not have to open ports on their firewall (assuming that the basic HTTPS port is open to the outside world). We have a GeoTrust RapidSSL CA V3 (algorithm: sha1 RSA) certificate that guarantees that the TraIT BMIA user is really communicating with the TraIT BMIA environment. Our infrastructure architecture has been optimized for data security; for example separate compartments are used for the web-, application and database environment. The BMIA database is backed up every night and every other year we perform a disaster recovery test. The last successful disaster recovery test was performed on April 2 2013.

BMIA takes security seriously at the application level. It works with controlled access through user accounts and authorization at the study and role level.

NBIA uses a dedicated application called the Common Security Module User Provisioning Tool (CSM-UPT). For more information about CSM-UPT please see <https://wiki.nci.nih.gov/pages/viewpage.action?pageId=4260067>.

XNAT in turn has similar authorization options. For each study (project in XNAT), the study owner decides which users to add and with which role. For more information, please see: <https://wiki.xnat.org/display/XNAT16/User+Roles+and+Permissions>.

Furthermore, the visibility of a project/collection can be set as:

- Public: all project visible to outside world (for NBIA and XNAT).
- Protected: project description visible to outside world, but image (derived) data not. Users can request access (XNAT only)
- Private: a user should be a member of the project to see it after login (NBIA and XNAT)

By default, a project is created with private visibility. The study owner can change this at the creation of the project, or at a later moment.

The data owner (data controller), generally the principal investigator of the research project, decides in both tools who gets access to the study in BMIA and indicates the role/authorization that should be applied to the user account. The institute or investigator that supplies the data to BMIA remains the owner of the data and access to the data is controlled by the owner. In order to comply to privacy regulations it is only allowed to store anonymized or pseudonymized data on the TraIT BMIA server.

Security at transport level, especially with regards to data collection/ingestion and data consumption, is covered by using standard ciphering protocols to provide encrypted communications over the Internet.

Application and Change Management

TraIT technical support staff is responsible for application management. Application changes (such as upgrades) are tested by TraIT technical staff on a test server and clear instructions how to perform the change are provided to Vancis. Vancis always first performs the change on an acceptance server and after verification by TraIT personnel the change will be performed on the production server by Vancis. All changes in the application are logged in TraIT logs. BMIA versions are synchronized between all (development/test/production) environments.

Compliance to rules and regulations

The tools and applications used by BMIA are trusted worldwide to power mission-critical clinical trials in highly regulated environments. They are developed according to a robust quality system consisting of procedures, controls, and documentation aligned with the US National Institute of Health (NBIA), Washington University (XNAT) and the Royal Society of North America (CTP) regulations and guidance and complies to HIPAA and GCP regulations. The Imagys viewer is CE marked by Keosys as a medical device class IIa and FDA 510k cleared.

Pricing model

Costs of hosting and user support are currently covered by the CTMM-TraIT project. Research projects can use the TraIT BMIA server free of charge until (at least) January 2016. However a fair-use policy applies: Projects having extraordinary demands with respect to computing capacity, disk space or network bandwidth should fund this from their own project budget.

Multi center access

The TraIT BMIA environments are accessible via the internet from all over the world. Therefore it is possible to capture data from different centres for one study in this BMIA environment.

Large user community

Since BMIA was adopted by TraIT as the preferred image data capture suite in 2011, its user base on the TraIT server has grown to over 20 clinical studies involving more than 2000 patients.

User Support

The CTMM-TraIT project supports users in the TraIT-BMIA environments. Support is provided for specific questions/problems related to the BMIA software, but the support model assumes a do-it-yourself attitude after the initial training provided by TraIT. Studies should take responsibility for quality control of the image sets uploaded to BMIA and specific questions about the validity and content of data or study subjects cannot be answered by TraIT staff.

There are manuals, guidance documents and how to's available in the TraIT helpdesk tool TOPdesk. All users of TraIT applications receive a user account for TraIT TOPdesk.

Conditions for use

Please consider the following conditions before setting up a study on CTMM TraIT BMIA.

Patient Identifying Data (PID)

Patient Identifying Data (PID) is any data (names, numbers, addresses, etc.) within clinical data that could potentially be used to identify subjects, either directly or by linkage to other systems. PID obviously includes names and initials, but also hospital system IDs or national health service / insurance IDs, numbers which in conjunction with those systems would identify an individual. Dates of birth can be PID, though normally not in a large data set and without other associated data (e.g. identifying source hospital) when identification would be difficult. *There is no absolute definition of PID* - it depends on the size of the data set and what data is present. Any clinical data can be PID if it is rare, in a small data set, or linked to other information (e.g. geographical location).

TraIT will check the use of PID for each study that starts on the TraIT BMIA production environment. If a patient has signed informed consent and specifically consented to the recording of her/his PID than it is allowed to record identifying data in BMIA. However, unless there is explicit reason to capture PID, no PID will be recorded.

If there is no informed consent and no approval of an accredited reviewing committee, a Privacy - or Security Officer from each participating site should give approval and take responsibility for capturing PID. Under no circumstances it is allowed to capture unencrypted BSN (Dutch social security number) unless the patient has given explicit informed consent to do so.

The Principal Investigator (PI) remains the controller and custodian of the data with all corresponding responsibilities regarding personal data

- TraIT is the data processor on behalf of the PI
- The PI (or a delegate assigned by the PI) determines who will get access to the data; TraIT will only execute those decisions

Please note that PID may **not** be part of the coding of study participants (the Study Subject ID in BMIA). For more information on encryption see the protocol model of the CCMO , section 12.1 (<http://www.ccmo.nl/en/standard-research-file>)

Use of validated de-identification profiles and full-circle test

TraIT requires a de-identification profile that is validated for each version of each modality (~scanner) in each participating site. Validation is required for both the completeness of the de-identification and for the usability of the de-identified images. The reason to do so is that there are many vendor specific implementations of the DICOM standard that may cause PID to be present at vendor / modality / version specific locations in the DICOM header. TraIT supports in this set-up of the de-identification profile using, amongst others, the De-identification Knowledge Base of The Cancer Imaging Archive (<https://wiki.cancerimagingarchive.net/display/Public/De-identification+Knowledge+Base>). For a given de-identification profile a full circle test (de-identification, upload, download and analysis) needs to be conducted by the study to ensure the de-identified images are not only properly de-identified but are also still usable for the analysis foreseen in the study. . A typical example of such a variable critical for analysis is the weight of a patient in a PET scan. Although the weight is a data element that is preferentially removed from the DICOM header (because it might identify a patient, esp. if the weight is exceptional), it causes many PET measures to no longer be calculable (e.g. Standardized Uptake Value) as the weight is needed for the calculation of that measure.

TraIT can advise how to set-up de-identification profiles and has 'standard' de-identification profiles, but the testing of these profiles in the specific environment of the study is ultimately the responsibility of the study staff.

Training

CTMM-TraIT does not organise formal training for BMIA at the moment. This may be done in the future.

Contact

If you are a TraIT BMIA user and require support please contact our Self -Servicedesk <https://trait.topdesk.net> all users of TraIT applications receive a user account for TraIT TOPdesk)

Or e-mail or call our help desk at:

E: servicedesk@ctmm-trait.nl

T: +31 (0)88-1167500

Useful links

NBIA main: <https://wiki.nci.nih.gov/display/NBIA/National+Biomedical+Imaging+Archive+-+NBIA>

NBIA documentation: <https://wiki.nci.nih.gov/display/NBIA/NBIA+Documentation>



XNAT main: <http://www.xnat.org/>

XNAT documentation: <https://wiki.xnat.org/display/XNAT16/Home>

CTP main: http://mircwiki.rsna.org/index.php?title=CTP-The_RSNA_Clinical_Trial_Processor

CTP documentation: http://mircwiki.rsna.org/index.php?title=CTP_Articles

Imagys: http://www.keosys.com/eng/visualize/workstation_nm.htm

TraIT TOPdesk Knowledge Base: <http://trait.topdesk.net>