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BONAPARTE : Bayesian networks for victim identification on the basis of DNA profiles

An ICIS valorisation project proposal
SNN, Nijmegen (the proposer and the executive)
NFI, The Hague (the costumer)

1 Summary of the project

The objective of the project is to improve NFI's (Netherlands Forensic Institute) missing person screening and matching routine for victim identification based on DNA profiles. A particular aim is to enable NFI to handle the screening and matching task in case of a large national disaster with many unidentified victims. An additional aim is to help ICMP (International Commission on Missing Persons, Bosnia) with software to improve their kinship analysis system, which is, for instance, used for analysis of data from mass graves in the Balkan and international disasters such as the tsunami in 2004 and the hurricane Katrina in 2005.

One of the tasks of forensic research --such as is performed at the NFI -- is the identification of unidentified victims through screening and matching of their DNA profiles against the DNA profiles from relatives of missing persons. In this task, the quality of the match is obviously of great importance for humanitarian reasons, and, to some extent, economic reasons as well. The matching task is often indirect (if there is no material of the missing person him/herself) and should be performed using statistical methods. Bayesian networks are very well suited to model the statistical relations of genetic material of relatives in a pedigree, and can be applied in kinship analysis such that whole pedigrees of relatives of the missing persons are used in the screening phase. As a result, with these models correct matches can be found at the cost of much less false hits than with more straightforward methods which do not take pedigree information into account. An additional advantage of a Bayesian network approach is that it makes the analysis tool more transparent and flexible, allowing to incorporate other factors that play a role - such as measurement error probability, missing data, statistics of more advanced genetic markers etc.

The proposed ICIS project *Bonaparte* will be part of NFI's *Napoleon* project. Napoleon's aim is to develop new software for the NFI for the identification of unidentified victims through screening and matching of their DNA profiles against databases with DNA profiles of relatives from missing persons. Bonaparte will be the technical core in Napoleon. The Bonaparte project will design and develop flexible and transparent models using automatically generated Bayesian networks and Bayesian inference methods, enabling to correctly do kinship analysis on the basis of DNA profiles combined with pedigree information. In addition, the Bonaparte project will develop a graphical user interface for forensic analysts. Means for communication with other NFI systems (e.g. for the DNA-data input) will also be implemented.

The project will have two phases. One in which the basic functionality will be implemented, to be finished in 12-2008, one for extended and advanced functionalities, to be finished in 10-2009.

2 Valorization checklist

2.1 *Project* participants and organization

- Who will lead the *project*? Which companies an*d/or or*ganizations (universities, industries, institutes) will participate? For which percentage of the effort?
    - SNN will lead Bonaparte and is the only participator
    - Bonaparte is a subproject of the larger Napoleon project of NFI. Effort in Bonaparte is 57% of the total Napoleon effort. Napoleon is lead by NFI. NFI and its subcontractors (IT companies) will carry out the other 43% of Napoleon.
- Do any of the *project* participants already participate in ICIS?
    - SNN already participates in ICIS.
- How will the *project* be run or embedded? For example by a consortium/proposer, within the ICIS I&D or other cluster, within an end user organization.
    - The Bonaparte project will be run as part of the Napoleon project lead by NFI. NFI will have other subcontractors in the Napoleon project as well. NFI and ICMP will be involved as end-user.
    - ICMP = International Commission on Missing Persons ("Bosnia", "tsunami", "Katrina"), see section 3.4

2.2 Customer and end users

- Who is the customer of the ICIS *contribution* such as ICIS knowledge or technology?
    - NFI is the customer of the ICIS *contribution.*
- Is there an end user or branch association involved in the *project*?
    - NFI and ICMP will be involved as end-user in the *project*.
- Is there any demand articulation activity foreseen or necessary?
    - There is a demand for effective, flexible, efficient and transparent software that can do large scale DNA matching of unidentified victims with a database of relatives of missing persons, in particular in case of disaster, where many data has to be handled. Currently available systems are considered inadequate by end-users.

2.3 Innovation and customer benefits of the project results

- Which aspects of innovation are targeted by the *project* and/or *the contribution*? For example 'newness' (new to the world, new for a market, new for a company) and 'innovation impact' ('schudt de markt wakker' or incremental improvement)
    - The resulting product will be new to NFI and ICMP ,and to other international forensic institutes as well. Important improvement is that forensic institutes can handle more data of missing persons more effectively, with much less false positives and much less manual post-processing.
- What are the more specific goals/objectives of the *project* and *the contribution*?
    - The objective of the project is to improve NFI's unidentified victims-missing persons screening and matching routine. An important objective in here is to enable NFI to handle the screening and matching task in case of a national disaster with many unidentified victims. A third aim is to improve ICMP's unidentified victims-missing persons screening and matching systems.
- What will be the social/economic effects of the *project*? For whom?

  - Social benefits: relatives of victims/missing persons will be helped better and faster. In particular in a disaster scenario this will have much social impact, since the identification of so many victims is almost impossible without an effective automated system. Who: relatives of victims of a national disaster (NFI), relatives of victims of international disaster and armed conflicts (ICMP).
  - Economic benefits: a more efficient routine at the NFI.

2.4 Utilization of ICIS assets

- What ICIS contributions will be utilized in this *project*? For example specific knowledge/technology assets previously developed in ICIS.
  - Automated Bayesian network modeling and efficient inference.
- What problem(s) will be (re)solved using these assets?
  - The problem of how to deal with large scale databases of DNA from victims and relatives of missing persons such as will occur in case of large disasters and the problem of many false hits that occur in current DNA kinships analysis on such data.
- Any spin-of research foreseen?
  - Implementation of Bonaparte at ICMP or other international institutes is expected to generate further demand for technological research and development.

2.5 What will be the outcomes of the valorisation?

- How will the *contribution* (utilization of ICIS assets) materialize in the project? For example transfer of knowledge, embedded in a proof of principle or in a product)
  - The contribution will materialize as the generic technological core in the Napoleon project.
- How will the *contribution* help to embed (verankeren) ICIS results?
  - The contribution will have a central role in a relevant application that will be used by the renowned NFI forensic institute and is foreseen to play a central role in ICMP and other international forensic institutes as well.
- Are there any separate/identifiable *project* deliverables that will contribute to the ICIS goals? Will the project contribute to the common ICIS demonstrator? How?
  - This project deliverable will be important for crisis management in national and international disaster scenarios. This project will not contribute to the common ICIS demonstrator. However, Bonaparte will contribute with a demonstrator system for ICIS.
- Are any patents or other type of IP foreseen? Will ICIS partners share is the revenues?
  - IP will remain at SNN.

2.6 Dissemination

- The project will deliver a publication.
  - This is not the first objective, but yes, we will publish about this work
- The project can contribute to the Scientific Book or Glossy Booklet. Will the *project* contribute to the Scientific Book or the Glossy Booklet?
  - If possible (in principle, after the delivery of the system)
- The project can contribute to special events.
  - The project can contribute to special events.

2.7 Costs and financial ICIS contribution

- What are the (minimal) total costs of the *project*?

  - Costs of Bonaparte: 10, 1, c & 10, 2, b
  - Napoleon’s specific costs for NFI developments outside Bonaparte: 10, 2, b
  - Total costs Napoleon 10, 1, c & 10, 2, b
- How much subsidy is requested out of the ICIS budget? What percentage of the total cost are ICIS partner costs? (This part is eligible for ICIS subsidy)
  - ICIS requested subsidy €130.000,=
  - SNN (=ICIS partner) costs is 100% of Bonaparte 10, 1, c
  - SNN costs is 57% of Napoleon.
- What percentage of the total *project* costs will be paid for by a customer or 3-rd party?
  - NFI will pay 10, 2, b of Bonaparte
    - This is about 50% of Bonaparte
  - NFI will pay 10, 2, b of Napoleon
    - This is about 72% of Napoleon

Effort by, cost to be paid to:			Cost to be paid by:			
Project	Subproject	Performer/ creditor	NFI	SNN	ICIS subsidy	Total
Napoleon		NFI	10, 2, b	-	-	10, 1, c 10, 2, b
	Bonaparte	SNN	10, 2, b	€10, 1, c	€130.000,=	
Total Napoleon			10, 2, b	10, 1, c	€130.000,=	

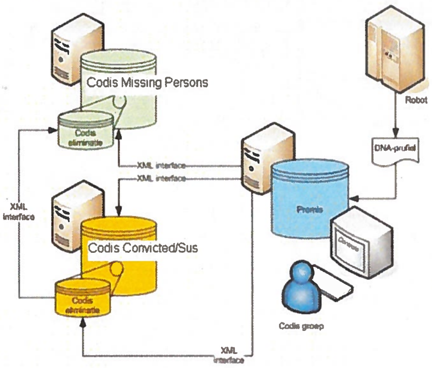
(*) costs based on rate of 10, 1, c hour
(**) costs based on rate c 10, 2, b /day

3 The project: background and objectives

Within the Napoleon research project the aim of the ICIS valorization project Bonaparte is to develop new software in which 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. This 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 network analysis approach. Bayesian networks offer a mathematically precise, powerful, transparent and flexible modeling approach in which model extensions are easily incorporated. In this way Bonaparte enables the Napoleon system to 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.

3.1 Background

3.1.1 Regular Forensic Cases - current situation



The NFI uses the database CODIS (Combined DNA Index System) in combination with the kinship analysis program DNAView in DNA identification work. CODIS is designed to identify criminal suspects from DNA registers and is designed for direct comparisons of DNA profiles. For regular forensic work CODIS works fine, as designed. But when it comes to identifying unidentified persons through a database of DNA profiles of relatives of missing Persons (indirect comparisons), it runs short, which will in particular a problem in the case of a large disaster. The kinship analysis program DNAView cannot use whole pedigrees with DNA profiles from the relatives of missing persons in the screening phase, it gives many false hits.

3.1.2 Catastrophes

World Trade Center in New York disaster on 11 September 2001

It is now estimated that 2,749 lives were lost in the terrorist attacks on the World Trade Center in New York on 11 September 2001. The software used in the first weeks after the disaster, CODIS, ran short in this particular case. For identification of the victims of this disaster the program M-FISys (Mass-Fatality Identification System) has been developed by Gen Codes Forensics. This software is very expensive, and not very transparent. Users of the software are dependent on the maintenance and support of Gen Codes Forensics.

Outside the US, only the Metropolitan Police in England has purchased the software, but their experience so far is not positive. Even the ICMP, an institute at which a lot of identification work is performed, has not purchased this M-FISys software.

The East Asia Boxing Day tsunami disaster
The East Asia Boxing Day tsunami disaster presented different challenges. Although few of the bodies were fragmented, the disaster was on a far larger scale and, with many members of some families being lost; proportionally fewer kinship records were available. It was sometimes possible to identify someone from records from a relative who was also a victim. A disaster on this scale also gives rise to an identification problem of a higher magnitude again.

3.2 Objectives of Napoleon

The main objective of the Napoleon project is to provide the NFI researchers and analysts an efficient and effective tool, which can help in the identification of unidentified persons through screening and matching of unidentified person's DNA profiles against the pedigrees of relatives from missing person's DNA profiles in large databases. In this way the Napoleon system will improve the quality and continuity of the services delivered by the NFI, and it should be able to handle data of a major disaster.

The basic productive system should be ready by 31-12-2008. A full and advanced production system that can handle complex pedigrees and partial DNA profiles should be available by 01-10-2009.

3.3 Objectives of Bonaparte

For efficiency, transparency and flexibility purposes Napoleon's core module will be based on a Bayesian network analysis approach. This will be developed in the Bonaparte project as ICIS valorization. The Bayesian network approach will significantly reduce the number of false hits, and thus streamline the process of identifying victims. In addition, it allows that (future) model extensions are easily facilitated, such as

- Measurement errors
- Mutations
- Population structure
- Missing data
- Advanced genetic markers (SNP's, CNV's)
- Alternative hypothesis testing

3.4 ICMP: International Commission on Missing Persons

The International Commission on Missing Persons (ICMP, www.ic-mp.org) was established at the initiative of U.S. President Clinton in 1996 at the G-7 Summit in Lyon, France. Its primary role is to ensure the cooperation of governments in locating and identifying those who have disappeared during armed conflict or as a result of human rights violations. ICMP has its headquarter and research lab in Bosnia. ICMP is responsible for identifications of victims in Bosnia, after Tsunami disaster, Katrina hurricane and after other disasters. Since its establishment in 1996 ICMP has been funded through voluntary grants, donations and contributions from participating governments and organizations.

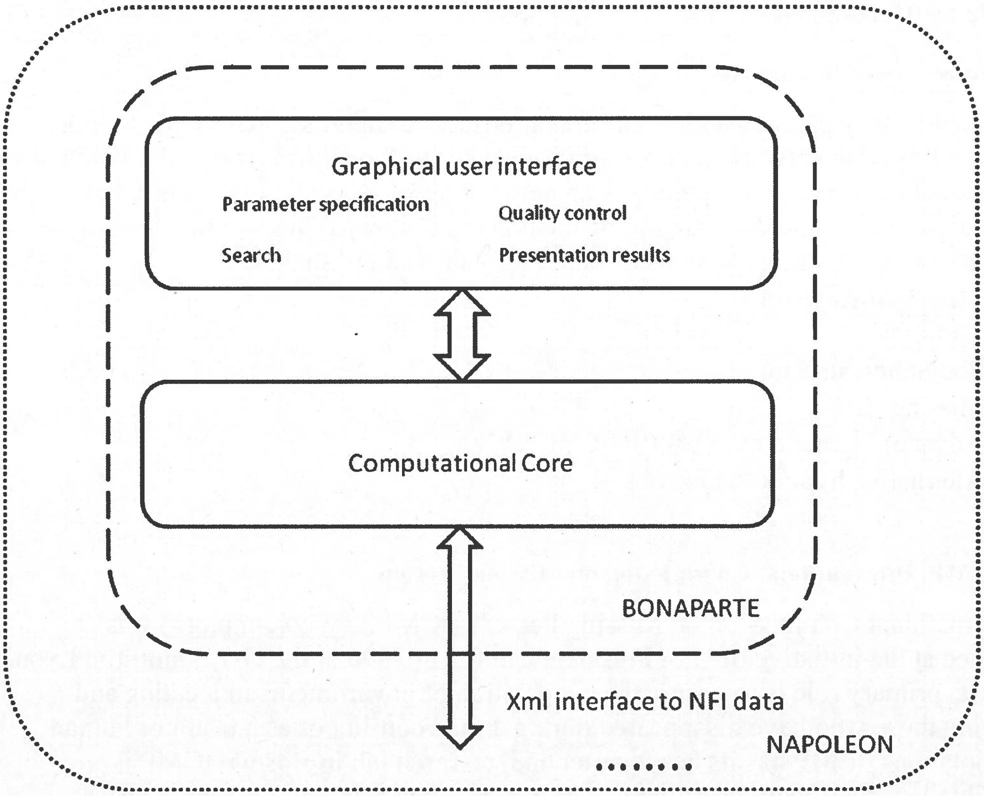
NFI wishes to offer the pedigree-functionality to be incorporated into the ICMP-system at no cost for ICMP and to grant the ICMP to use this algorithm without license fees under specific conditions. NFI researchers explicitly expressed to consider it to be an honor to work together with the ICMP on its humanitarian mission. We sympathize with this idea and would like to cooperate with NFI in this issue. In our opinion this would suit very well in the context of the ICIS project, using public money to valorize technology for the benefit of victims of armed conflicts and disasters. Beside this, it would be a perfect opportunity for ICIS publicity.

4 The contribution: description of the proposed system

The Bonaparte system that we propose to contribute will be part of the Napoleon system. The system will have two components (see figure below):

- Computational core (Bayesian modeling and inference)
- Graphical User Interface

The system interacts with the other NFI systems, such as database via XML protocols.



4.1 Operation of the system

The system will operate as follows:

Relevant data needed for the kinship analysis (victims' DNA data, DNA data from objects and relatives and possibly relations in families of missing persons) will be imported from other NFI systems into the system via xml protocols. On the basis of these data supplemented with specifications provided by the forensic analyst via the GUI, the computational core generates a series of Bayesian networks. With these networks likelihoods for the matches that are to be screened. Results are presented via the GUI and can be communicated to other NFI systems via XML.

The system can be controlled via the GUI: configuration of parameters, inspection of results, quality control of data, options to provide the system with alternative hypotheses, search commands, and presentation of results. Furthermore, the system will have features such as the inclusion of annotations, authorization of matches, and history of analysis.

The system will be implemented as a multi-client system. It should be able to run on a standard laptop.

4.2 Embedding of the system within NFI

Other parts of the Napoleon project include the further embedding and integration of the system with other NFI systems and processes, end-user part of the GUI design etc. These are not further discussed here. Also integration with ICMP systems and processes will fall under other parts of Napoleon, not discussed here. For a detailed description of the functionality of Napoleon system we refer to Appendix I.

4.3 Intellectual property rights and licenses

Intellectual property rights of Bonaparte remain with SNN. NFI will obtain a non-exclusive license. Our intention is to grant ICMP a non-exclusive license free of charge under conditions to be agreed.

5 Time schedule, effort and budget

5.1 Time schedule

The proposed project will be carried out in 2 phases. In the first phase, we will realize the basic functionalities. In the second phase, we will realize additional functionality, such as the clustering of partial DNA profiles, and the handling of more advanced DNA markers. NFI strongly requested that the first phase is finished by the end of 2008 and the second phase by 10-2009

Phase	End date
1	31-12-2008
2	1-10-2009

5.2 Effort

Task	Person-months	
	Phase 1	Phase 2
Modeling, design	7	4
Implementation, testing	7	4
Manual, reports	1	1.5
Project management	1	0.5
Total	16	12
Total project	28	

These estimate are partly based on our experience in the SHELL ICIS valorization project. In particular the SHELL project has that we can compare with this project. We satisfactory completed the SHELL project in about 20 person-months, and by comparing innovation and complexity levels, we can get an estimate for the required effort in this project. Our estimate is that phase 1 is a bit less innovative but somewhat more complex than the Shell project. However in the SHELL project, the overall approach to the problem was initially less clear than that we expect in this project. This required a few months extra in the SHELL project. Thus we think that in this project 16 months is a fair estimate. Phase 2 will be more complex than phase 1, but we can build to a large extend on the results and experiences of phase 1.

5.3 Budget

For application projects, SNN charges standard a commercial rate of 10, 1, c 10, 2, b Budgets are computed assuming 20 days per month.

The total effort is 28 months. The budget for Bonaparte is therefore 10, 1, c & 10, 2, b SNN is willing to invest 10, 1, c in Bonaparte. ICIS subsidy of €130.000,= is requested. If subsidy is granted, the remainin 10, 1, c & 10, 2, b for the Bonaparte project is payable by NFI to SNN.

The additional NFI effort to Napoleon is estimated to be 3292 hours, partly to be carried out by NFI and partly outsourced by NFI to other parties. For these hours, NFI calculates a rate of 10, 2, b per hour. So, the additional NFI efforts are estimated to b 10, 2, b The total budget of the Napoleon project is the sum of the Bonaparte budget 10, 1, c & 10, 2, b and the additional effort in Napoleon, 10, 2, b which equals a total of 10, 1, c & 10, 2, b

The requested ICIS subsidy is about 15% of the total Napoleon budget, which corresponds to a valorization part of about 30% of total Napoleon budget.

Effort by, cost to be paid to:			Cost to be paid by:			
Project	Subproject	Performer/ creditor	NFI	SNN	ICIS subsidy	Total
Napoleon		NFI	10, 2, b	10, 1, c	-	10, 1, c 10, 2, b
	Bonaparte	SNN			€130.000,=	
Total Napoleon					€130.000,=	

(*) costs based on rate of 10, 1, c 10, 2, b /hour
(**) costs based on rate of /day

6 Project team

6.1 SNN Team

For phase 1, we will have about 10 months time for a 16 person-month project. So we need a project team with about 2 persons per tasks to carry out the project. This project team will consists of the following people.

- Modeling: 10, 2, e
- Programming: 10, 2, e
- Manual and reports: 10, 2, e
- Project management: 10, 2, e

6.2 Experience of SNN team

- Drs 10, 2, e has been responsible for the succesful software implementation in valorization project with SHELL, " A Petrophysical Decision Support System". In this project, 10,2,e 10,2,e acted as supervisors/advisors.
- 10, 2, e has been responsible for the BayesBuilder JAVA implementation (ICIS-CDM), supervised by 10, 2, e and the JAVA implementation of Promedas, a system applying Bayesian networks for medical diagnosis (supervised by 10, 2, e
- Drs 10, 2, e has performed his PhD research at SNN in the field of genetic applications of Bayesian networks 10, 2, e acted as his advisors.

- Dr 10, 2, e is researcher at SNN in the field of Bayesian networks. He also carried out and supervised research in genetic applications of Bayesian networks. He has ample experience with database application in genetic anthropology. Currently he is director of Promedas BV, applying Bayesian networks for medical diagnosis.
- Dr 10, 2, e is researcher at SNN in the field of Bayesian networks. He also carried out research within the ICIS-CDM, and has been supervised other ICIS projects. Currently he is vice-director of Smart-Research BV, for commercial applications of neural networks and Bayesian networks.
- Prof 10, 2, e is professor "Neurale netwerken en machine intelligentie" and director of SNN. He supervised many projects, including ICIS projects.

6.3 Relevant publications of SNN team

Albers CA, Stankovich J, Thomson T, Bahlo M, Kappen HJ (2008)
Multipoint approximations of identity-by-descent probabilities for accurate linkage analysis of distantly-related individuals
American Journal of Human Genetics (in press)

Albers CA, Heskes T, Kappen HJ (2007)
Haplotype inference in general pedigrees using the cluster variation method
Genetics 177:1101-16

Albers CA, Leisink MA, Kappen HJ (2006)
The cluster variation method for efficient linkage analysis on extended pedigrees
BMC Bioinformatics 7(Suppl 1):S1

Albers CA, Kappen HJ (2007)
Modeling linkage disequilibrium in exact linkage computations: a comparison of first-order Markov approaches and the clustered-markers approach
BMC Proceedings 2007, 1(Suppl 1):S159

de Vries BB, Pfundt R, Leisink M, Koolen DA, Vissers LE, Janssen IM, Reijmersdal S, Nillesen WM, Huys EH, Leeuw N, Smeets D, Sistermans EA, Feuth T, van Ravenswaaij-Arts CM, van Kessel AG, Schoenmakers EF, Brunner HG, Veltman JA (2005)
Diagnostic genome profiling in mental retardation.
Am J Hum Genet. 2005 Oct;77(4):606-16. Epub 2005 Aug 30.

6.4 NFI team

The following persons from NFI are involved in the Napoleon project from which the ICIS project will be a subproject.

- Executive Napoleon: 10, 2, e (Head of department BSO - "Biologisch Sporen Onderzoek")
- End-user Napoleon, forensic scientist, specialist kinship analysis: Dr 10, 2, e 10, 2, e
- Software project leader Napoleon: 10, 2, e

Appendix I Napoleon functionality

As defined in collaboration with NFI (including the non-ICIS parts)

Basic Functionality

- Operation in a network environment with multiple users, or as a standalone system that can be run entirely on a common laptop.
- Databases with DNA-STR profiles configuration and maintenance
  Add database; Delete database; Convert old database to new database. [With database-creation and ETL scripts]; Import DNA profiles [per group/cluster?]; Export DNA profiles. [per group/cluster?]
- Static Data configuration and maintenance:
  Population STR data (frequencies): Adding; Search; Update; Delete
  Locus table: adding/update/delete locus
  Amplification Kit table: adding amplification kit loci specifics
  Maximal 25 STR
  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
- Static Data configuration and maintenance:
  Population mutation data for STRs: Adding; Search; Update; Delete
- DNA profile tables (authorized) modifications [per group/cluster?]
  Add loci, alleles, unique DNA identity number, casenumber
  Search, Update, Delete
- Option to compatible file exchange with CODIS
- Automatic screening of all samples against Elimination Known profiles (e.g., laboratory personnel), reducing the chance of misidentification through laboratory contamination of samples: could be performed by CODIS itself
- User (Role Based) Access Control
  DBA function
  Multiple levels of secure access privileges including "Administrator Only" functions. Specific operators can be assigned to samples or groups of samples
- Pedigree:
  Kinship (table) configuration: Adding; Search; Update; Delete
- Matching options: options are optional and can be configured by the user [defaults to default values]
  - option to select DNA profiles and pedigrees for searching
  - option to select a population for statistics
  - option to select a subpopulation correction
  - option to chose a frequency for rare alleles
  - option to add the maximal number of mutation loci in a case
  - option to include null alleles in match
  - option to include mutation model of K. Ayres and C. Brenner
  - option to give the minimum required loci in match
  - option to add a prior probability

  - option to calculate beside LR, the posterior probability
  - option to chose thresholds for reporting results
- Direct searches:
  One-to-many and *many-to-many* searches between DNA profiles of Missing Persons against DNA profiles of Unidentified Persons
  One-to-many and *many-to-many* searches between DNA profiles of Unidentified Persons (/bodies parts) against DNA profiles of Unidentified Persons (/bodies parts) in order to group profiles
- Indirect searches:
  One pedigree-to-many-profiles and *many pedigrees-to-many-profiles* searches between DNA profiles of Reference Samples against DNA profiles of Unidentified Persons
- Automatic Calculation of likelihood ratios and posterior probabilities with flexible, intuitive parameters based on Bayesian Stochastic Network Analysis. Results are ranked and results above a selected threshold are reported
- Kinship matching to family references. Samples can contribute to more than one case and Napoleon can handle complex pedigrees. Profiles can have multiple roles, allowing a direct reference or newly identified person to be used as a reference for another. Profiles can be reassigned to other references if needed, greatly increasing their flexibility
- Generate user specified Reports from Matching-Results-table
  Report options: searching defaults (see matching options)
  Print Reports; Save Reports
  Export matching results from Matching-Results-table
- Reassignment of DNA profiles of missing persons found matching
- QA tools allowing you to spot inconsistencies and errors in the data that may be the result of commingled remains, sample switches or contamination and greatly reduce the chance of a false-identification
- User's friendly GUI: Menu's, Options and defaults set up, search and filter commands
- Documentation
- Back-up

Extended functionality:

Extended functionality will be completely described after stage 2 has been finished.

- Includes all basic functionality
- Databases with DNA-Y chromosomal STR profiles configuration and maintenance: Adding; Search; Update; Delete; Import; Export
- Static Data configuration and maintenance: population Y-chromosomal STR data:
  Adding; Search; Update; Delete
  Locus table: Adding/Update/Delete locus
  Amplification Kit table : adding amplification kit loci specifics
  Maximal 20 Y-chromosomal STR

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

- DNA Y-chromosomal profile tables (authorized) modifications [per group/cluster?]:
  Adding; Search; Update; Delete
  Option to compatible file exchange with other external databases (not only CODIS)
- Analyses can be grouped using variable parameters to identify fragments belonging to the same person and to build up a consensus DNA profile from badly damaged remains
- Virtual Profiles, combining multiple test results from a single sample, with concordance & conflict reporting. This greatly simplifies work with fragmented samples, or degraded samples that have been assayed many times
- Matching options: options are optional and can be configured by the user [defaults to default values])
  - option to chose more that one population for the statistics
  - option to include Y chromosomal data for screening
  - option to use fatherless calculation for loci with paternal exclusion
  - option to use motherless calculation for loci with paternal exclusion

Advanced functionality
Advanced functionality will be completely described after stage 2 has been finished.

- Includes all extended functionality
- DNA profile tables (authorized) modifications [per group/cluster?]
  Add: include peak heights; Search; Update; Delete
- Databases with DNA-SNP data and maintenance
  Add database; Delete database; Convert old database to new database. [With database-creation and ETL scripts]; Import DNA profiles. [per group/cluster?]; Export DNA profiles. [per group/cluster?]
- Static Data configuration and maintenance: population SNP data
  Adding; Search; Update; Delete
  Locus table: adding/update/delete locus
  Amplification Kit table : adding amplification kit loci specifics.
  Maximal 200 SNP
  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
- DNA profile tables (authorized) modifications [per group/cluster?]
  Adding; Search; Update; Delete
- Matching options: options are optional and can be configured by the user -
  option to include mtDNA data for screening
  - optionto include SNP data
  - option to use other mutation model (Xu et al 2000)