

Programme of Requirements



Project Napoleon

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Project Name	: Napoleon
Project Number	: 310.158
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TABLE OF CONTENTS

1	DOCUMENT INFO	3
2	INTRODUCTION	4
3	NAPOLEON	5
3.1	PURPOSE OF THE NAPOLEON PRODUCT	5
3.2	FUNCTIONAL REQUIREMENTS	5
3.3	CONSTRAINTS	6
3.4	OPERATIONAL REQUIREMENTS	6
3.5	RELIABILITY REQUIREMENTS	7
3.6	MAINTENANCE REQUIREMENTS	7
3.7	SYSTEM REQUIREMENTS	8
3.8	SECURITY REQUIREMENTS	8
3.9	USABILITY	8
4	BONAPARTE	9
4.1	PURPOSE OF THE BONAPARTE PRODUCT	9
4.2	FUNCTIONAL REQUIREMENTS	9
4.2.1	<i>Computational Core</i>	9
4.2.2	<i>GUI</i>	10
4.2.3	<i>Communication Protocol</i>	12
4.3	CONSTRAINTS	13
4.4	OPERATIONAL REQUIREMENTS	13
4.5	RELIABILITY REQUIREMENTS	13
4.6	MAINTENANCE REQUIREMENTS	13
4.7	SYSTEM REQUIREMENTS	13
4.8	SECURITY REQUIREMENTS	13
4.9	USABILITY	14
5	WORKFLOW	15
5.1	DNA-MATCHING	15
5.1.1	<i>Start up</i>	15
5.1.2	<i>Select or create a Project</i>	15
5.1.3	<i>Match Preparation</i>	16
5.1.4	<i>Match and Analyze Match results</i>	17
5.1.5	<i>Adapt Match configuration</i>	17
5.1.6	<i>Report and Store Match results</i>	17
5.1.7	<i>Save the Project</i>	18
5.2	MAINTENANCE FUNCTIONS	18
5.2.1	<i>Start up</i>	18
5.2.2	<i>System Maintenance</i>	18
5.2.3	<i>User Administration</i>	18
5.2.4	<i>Database Administration</i>	18
5.2.5	<i>Project Administration</i>	18
6	BIJLAGE	19



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

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. <i>Describes requirements for phase 1, with basic functionality.</i>
0.2	05-06-2008	Concept	10.2.e	After discussion with 10.2.e

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
Batch	Search definition within all DNA-profiles in a database, based on a selection of characteristics, such as gender, finding-place, etc.
BSO	Biologisch Sporen Onderzoek
CODIS	Combined DNA Index System, NFI-database containing DNA-profiles of missing persons and reference persons. (Allele-based and not containing mixed profiles)
GUI	Graphical User Interface
ICMP	International Committee for Missing Persons
Locus	Position of a STR on the DNA
Metaproject	Set of projects with a common factor, such as a time-period or a geographical location.
Mixed profile	DNA-profile of a contaminated specimen, containing DNA-material of more than one individual
MP	Missing Person
NFI	Nederlands Forensisch Instituut
Pedigree	Family of AM-profiles, with their mutual relations
PM	Post Mortem, data used for identifying (remains of) persons
Project	Workset within Napoleon, consisting of one or more DNA-profiles e.g. linked to the same NFI#. A project consists of <ul style="list-style-type: none">1 or more targets (PM)0 or more References (AM/PM)0 or more Pedigrees
PROMIS	LIMS system of the NFI
SearchSet	Set of profiles to be matched
SIN	Specimen Identification Number, represents a SVO
SNN	Stichting Neurale Netwerken
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 person
Virtual profile	Constructed profile, combining two or more partial DNA-profiles



Owner	: NFI
Project Name	: Napoleon
Project Number	: 310.158
Version	: 0.2
Status	: Concept
Date	: 05-06-2008

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:

Fout! Onbekende naam voor documenteigenschap. (NFI)

- Department Biologisch Sporen Onderzoek (BSO)
- Department Digital Technology and Biometrics (DTB)

Radboud University of Nijmegen (RUN)

- SNN: 'Stichting Neurale Netwerken', the Dutch Foundation for Neural Networks, a national network of research groups on neural networks and affiliated techniques

International Commission on Missing Persons (ICMP)

- Research lab in Bosnia which is responsible for identifications of victims in Bosnia, 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 the screening 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.



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

3 Napoleon

3.1 Purpose of the Napoleon product

3.2 Functional requirements

[NF001]

Identification fields used in database structures, such as SIN-numbers, must be flexible so that data from various sources can be processed.

Minimal sources are CODIS, the ICMP-database and Testdatabases.

[NF002]

Backups can be made. The backup only concerns the internal Napoleon database.
An automatic backup is made daily.

[NF003]

Napoleon can deliver the following user specified Reports:

1. ...
2. ...
- 3.

[NF004]

Napoleon can manipulate databases in the following way:

- Add a database
- Delete a database
- Convert a database with e.g. ETL-scripts (how? which types are to be supported?)
- Import DNA-profiles from foreign databases (which types are to be supported?)
- Export DNA-profiles (which formats are to be supported?)

[NF005]

Napoleon shall be able to manipulate DNA-profile tables (organised as?)

- Search
- Update
- Delete
- Add

[NF006]

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



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

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 database structure and datamodel of Napoleon should be aligned with those of the ICMP-system. In a later stage the pedigree module to be developed should be integrable in both systems.

[NC005]

Data-structure for DNA-profiles shall be compatible to the CODIS-datastructure.

In this structure the *specimen* (or Sample) is central.

A specimen is identified by a Specimen ID (KLPD number + SIN number), and carries a CASE ID, which is a unique key for a case in PROMIS (het DNA-zegelnummer?)

[NC006]

Napoleon must be validated with a proper test-set to be defined by NFI.

[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. Interfacing is implemented through database export-files (XML)

[NC009]

Linkage (relations between alleles) is not applied within Napoleon.

3.4 Operational requirements

[NO001]

Napoleon will be able to run standalone (phase 2) on a commodity laptop as well as in a network environment with multiple users. The maximum number of concurrent users is 8.



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

[NO002]

All searches and decisions made by the user shall be logged.

[NO003]

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

3.5 Reliability requirements

[NR001]

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.

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] 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.

[NM003] Documentation

Clear design documentation and manuals are needed for the use and maintenance of Napoleon.



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

3.7 System requirements

[NS001]

- Napoleon will have database interface modules allowing it to interface with CODIS, ICMP and other foreign DNA-databases.

[NS002]

Napoleon shall contain rudimentary static data to be used for Matching:

- Population Sets (some 10 sets of population-related allele frequencies)
- Mutation models (some 5 sets)
- Size bias models
- Testdata

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

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.

[NX002] Privacy

Privacy-sensitive information shall be encrypted such that it cannot be interpreted without using Napoleon as the access provider.

It is preferred that no privacy-sensitive information is contained in Napoleon at all.

[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.



Owner	: NFI
Project Name	: Napoleon
Project Number	: 310.158
Version	: 0.2
Status	: Concept
Date	: 05-06-2008

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
- Graphical User Interface (GUI)
- Communication Protocol

4.2 Functional requirements

4.2.1 Computational Core

The computational core performs the 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 Ayres and Brenner)
2. Genotype observation
 - a. Alleles, KIT
 - b. peak heights
3. Population allele frequencies
4. Theta-correction
5. Rare alleles (such as null-alleles)
6. Size bias correction

[BF003] Elementary matching

Elementary matching options (SearchSet vs. Batch), where x, y are numbers [1,N]

1. x PM vs. y AM(pedigree); match PM-profiles into (putative) pedigrees
2. x PM vs. y PM (to detect doubles)
3. x PM vs. y PM (to detect parents and siblings)
4. x PM vs. y AM (1:1) to detect parents and siblings
5. x PM vs. y AM(false pedigree); the Father-role has a percentage of likelihood



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

4.2.2 GUI

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

[BF010] Profile Management

The following operations are possible with profiles. Reference is the Napoleon database. Adapted profiles are not fed back into the source-database.

- 1) Add a profile
 - a) Relatives of MP (AM)
 - b) Victim (PM / UI)
 - c) Body Part (PM / UI)
- 2) Edit / Change a profile
 - a) Population
 - b) Pedigree reference(s)
 - c) Alleles
 - d) Add Loci
- 3) Import profiles from an external source (XML-interface t.b.d.)
- 4) Export profiles to an external file (XML-interface t.b.d.)
- 5) 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”
- “MP” = red,
- “identified PM” = blue.

Pedigrees are limited to 5 generations, and 6 siblings wide.

Virtual pedigrees may be composed by dragging profiles from either the SearchSet of the Batch onto positions in the pedigree.

A pedigree (that passes the consistency check) can be saved, printed and stored.

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.

Construction of pedigrees (for 1:1 PM-PM AM-PM matches) pi and si matching should be possible.



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

[BF005] Pedigree Consistency Check

A (read or constructed through the Bonaparte GUI) pedigree can be parsed for consistency. 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 can't 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 project is going to be processed.

The list of present NFI cases and earlier defined projects will be imported from the DNA-database. (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.

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

Next a Batch can be selected or created with the GUI.

The following criteria can be used to create a batch:

- Date (interval) of entry
- Location (remains, or address of MP)
- Complete DNA-profile (Y/N)
- Gender
- Project name
- Pedigree
- Role (in pedigree)
- Age (target)
- Specimen Type

The selected/created batch is the matching set for the Search Set.

The user may now select the option "match", to start the Match-Setup dialog.



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

[BF007] Match Setup

- 1) Loci (per profile in SearchSet adaptable)
 - a) Add, update, delete locus
- 2) Select population allele frequencies per profile
- 3) Select mutation model (per SearchSet) or create a mutation model
- 4) Select model for subpopulation correction
- 5) Select model for size bias correction or create a size bias correction model
- 6) Select model for null alleles
- 7) Select model for rare alleles
- 8) Percentages for the default probability on a false pedigree for father- and mother-role.
- 9) Thresholds to filter possible hits (such as LR, minimum number of loci, max. number of mutations)
- 10) Statistics type
 - a) LR (likelihood Ratio)
 - b) Posterior odds
- 11) Other parameters (t.b.d.)

[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, Search Set, Batch, Match strategy summary, Caseld
- 2) List of hits 1 { UI/MP | Reference | LR } N

When a hit is selected by double clicking a detail screen pops up, showing:

- Date, Issuer, Project, Search Set, Batch, Match strategy summary, Caseld
- 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:

.....

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.



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

The content of the XML-files is <t.b.d.>

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 (DNA peakheight) instead of interpretations.

[BC003]

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

4.4 Operational requirements

4.5 Reliability requirements

[BR001]

The number of false hits per match shall not exceed 0.01%

[BR002]

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

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.



Owner	: NFI
Project Name	: Napoleon
Project Number	: 310.158
Version	: 0.2
Status	: Concept
Date	: 05-06-2008

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.



Owner	: NFI
Project Name	: Napoleon
Project Number	: 310.158
Version	: 0.2
Status	: Concept
Date	: 05-06-2008

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) requirements may be formulated “fit for purpose”.

The described workflow was defined together with BSO-personnel.

5.1 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)
    • 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.

5.1.1 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.

....

5.1.2 Select or create 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.



Owner	: NFI
Project Name	: Napoleon
Project Number	: 310.158
Version	: 0.2
Status	: Concept
Date	: 05-06-2008

Projects can be selected from a list to continue previous work with Napoleon, or created new. 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-casenummer. 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.

5.1.3 Match Preparation

5.1.3.1 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 exits of PM-profiles (post mortem victim profiles)

Per Match there is always one current SearchSet. A SearchSet belongs to the Project.

5.1.3.2 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 PM 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



Owner : NFI
Project Name : Napoleon
Project Number : 310.158

Version : 0.2
Status : Concept
Date : 05-06-2008

- Specimen Category
- Future use fields

Per Match there is always one 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.

5.1.4 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.

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.

5.1.5 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.

5.1.6 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



Owner	: NFI
Project Name	: Napoleon
Project Number	: 310.158
Version	: 0.2
Status	: Concept
Date	: 05-06-2008

- 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.

5.1.7 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.

5.2 Maintenance functions

These functions are divided into “basic functions” and “advanced functions”.

This section describes the workflow for the roles “Administrator” (all), “Data Enterer” (basic only) and “Forensic Researcher” (basic only).

To be detailed.

5.2.1 Start up

Start the Napoleon application and Log In as Administrator.

....

5.2.2 System Maintenance

5.2.3 User Administration

5.2.4 Database Administration

5.2.4.1 Profiles

5.2.4.2 Batches

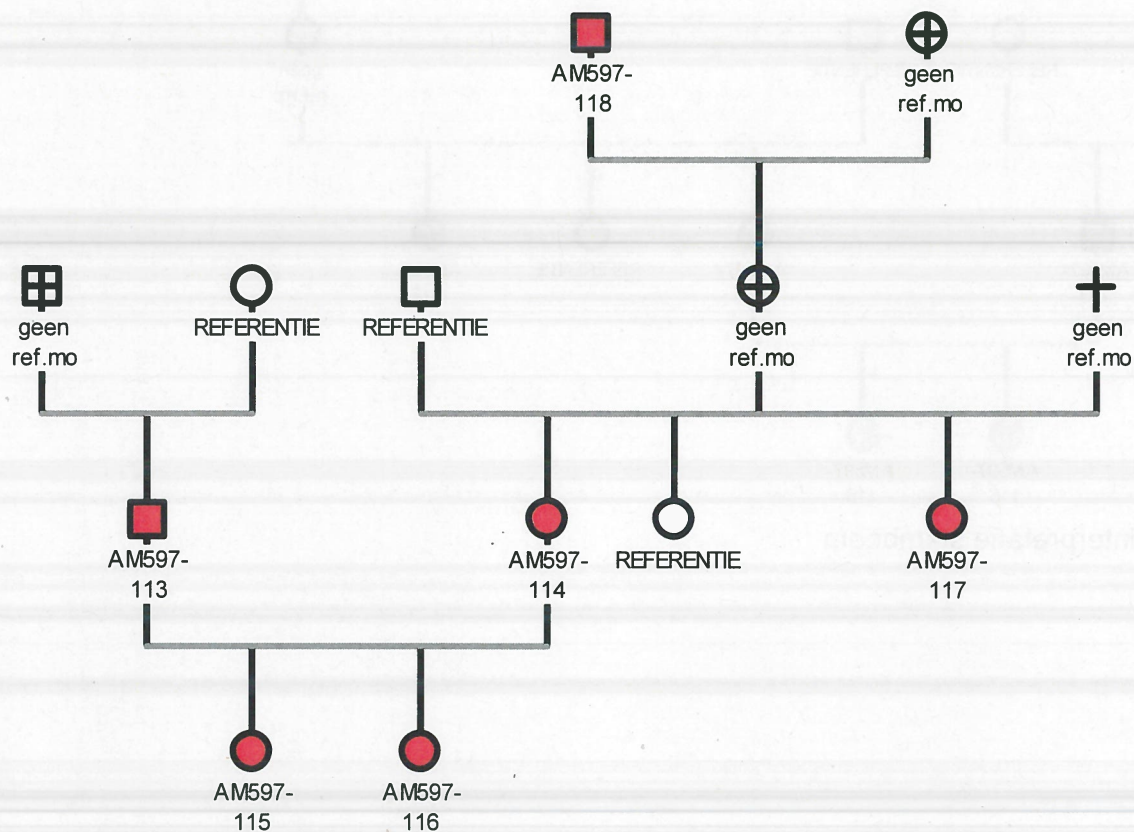
5.2.5 Project Administration



Owner : NFI
Project Name : Napoleon
Project Number : 310.158
Version : 0.2
Status : Concept
Date : 05-06-2008

6 Bijlage

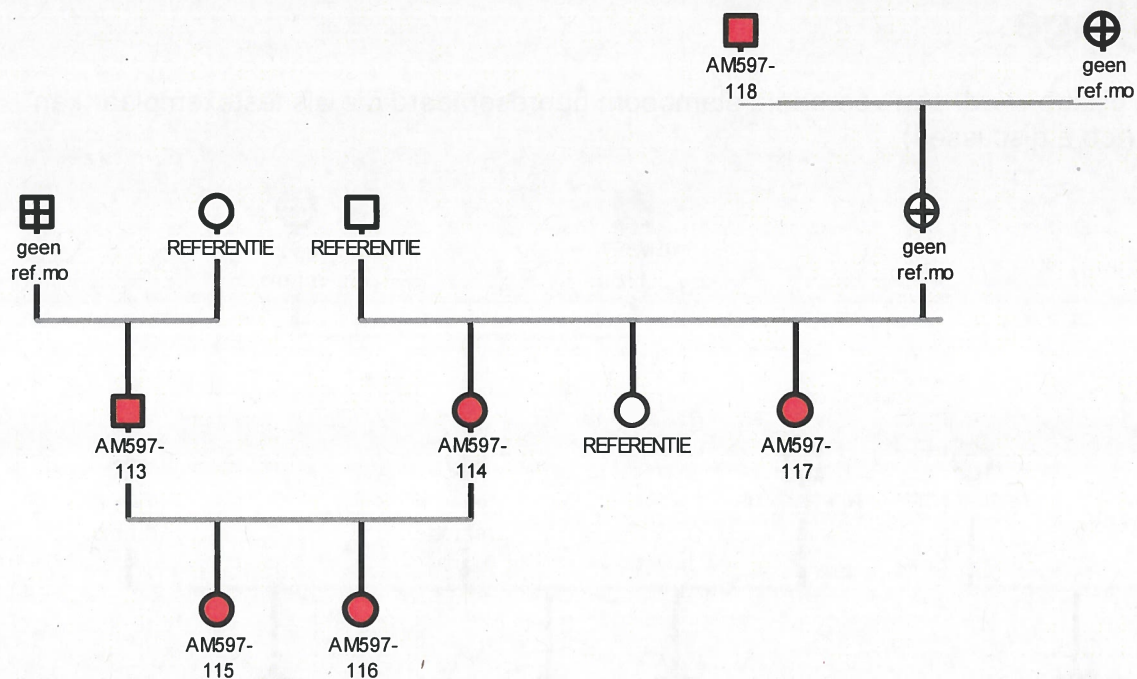
In deze bijlage wordt een voorbeeld stamboom gepresenteerd die als testexemplaar kan dienen (tob e discussed).



Uiteindelijke interpretatie stamboom



Owner : NFI
Project Name : Napoleon
Project Number : 310.158
Version : 0.2
Status : Concept
Date : 05-06-2008



Initiële interpretatie stamboom