Program of Requirements

Project Napoleon

Owner	:	Netherlands Forensic Institute
Project Name	:	Napoleon
Project Number	:	310.158
Version	:	0.5
Status	:	Concept
Date	:	23-06-2008

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1 Document Info

Document History

Version	Date	Status	Author	Change description
0.1	29-05-2008	Concept	10, 2, e	Draft; after discussions with SNN on 22-05-2008 and 10, 2, e on 26-05-2008. *Describes requirements for phase 1, with basic functionality.*
0.2	05-06-2008	Concept		After discussion with 10, 2, e and 10, 2, e 10, 2, e
0.3	07-06-2008	Concept		After discussion with SNN on 05-06-2008. Revised by 10, 2, e
0.4	13-06-2008	Concept		Comments SNN processed.
0.5	23-06-2008	Concept		Comments of 10, 2, e (ICMP) processed.

Table of References

Reference [ref]	Title	Author	Version	Comments
Napoleon	Research Proposal Napoleon (PID)	NFI	1.1	
Bonaparte	Bonaparte: Bayesian networks for victim identification on the basis of DNA profiles	SNN	2.1	

Acronyms en definitions

Acronym	Description
Allele	Number of repeating DNA-blocks on a Locus
AM	Ante Mortem, data used for identifying missing persons
AM profile	DNA-profile of a relative of a MP or a personal item belonging to a MP
Batch	Search definition within all DNA profiles in a database, based on a selection of characteristics. Batches are not bound to Projects or Folders
BSO	Biologisch Sporen Onderzoek
(CODIS) Case ID	CODIS-key: NFI-case ID + KLPD#
CODIS	Combined DNA Index System
CODIS DBV	NFI Database containing DNA profiles of missing persons, family members of missing persons and of unidentified bodies based on CODIS
DNA profile	See Profile
ETL	Extract, Transform Load, technology for information exchange with minimal technical and semantic coupling between the systems involved.
Folder	Collection of Projects with a common characteristic, such as: "Srebrenica", "Suriname" resp. "DBV".
GUI	Graphical User Interface
Individual	Individual person (can be either a UI or a person in a pedigree)
ICIS	Interactive Collaborative Information Systems
ICMP	International Commission on Missing Persons (http://www.ic-mp.org)
Locus	Position of a STR on a chromosome
Mixed profile	DNA profile of a contaminated specimen, containing DNA material of multiple individuals
MP	Missing Person
NFI	Netherlands Forensic Institute
NFI#	NFI case number

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Pedigree	Construction of the mutual relations between missing persons and their relatives
PM	Post Mortem, data used for identifying (remains of) persons
PM profile	DNA-profile of a victim
Profile	Anonymous DNA profile related to a case. A UI *profile* is PM, collected from unidentified remains An AM *profile* is either: • collected from a family member of a missing person • collected from a personal item, such as a toothbrush of a missing person
Project	Work set within Napoleon, consisting of one or more DNA profiles e.g. linked to the same missing person, pedigrees or unidentified person. A project consists of : • 1 unidentified individual • 0 or more (putative) AM profiles. (A putative AM profile can be a PM profile) • 0 or more (putative) pedigrees If a pedigree consists of more missing persons, it could be stored in one Project.
Role	Role in a pedigree, relative to the UI (such as "father" or "sibling")
SearchSet	Set of profiles to be matched
SIN	Specimen Identification Number, represents a SVO
SNN	Stichting Neurale Netwerken
SNP	Single Nucleotide Polymorphism
CODIS Specimen ID	Unique ID for a DNA profile (Database specific, e.g. in CODIS: SIN# + Rol + Aanvraagnummer
CODIS Specimen Data	Data belonging to a Specimen (such as #Loci, profile, alleles etc.)
Specimen Type	A.k.a. Specimen Category. Attribute designating the type of a DNA profile, such as "MP", "BM", "BF", etc.
Search Count	Number of times a profile was searched for
STR	Short Tandem Repeat, repetitions of tiny pieces of DNA, used for matching because they can vary strongly between individuals
SVO	Stuk van Overtuiging
UI	Unidentified individual
Virtual profile	Constructed profile, combining two or more partial DNA profiles
XML	Extended Markup Language

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2 Introduction

Napoleon is a system for identification of unidentified victims through screening and matching of their DNA profiles against pedigrees of Missing's Persons DNA Profiles in large databases based on a Bayesian statistical network analysis approach.

The development of Napoleon will be performed and supported by the following parties:

Netherlands Forensic Institute (NFI)
- Department Biologisch Sporen Onderzoek (BSO)
- Department Digital Technology and Biometrics (DTB)

Stichting Neurale Netwerken (SNN)
the Dutch Foundation for Neural Networks, a national network of research groups on neural networks, machine intelligence and affiliated techniques. SNN Nijmegen, the research group 10.2.g will be involved in this project.

International Commission on Missing Persons (ICMP)
- Research lab in Bosnia which is responsible for identifications of victims in former Yugoslavian countries, after Tsunami disaster, Katrina hurricane and after other disasters.

Within the Napoleon research project the aim is to develop new software in which the whole pedigrees of the relatives of missing persons are used in both the screening and the matching phase. The main advantage of this approach is that the number of false hits will be much lower than conventional methods. The software will consist of database functions, a graphical user interface and screening and matching functionality. The Matching of Missing Persons against its Pedigree's in large databases will be based on a Bayesian statistical network analysis approach. In this way the Napoleon system will improve the quality and continuity of the services delivered by the NFI, even in case of a major disaster. The combination of both the Pedigree Approach and the Bayesian Approach is an unique method in DNA Identification Work.

Within the Napoleon project two complementary products will be developed:
- Napoleon-product: the Logistics modules to be developed by NFI
- Bonaparte product: the Calculation core to be developed by SNN

These products will be specified in the following chapters. As a rough indication, the domains of both products are sketched globally in the picture below.

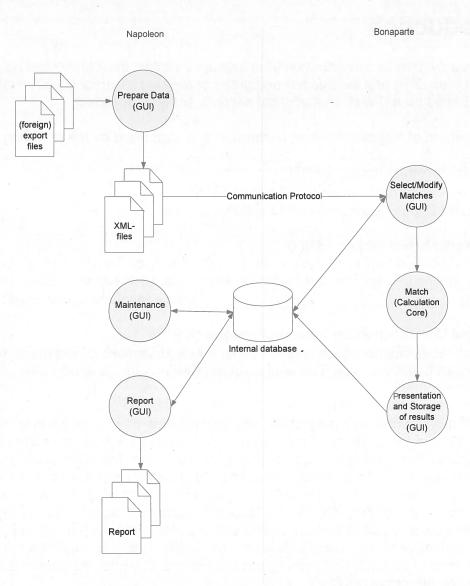| Owner | : NFI |
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Figure 1: the Napoleon and Bonaparte domains

The project is divided into two phases :
- Phase 1: Autosomal DNA profiles
- Phase 2 : Extended profiles

The distinction between these two phases is indicated in the text, where relevant.

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3 Napoleon

3.1 Purpose of the Napoleon product

The Napoleon software takes care of the logistic handling of data and results:
- Preparing the input data for Bonaparte
- Maintaining the Napoleon database
- Reporting the Bonaparte match results

3.2 Functional requirements

3.2.1 Data Preparation

[NF007] Import data from XML-files
Napoleon shall be able to read the export files of several native and foreign databases.
(phase1: CODIS DBV, ICMP and some proprietary formats used for gauge purposes).
Independent on the source database Napoleon shall translate the export file into a XML-file
with a standard syntax <t.b.d>.
This is a one-way interface. No information shall be fed back into the data sources.

3.2.2 Maintenance

[NF001] Format flexibility
Identification fields used in database structures, such as Specimen ID numbers, must be
flexible so that data from various sources can be processed.
Minimal sources are CODIS DBV, the ICMP database and Test databases.

[NF004] Database Manipulation
Napoleon can manipulate databases in the following way:
- Add a database
- Delete a database
- Convert databases with e.g. ETL-scripts <t.b.d.>
- Process exported DNA profiles from foreign databases <t.b.d.>
- Export DNA profiles in several formats <t.b.d.>

[NF005] DNA-profile manipulation
Napoleon shall be able to manipulate DNA profile tables (organised as?)
- Search
- Update
- Delete
- Add

[NF006] Static Data Configuration

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Napoleon shall support the following Static Data configuration and maintenance options:

- Locus table : adding/update/delete locus
- Amplification Kit table : add amplification kit loci specifics. Data compatibility with all current commercially available kits and markers and extensible for custom systems and marker sets as needed, to ensure long-term usability.
- Population Statistics table: search/add/update/delete population statistics
- Kinship table configuration : add/update/delete kinships
- Mutation Models
- Size bias models
- Test data
- Minimum frequency of rere alleles
- Null alleles
- Dropout alleles (phase 2)

It shall be possible to enter and maintain these sets through a basic GUI.

3.2.3 Reporting

[NF003] Reporting features
Napoleon can deliver the following user specified Reports using data from the Napoleon internal database:
1. Match Reports (NFI)
2. Match Reports (ICMP)
3. Match Reports (ad-hoc)

3.3 Constraints

[NC001]
The technical environment in which Napoleon is developed should be Oracle/Java and Flexible or Open source platforms.

[NC002]
The methodological environment of the Napoleon development should be UML, OOD

[NC003]
The management environment for the Napoleon project should be Prince2.

[NC004]
The XML-conversion of databases to be imported should be compatible to the DNA profile structures used by CODIS DBV and the ICMP (phase 1) as well as Excel Validation data in ad-hoc formats. In a later stage other conventions may be added.

In this structure the *Individual* is central.

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An Individual (with a DNA-profile) in CODIS is uniquely identified by a CODIS Specimen ID and carry info about the NFI-case ID and the Specimen Type.

[NC006]
Napoleon must be validated with a proper test-set to be defined by NFI and ICMP.
Note: DNAview can not be used as a formal (commercial) validation reference.

[NC007]
The interfaces with databases containing DNA profiles, or exports from databases, are read-only and limited to DNA profiles. Napoleon does not feed back any information into its source data.

[NC008]
There is no direct interface between Napoleon and its source databases.

[NC009]
Linkage (relations between alleles) is not applied within Napoleon, except possibly for phase 2 when SNP is included.

3.4   Operational requirements

[NO001] Client-server and standalone mode
Napoleon will be able to run standalone (phase 2) on a commodity laptop as well as in a network environment with multiple users (phase 1) in a client-server architecture.
The maximum number of concurrent users is 20 .

[NO002] Logging of actions
All searches and decisions made by the user shall be logged, specifying time, user and action.

[NO003] User administration
A user-administration must be set up. This administration contains the known users and their according rights to operate Napoleon and provides Role Based Access Control.

The following Roles and according privileges are identified:

Role	Privileges	Comments
Administrator	all	System administrator
Data Enterer	Basic maintenance	Data Entry (profiles, pedigrees, etc.)
Forensic Researcher	Matching, Basic maintenance	e.g. BSO personnel
SNN-user	Maintenance	e.g. for maintenance
Foreign user	Matching	e.g. ICMP-personnel

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3.5 Reliability requirements

[NR001] Backups
There shall be periodic automatic backups so that little work will be lost in case of problems. After recovery at most one hour of work can be lost.
The backup only concerns the internal Napoleon database.
An automatic permanent backup is made daily.

3.6 Maintenance requirements

[NM001] Compatibility
Napoleon's interface conversion modules must keep up with:
- new releases of source databases
- new statistical models
- new DNA kits

[NM002] Export
For each selected database source, Napoleon shall supply export functionality, as far as not contained in the source database itself.

[NM003] Use of 3rd party products
All 3rd party products applied in Napoleon should be acquired from reliable suppliers, offering transparent conditions for usage, upgrade and maintenance.

[NM004] Documentation
Clear design documentation and manuals are needed for the use and maintenance of Napoleon.

3.7 System requirements

[NS001] Interfacing with databases
Napoleon will have database interface modules allowing it to read CODIS DBV, ICMP and other foreign DNA-databases.

3.8 Security requirements

[NX001] Authorization
Only authorized users may gain access to Napoleon through a login procedure.
Napoleon starts up with an authorization-dialog.
After a configurable period of inactivity the authorization dialog reappears, so that the user has to log in again.

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[NX002] Privacy
It is preferred that no privacy-sensitive information is contained in Napoleon at all.
If this might turn out to be inevitable, information shall be encrypted such that it cannot be interpreted without using Napoleon as the access provider (phase 2)

[NX003] Secure connections
No insecure open internet connections may be applied.

3.9 Usability

[NU001] Look and Feel
The GUI is designed to be intuitive, conforming to universal GUI-guidelines.

[NU002] User Profiles
Napoleon shall support user-profiles containing preferred settings, etc.

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4 Bonaparte

4.1 Purpose of the Bonaparte product

The project "Bonaparte" will deliver a system for kinship analysis in DNA-files as described in the ICIS valorisation proposal [Bonaparte].
This system, the computational core of Napoleon, will be referred to as "Bonaparte".

Bonaparte consists of 3 elements:
- Computational core
- Preparing the Match
- Communication Protocol

4.2 Functional requirements

4.2.1 Computational Core

The computational core performs the screening and matching and shall support the following features:

[BF001] Network builder
Build Bayesian network family – per locus
1. Paternal/Maternal inheritance
   a. Mutation model (such as from Ayres or Brenner)
2. Genotype observation
   a. Alleles, KIT
   b. Multiple genotypes with their according probabilities[1]
3. Population allele frequencies
4. Theta-correction
5. Rare alleles
6. Null-alleles
7. Size bias correction models

[BF003] Elementary matching
Elementary matching options (SearchSet vs. Batch), where x, y are numbers [1,N]
1. x UI vs. y pedigrees; match UI-profiles into (putative) pedigrees
2. x UI vs. y UI (to detect doubles)
3. x UI vs. y AM references (1:1) to detect parents, children and siblings in pedigrees, with the same role as in the current pedigree: this means that for the screening to detect parents and children only the family members with the roles F, M and C are involved. To detect siblings only the family members with the role S are involved.

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[1] Possibly to be related to peak-heights in a later stage (phase 2 or later). NB mixed profiles are excluded from the computational core in both phase 1 and 2. However the data-storage should be prepared for storing mixed profiles which may be dealt with in future versions.

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4. (phase 2) x UI vs. y UI (to detect parents, children and siblings)

4.2.2 Preparing the Match

The GUI shall allow the user to
- enter configuration data and selections for the computational core
- perform basic manipulations on profiles, models and sets
- manipulate pedigrees

[BF011] Profile Management[2]
The following operations are possible with profiles. Reference is the Napoleon internal database. Adapted profiles are not fed back into the source-database.

For profiles constructed through the Napoleon GUI:
1) Add a profile (NB: an artificial profile must be clearly marked as being artificial)
    a) Relatives of MP (AM)
    b) Victim (PM / UI)
    c) Body Part (PM / UI)
2) Edit/Change a profile (NB: an adapted profile must be clearly marked as being artificial)
    a) Population[3]
    b) Pedigree reference(s)
    c) Alleles
    d) Add Loci
For external profiles:
3) Import profiles from an external source (XML-interface t.b.d.)
For any profile:
4) Export profiles to an external file (XML-interface t.b.d.)
5) (phase 2) Construct a virtual profile (e.g. add up of profile parts supposedly belonging to the same victim, or making a test-profile)

[BF004] Construction of Pedigrees
The Bonaparte GUI offers a tool to construct pedigrees graphically. Pedigrees consist of squares (males) and circles (females), where the color represents their status being either
- "no DNA sample" = checked square,
- "Reference AM sample present = "blank"
- "unidentified MP" =red,
- "identified MP" = blue.

Pedigrees may be composed by dragging Individuals from the Project onto positions in the pedigree.
A pedigree (that passes the consistency check, see other requirement) can be saved, printed and stored.

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[2] The system will compute with at most one (maybe virtual) profile per individual.
[3] For phase 1 Population is coupled to a Match, not to an individual profile, In later stages the default Population-value of a Match might be overruled by a profile-bound Population-value. For phase 1 however, this field is unused.

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It shall be possible to define relations within the pedigree such as: there is a 10% chance that a particular child is not of the supposed biological father.

For phase 1 there will only be input/output of pedigrees through the Napoleon GUI.

Note that a pedigree can "evolve" by dragging Individuals onto its positions. A PM-profile may act as an AM reference profile when it is dragged onto a reference-position. See also "Appendix on Pedigrees".

One project may contain several (putative) pedigrees.

[BF005] Pedigree Consistency Check

A pedigree can be parsed for consistency. Any change in the pedigree (such as by editing it) will be checked in the background. The system will return a consistency measure after each update of the pedigree.

When an inconsistency is found, the user shall be hinted towards the problem.
Only pedigrees that pass this consistency check without errors shall be stored and/or used for matching. The Bonaparte GUI shall disable the use and storage of inconsistent pedigrees.
The consistency check may result in a user-warning :
– Parent inconsistency (supposed parent is not the real parent)
– Sibling inconsistency (supposed siblings cannot all be siblings)

The inconsistency is detected when the number of mismatches above threshold value, which is configurable by the user.

The following inconsistencies shall be detected and reported as a result of parsing a pedigree:
1. (grand)child cannot be of a mother / grandparents
2. (grand)child cannot be of a father / grandparents
3. 2 or more siblings cannot be full siblings

The user may adapt the pedigree and check again until the pedigree is considered consistent.

[BF006] Match Preparation

The Bonaparte GUI will come up asking which folders and/or projects are going to be processed.

The list of new imported data/new projects and earlier defined projects will be presented by the Napoleon GUI. (Individuals can belong to one or more projects/batches/SearchSets)

The user can select from this list.

A (set of) NFI-case(s) may be given a name so that the project can be easily found again.

New imported data: user should define a project name and add pedigree(s).

For the match preparation the user should define the SearchSet

Now the list with specimens belonging to the selected project is presented in a list, together with the attribute Specimen type, for the SearchSet.

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Next a Batch can be selected within a Folder or created with the GUI.
The following criteria can be used to create a batch:
- Folder Name
- Project name
- Specimen Type

The selected/created batch is the matching set for the SearchSet.
The user may now select the option "match", to start the Match-Setup dialog.

[BF007] Match Setup
1) Select Loci
2) Select population for this Match
3) Select mutation model or specify a customized mutation model
4) Select model for subpopulation correction
5) Select model for size bias correction of specify a customized size bias correction model
6) Select model for null alleles
7) Select model for rare alleles
8) Prior odds

[BF008] Match and Presentation of results
The results of the match are presented to the user.
Minimal content of the Hitlist (layout is to be determined):
1) Date, Issuer, Project, SearchSet, Batch, Match strategy summary, Case ID
2) List of Hits 1 { UI/MP | Reference | LR } N

The Hitlist may be filtered as follows:
- Thresholds, such as LR, min. # loci, max. # mutations
- Statistics type
    o LR (likelihood Ratio)
    o Posterior odds

When a hit is selected by double clicking a detail screen pops up, showing:
- Date, Issuer, Project, SearchSet, Batch, Match strategy summary, Case ID, Folder
- The pedigree
- LR per Locus
- DNA profiles

The detail report can be exported and printed.
The DNA profiles of the Set can be exported for comparison purposes.

[BF009] Store the Match Results
Match results can be stored within the Napoleon database, as part of a Project.
The following data must be saved:
.....

[BF010] Creating Folders and Projects

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Projects are formed around one or more MPs (if those MPs are present in the same pedigree) and/or one or more UIs. Projects can be grouped in Folders.
Both Folders and Projects can be created new.

[BF012] Refresh Folders and Projects
Overnight, the contents of the export of source database may have changed, e.g. profiles were added. These changes may affect Projects and/or Folders.
Napoleon should warn the user for this and present the list with possibly affected Projects/Folders.

All new data should be either:
- Added to existing Project
- Put into new Project

The user may now decide to (automatically) update the affected Projects/Folders with a new Search.

4.2.3 Communication Protocol

The communication protocol between Napoleon and Bonaparte is implemented through exchange of XML-files, containing DNA profiles from source databases.

The content of the XML-files is <t.b.d.>.
Napoleon is responsible for preparing the input data in XML-format.

Furthermore information can be exchanged through the internal Napoleon database.
The data model of this internal database is <t.b.d.>

4.3 Constraints

See Constraints in paragraph 3.3.

[BC001]
Mixed profiles are excluded from the computational core.
However the data-storage should be prepared for storing mixed profiles.

[BC002]
The Bonaparte database shall store percentages (peak heights) instead of interpretations.

[BC003]
The interface between Napoleon and Bonaparte (communication protocol) shall be specified and implemented in XML.

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4.4 Operational requirements

4.5 Reliability requirements

[BR001]
The number of false hits per match shall not exceed 0.01%.
This is a flexible, multi-interpretable requirement. Must still be stated more precisely

[BR002]
The number of searches performed on a specimen shall be written in the specimen data
(like the search count in CODIS DBV).

4.6 Maintenance requirements

4.7 System Requirements

4.8 Security requirements

Napoleon's security requirements (paragraph 3.8), as far as applicable, apply to Bonaparte
as well. In particular, Bonaparte will not be provided privacy sensitive information.

4.9 Usability

[BU001]
Bonaparte shall support the use of user-profiles, such that Napoleon user-preferences
connected to a user-profile (see requirement NU001) are automatically applied.

[BU002]
The statistical model usage shall be transparent to the user.
This means that all relevant parameters used in the model shall be presented to the user
and adaptable where relevant.

[BU003]
A user training shall be part of the delivery.

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4.10 Phase 2

This paragraph describes the requirements for the second phase of the project.
These requirements are not yet detailed any further.

In general:

1. Working with:
   1.1. Y-chromosome profiles
   1.2. SNP profiles
   1.3. mtDNA profiles

2. Construction of consensus profiles: combining test results / test profiles of more than one sample to one profile.

3. Construction of virtual profiles: combining partial results / test profiles of one sample to one profile.

4. Exclusion of paternal or maternal relation in a match

For the Calculation core:

5. Expand the Bayesian network with:

   5.1. linkage between SNP-markers
   5.2. Y-chromosomal data
   5.3. mtDNA data
   5.4. mutation model of Xu et al, 2000
   5.5. genotype observation model with kit-specific parameters (possibly STR peak heights)
   5.6. combining observations for a sample (virtual profiles)

6. Expand the Matching with:
   6.1. virtual profile calculation
   6.2. clustering of profiles into consensus profile

7. QA calculation
   7.1. posterior probability genotype error
   7.2. posterior probability mutation

For the Preparation of Match:

8. Add profile functionality for
   8.1. Create profile groups
   8.2. Convert profiles (ordered in groups/databases)

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8.3. Y-chromosomes
8.4. SNP-data
8.5. mtDNA data
8.6. management of virtual profiles
8.7. management of consensus profiles

9. Static data configuration
9.1. specify DNA-kit parameters per locus and/or group of loci
9.2. functionality for Y-chromosomes
9.3. functionality for SNP-data
9.4. functionality of mtDNA-data

10. Analysis: Construction of virtual profiles

11. Matching: Construction of consensus profiles
Identify/cluster all profiles belonging to one individual

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5 Workflow

This chapter globally (non-SMART) describes the way of working for Napoleon (forensic) users. Its purpose is to provide context to the Napoleon and Bonaparte functionality, so that the (SMART) engineering requirements may be formulated "fit for purpose".

The described workflow was defined together with BSO-personnel.

5.1 Creating Folders and Projects

Use of Folders and Projects is meant to ease working with large sets of profiles.

A Project is always centered around an unidentified Individual.
A Folder is a logical set of Projects related by a common characteristic.

A Project may be considered as a workspace containing profiles, configurations, match results, etc. related to matches performed on the Individual.

It can be defined by the user by selecting a profile and giving it a unique name.
Information can be added to a Project by selecting (e.g. SearchSets), configuring or matching.

A Project can reside in a Folder, bringing together related Projects.
For example, the unidentified profiles of a mass grave in Srebrenica may be clustered in a Folder called "Srebrenica MG", containing several Projects with UI profiles. Each of these Projects contain the profiles associated with one Individual.
Another Folder might be all the Missing Persons registered in Srebrenica.

Projects and Folders are used in the Bonaparte function "Match Preparation".

5.2 DNA-matching

This section describes the workflow for the roles "Forensic researcher", "Data Enterer" and "Foreign User".

Matching with Napoleon globally consists of the following steps:

Start up and Login
{
    Select or create a Project
    {
- Preparation of Match ("what": select a SearchSet and Batch)
- Setting up the Match ("how": select the parameters and settings for the Match)

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- Match and Analyze Match results
- (if necessary) Adapt Match configuration
- Report and/or Store Match results

}
Save the Project
}
Logout and Close

These steps are described below.

5.2.1 Start up

Start the Napoleon application and log In as a Forensic Researcher.
Napoleon comes up in the same state as this user left it behind after the previous use.
….

5.2.2 Select a Project

The user first defines the environment in which DNA-matching is to be performed: the *Project*. The Project only exists in Napoleon, not within the source DNA-databases.

Projects can be selected from a list to continue previous work with Napoleon, or created new (see earlier). New projects should be given easily recognizable names by the user, for later reference.

Profiles can be added to the Project from the source databases. This is done by selecting Profiles with selection-attributes such as a NFI-casenumber. All Profiles having this attribute are then added to a Project.

A new or adapted Project must be saved before Matches can be performed within it.

5.2.3 Match Preparation

5.2.3.1 Create or Select the SearchSet

The SearchSet is the set of target-profiles which is to be matched against a Batch.
It can either be created or selected from a list of previously defined SearchSets.

Creating a SearchSet: select a set of Profiles from the Project by entering a search-category, such as entry-date, gender or NFI-case#.
Save this SearchSet under a straightforward name, say "MP".

SearchSets exist of UI-profiles (post mortem victim profiles)

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Per Match there is always <u>one</u> current SearchSet. A SearchSet belongs to the Project.

5.2.3.2 Create or Select the Batch

The Batch is a characteristics-based collection of Profiles. Batches exist outside Projects, because they extend over the complete set of currently available Profiles.
It can either be created or selected from a list of previously defined Batches.

Creating a Batch: select a set of Profiles from the source database(s) by entering one or more search-criteria, such as the entry-date (example: "all Profiles entered in April 2007"). Save this Batch under a straightforward name, say "April 2007".

Batches consist of MP and/or UI profiles and can be created using multiple criteria such as:
- Project
- Case ID
- KLPD#
- Aanvraag#
- Pedigree
- Role in Pedigree: O (unidentified), F (father), M (mother), A (personal item)
- Gender
- Profile complete?
- Location
- Date
- Specimen Category
- Future use fields

Per Match there is always <u>one</u> current Batch. A Batch is independent of the Project.

Match Setup

Now that the current SearchSet and the current Batch are identified, the user must define *how* the Match is to be done.
Several parameters and selections can be entered (see requirements) to model the calculations.

Optionally all Match-data can be exported for comparison purposes (outside Napoleon).

The Match is now ready for execution.

5.2.4 Match and Analyze Match results

After pressing the "Match" button, Bonaparte will calculate the Match results and present them in a Hit-list with only the essential information per Hit: Profile IDs and proof-value.
This provides the user with a summary of the Match results, e.g. :
1 { [tags] PM 597.001 – AM597.001 LR= 10^6} N

The Hit-list can then be analyzed by the user.

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The user may double-click on a Hit to see the match-details (or press "Details")

Optionally Hit-data can be exported for comparison purposes (outside Napoleon).

Hits may be provided with [profile-tags] to indicate whether a profile "was matched X-times before", is irrelevant, or other (to be determined). Profile-tags can be attached to SearchSet-profiles as well as Batch-profiles.

The Hit list may be saved, if relevant.

5.2.5 Adapt Match configuration
If the Match did not deliver satisfactory results, the user may go back to step Match Preparation, to define another Match and repeat the step Match and Analyze.
Default selections are the previously chosen selections.

The new Hit-list will replace the actual hit-list.

5.2.6 Report and Store Match results
Once the user is convinced that a Match is relevant and complete, it can be reported and stored in the Project

When a Match is stored, the following information is saved:
- SearchSet,
- Batch
- Match-configuration,
- Hits
- Pedigrees (if applicable)

To continue Matching the user can now go back to "Select a Project" to switch Project, or "Match Preparation" to continue within the same Project.

5.2.7 Save the Project
After the matching work is finished, the Project should be saved.
The saved Project contains all SearchSets, Batches and Match results used in the Project so far.

5.3 Maintenance functions

These functions are divided into "basic functions" and "advanced functions".
This section descries the workflow for the roles "Administrator" (all), "Data Enterer" (basic only) and "Forensic Researcher" (basic only).

To be detailed.

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5.3.1 Start up

Start the Napoleon application and Log In as Administrator.
….

5.3.2 System Maintenance

5.3.3 User Administration

5.3.4 Database Administration

5.3.4.1 Profiles

5.3.4.2 Batches

5.3.5 Project Administration

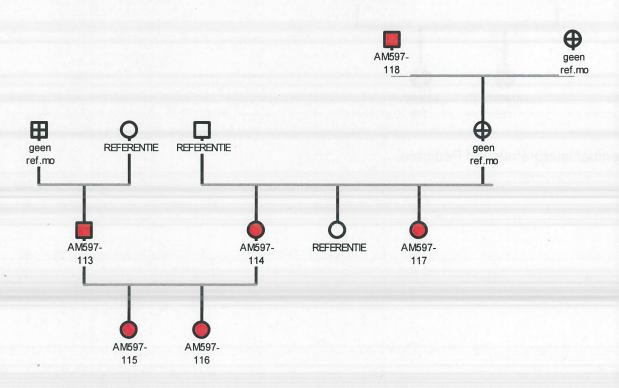| | Owner | : NFI |
	Project Name	: Napoleon
	Project Number	: 310.158
	Version	: 0.5
	Status	: Concept
	Date	: 23-06-2008

6 Appendix on Pedigrees

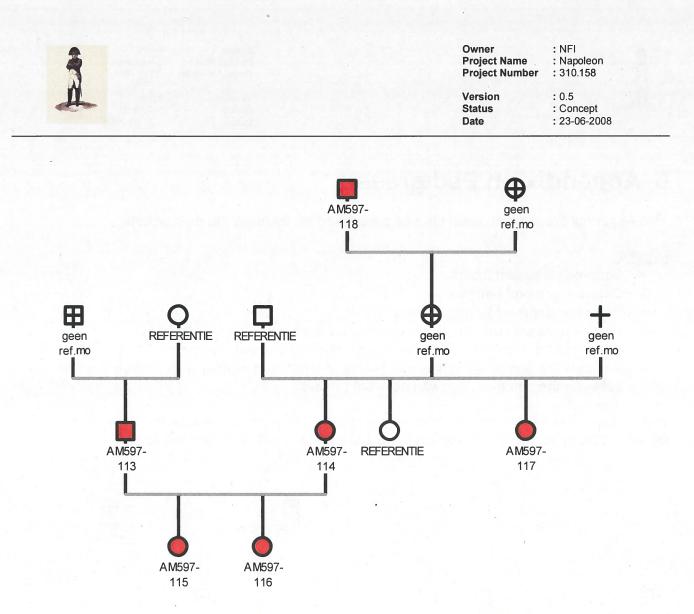This Appendix presents an example pedigree, used for focusing the discussions.

Legend:
- Squares represent males
- Circles represent females
- Red represents a Missing Person
- White represents that there is a reference profile available (AM-profile)
- Strikethrough represents that there is no reference profile available
- Children are positioned below and between father and mother (e.g. half-sisters are between the same mother with different fathers)

The example below concerns an putative pedigree , which had to be adapted during the match-process, because it turned out to be contradicting with 1:1 matches found.

Initial interpretation of Pedigree (a putative pedigree).

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Eventual interpretation of Pedigree.