

Introduction to Poster Presentation

Examples

Assistive Technologies for Dialysis Patients

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Abstract

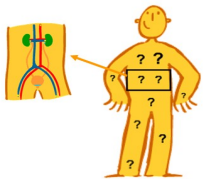
Dialysis patients can only consume 1 liter of fluid and a two grams of sodium each day. Currently, patients try to remember or write down in a food diary their fluid and sodium consumption. However, these techniques are insufficient because 80% of patients are unable to restrict their fluid intake. If patients miscalculate their fluid intake they run the risk of hypertension, pulmonary edema, and death.



Our research focuses on creating a personal digital assistant application to assist dialysis patients accurately monitor their fluid and sodium intake. Our application will:

- allow patients with *reduced cognitive skills* to easily record dietary information
- allow patients to get *immediate feedback* on their fluid and sodium intake
- *reduce the stigma of disease* as a medium for recording dietary information
- assist researchers gain information about patient *fluid and sodium compliance*

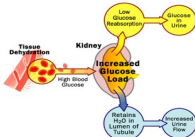
Why are kidneys important?



- Acts as a filter system
- Gets rid of waste products
- Balances the body's fluid content
- Produces hormones that control blood pressure
- Produces the hormone Erythropoietin to help make red blood cells
- Activates vitamin D to maintain healthy bones

Why do kidneys fail?

- Diabetes
- High blood pressure
- Glomerulonephritis
- Polycystic kidney disease
- Scarring from kidney infection in childhood
- Obstruction



A day in the life of a dialysis patient?

Early on patients get a *fistula* – an artery and vein are connected for good blood access



End-stage renal patients use a dialysis machine **three** days a week for **four** hours!

How we are developing assistive technologies

1. Evaluate users needs and technology available

- Users may have poor eyesight (large display)
- Users may have varying computer literacy (easy to use interface)
- Doctors want to monitor user compliance (download information)
- Users may have varying literacy rates (more memory to store images)

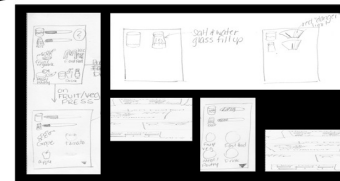


2. Allow users to test the selected technology

- Do users feel comfortable with technology?
- Can the user press the buttons?
- How large do icons have to be for easy recognition?
- Can the user use the voice recorder?
- Can the user use the barcode scanner?

3. Develop the interface -with the users in mind

- How do users record dietary information?
- How do we display a lot of information in a readable format?
- How do we convey how much fluid and sodium has been consumed?
- How can we educate patients about fluid and sodium intake?



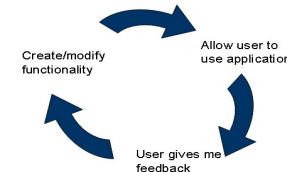
4. Create the backend of the application

- Transfer UPC database to Palm database
- Integrate scanner with UPC database
- Integrate UPC database with nutritional database
- Connect backend with interface



5. Iterative development of application

- Implement a small subset of functionality for the application
- Allow users to use the application
- Use user feedback to improve functionality and add more functionality
- Iterative development allows users to learn about the application



What are we doing now?

We recently finished a study examining the usability of personal digital assistants. We compared how well novice PDA users 25-30 years old, 75-85 years old, and people with chronic illness completed five tasks: pushing buttons, viewing icons, recording a voice message, and scanning barcodes with two scanners.



We found there are no major differences in performance between groups.

We are currently working with dialysis patients to find out how they keep track of their dietary intake. We are using our results to create picture cards and conduct usability tests on our initial interface designs.

Future Work

- Meet with nurses at Indiana University-Purdue University Indianapolis (IUPUI) hospital to discuss the interface clinicians will use to view compliance information
- Integrate complete UPC database with nutritional database
- Meet with renal dieticians at IUPUI to discuss how precise the application must be when monitoring fluid and sodium consumption
- Ensure application meets renal dietician requirements for accuracy
- Create a test suite of personal digital assistant applications for patients to learn how to use the technology
- Teach nurses how to use the test suite and introduce the technology to the participants
- Begin iteratively designing software and interface

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A General Framework for Wireless Smart Distributed Sensors

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The Problem

Many situations call for the use of sensors monitoring physiological and environmental data. In these situations, it is beneficial to have intelligent agents analyze the large amounts of sensor data, recognize cues from the data, and communicate the results to humans and other computers.



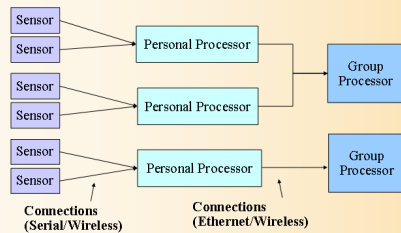
An awareness and warning tool – comprised of heterogeneous sensors, small light-weight, wearable processors, embedded intelligent software, and a wireless network connecting these processors and computers – is being piloted at Sandia National Laboratories. This tool has broad applicability to emergency teams, military squads, individual exercise and fitness monitoring, health monitoring for sick and elderly, and environmental monitoring in public places.

The Approach

Rather than create a custom software/hardware package for each application, we are developing an integrated generic system which can be configured by developers of different applications. The system is constructed of standard off-the-shelf hardware and software (Linux, ANSI C, and Java) platforms.

The flexible hardware infrastructure consists of sensors, small personal processors (e.g. handheld microprocessor devices), and larger group processors.

Integrated Hardware/Software System



As handheld devices become more powerful, this architecture becomes an impressive, albeit non-traditional, distributed computing cluster for mobile applications and pervasive computing. These small devices can process large amounts of sensor data, execute complex intelligent algorithms, and collectively communicate using a wireless network.

About the Embedded Reasoning Institute

"...In the 21st century the technology revolution will move into the everyday the small and the invisible..."

Mark Weiser, XEROX PARC

The Embedded Reasoning Institute (ERI) is a new research initiative for Sandia National Laboratories in the area of intelligent wireless pervasive devices (i.e., sensors, PDAs, micro-processors). The ERI seeks to explore, integrate, and advance technologies from the areas of wireless adaptive networks, wireless sensor technology, distributed sensor data integration, computer-enhanced situational understanding, and the flexible software/hardware systems to support these diverse areas. An important component of the ERI is the ERI-student program providing researchers and student interns with a collaborative environment to investigate capabilities in information technology, distributed computing, embedded systems, sensor technology, wireless technology, and information protection.

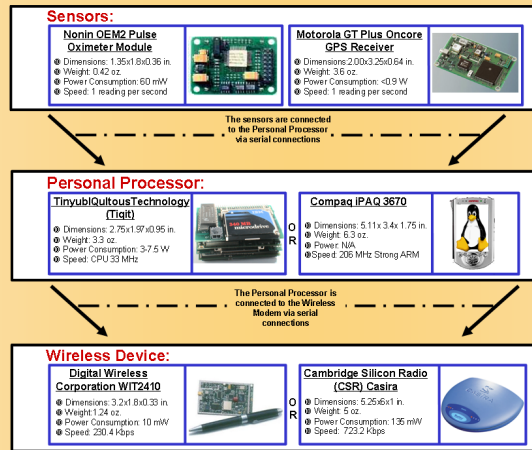


Sandia is a multiprogram laboratory operated by Sandia Corporation, a Lockheed Martin Company, for the United States Department of Energy under contract DE-AC04-94-AL85000.



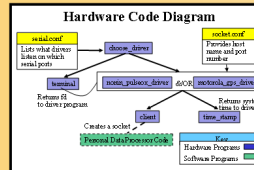
The Hardware Aspect

We considered weight, size, power consumption, computing power, operating system availability, support for high-level languages, reliable network support, and human factors when evaluating the equipment required for this system. Based on these specifications, we decided to use the following design:



We built middleware to interface the sensors with the intelligent agents. The hardware interfaces are shown in the code diagram:

- **Driver** programs for each sensor (nonin_pulseox_driver and motorola_gps_driver).
- **Configuration files** to assist user input changes.
- A **time stamp** module to ensure synchronized sensor measurements.
- A **client socket** module to communicate with the intelligent agent software.



Future Work

As faster, smaller processors become available, the platform will be upgraded. We plan to employ Bluetooth modules as a substitute for the wireless modems in order to reduce power, conserve space, and provide a better packaged tool. Furthermore, we plan to provide an IP-based wireless transmission protocol with 128-bit encryption between all personal processors and the group processors. We are also incorporating additional sensors in order to pilot awareness tools for different applications.

Most of our future work will focus on the intelligent algorithms. We plan to develop additional agents and to add capabilities to existing agents. We will experiment with customized SOMs for individual users and situations.

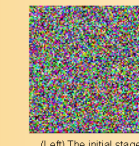
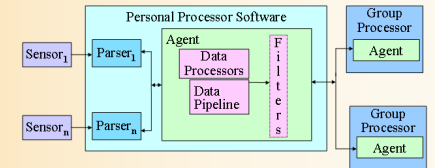
The Software Aspect

The software architecture combines generic agents and a reusable, core software infrastructure which manages the available hardware resources. The agents within the personal and group processors integrate several intelligent components that may be added and adapted to customize new applications. Furthermore, the software may be modified to include new sensors with minimal changes to the system.

Personal Processor Software

Although personal processors are typically smaller and less powerful than group processors, their power lies in the fact that as a group they are able to process and react to data from a set of sensors in parallel. An agent, executing on the personal processor, controls the flow of sensor data through the different intelligent data processors and employs filters to regulate the flow of information to the group processors.

- **Parsers** convert output from any sensor to standard format.
- **Data processors** add tags or flag interesting data (see SOM example below).
- **Filters** reduce the flow of data to the group processors.



(Left) The initial stage of a Self Organization Map.



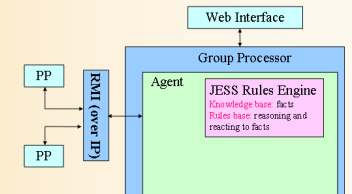
(Right) The final stage. Notice how similar colors are clustered together.

Intelligent Data Processors

One type of intelligent algorithm that an agent can employ to process sensor data is a Self Organizing Map (SOM). The map is trained to recognize typical sensor data. If the training data is labeled, the map may label new sensor data accordingly. If there is only unlabeled training data, a simpler tag which identifies any data dissimilar to the training data as "abnormal" may be used.

Group Processor Software

Each group processor is wirelessly connected to a set of personal processors (PP). The group processor contains one or more high-level reasoning agents. These agents can analyze patterns in data across many personal processors, and use past data and simulations in order to recognize scenarios. Data is archived for future use in a separate database.



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A Simple Approach for Finding the Globally Optimal Bayesian Network Structure

Tomi Silander and Petri Myllymäki, CoSCo Research Group, University of Helsinki



But that is NP hard!

True, but with a decomposable score it is manageable up to about 30 variables.

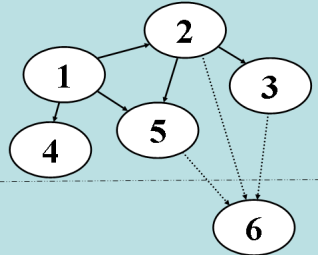


With the best ordering and the best sink available it is easy to build an optimal net.

For i in $\{1, \dots, |V|\}$:

$$Pa_G(ord(i)) = bps^1(ord(i), \underbrace{\bigcup_{j=1}^{i-1} \{ord(j)\}}_{\text{Predecessors of } ord(i)})$$

$$GS(G, V) = \sum_{v \in V} LS(v, Pa_G(v))$$



Best network = best for the rest + best parents for the best sink



Find the best order for variables; consistent with a best net.

For i from $|V|$ down to 1:

$$ord(i) = bsk^1(V - \underbrace{\bigcup_{j=i+1}^{|V|} \{ord(j)\}}_{\text{Variables already ordered}})$$

But why are you guys doing this stuff?

For all variable subsets W , find the best variable to act as a sink in a net with nodes W .

For each subset W of V in order:

$$bsk(W) = \max_{w \in W} \left(\underbrace{bps^0(w, W - \{w\})}_{\text{Score of the best parents of } w \text{ in } W - \{w\}} + \underbrace{bsk^0(W - \{w\})}_{\text{Score of the best net for } W - \{w\}} \right), w$$

Score of the best network for W with w as a sink

Sure, but how do you find the best sink and its best parents?

For each variable, find the best for all possible parent candidate sets.

For each variable v :

For each subset W of $V - \{v\}$ in order:

$$bps(v, W) = \max \left(\underbrace{LS(v, W, W)}_{\text{The whole } W \text{ as parents}}, \underbrace{\bigcup_{w \in W} bps(v, W - \{w\})}_{\text{The best parents of subsets}} \right)$$



Calculate local scores for all variables $v \in V$ and all subsets $W \subset V - \{v\}$.

Data	#
0 1 1 0 1	3
0 1 1 1 0	15
0 1 1 1 1	3
1 0 1 0 0	1
1 0 1 1 0	4
1 0 1 1 1	7

Marginalize

Data	#
0 1 1 1	6
0 1 1 0	15
1 0 1 0	5
1 0 1 1	7

Conditional frequencies

Data	#
0 1 1	(15, 6)
1 0 1	(5, 7)

A free demo and ANSI C source code at <http://b-course.hiit.fi/bene>

Poster presentation

- Informal event.
- Encourages interaction and exchange of ideas.
- Different from paper and talk.
- Way of presenting your topic in illustrative way:
 - Outline of your work.
 - Detailed enough to be self-contained.
 - For varying general audience.
- Goal is to share information and attract interest to your work!

Designing the poster

- Spend a few minutes thinking about :
 - What is the story you want to tell.
 - Motivation
 - Statement of the problem
 - Method and approach
 - Results and conclusion
 - Don't forget the references
 - How the poster looks visually
 - Graphics, colors, images, graphs.
- **Simplicity is the key.**

Designing ... (cont'd)

- Layout and modularity
 - To support your story.
 - Guide the reader.
 - Avoid congestion in audience.
 - Horizontal vs. vertical vs. cyclic vs. radial
- Typeface
 - Text should be visible from a few meters apart.
 - Title and author names should be prominent.

Designing ... (cont'd)

- Figures and diagrams preferred over text and tables.
 - Bulleted lists instead of running text.
- Use colors
 - To make your poster more attractive.
 - To support your story.
 - Sparingly —never use **RED** and **GREEN** in graphs to illustrate your point.
- More guidelines:
 - Google, for instance, “scientific poster design”

Presenting your poster

- Do not stand in front of your poster.
- Use graphics in your presentation.
- Be sensitive to the background of your audience.
- Finish with one listener first, then start with newly come.
- Don't be cheesy - Bad jokes are worse than no jokes.
- To support you presentation, you may have
 - Hand-outs (or even full papers) available
 - Computer demos
 - Contact information

If you want to make a

- Bad poster
 - Design for one audience
 - your competitor
 - Layout in rows
 - Obscure the sequence
 - Have a lot of small text
 - Be wordy, but avoid explanation
- Excellent poster
 - Design for varying audience
 - competitors, colleagues, people from outside your field
 - Layout in columns
 - Indicate the sequence
 - Use graphics
 - Emphasize important info
 - Organize your message
 - KISS

Some more examples

Identifying WRKY protein-protein interactions in *Arabidopsis thaliana*

PURDUE UNIVERSITY

Moyer, Michelle¹ and Chen, Zhixiang²

¹Summer Intern, Department of Botany and Plant Pathology, Purdue University, West Lafayette, Indiana
²Department of Botany and Plant Pathology, Purdue University, West Lafayette, Indiana



Introduction

Knowing how plants respond to invading pathogens is key in understanding the basics of plant physiology. This quest for knowledge is now beyond the observable macroscopic phenotypic responses; it has delved into the microscopic world since plant pathological research began to study the biochemical and genotypic interactions between the host plant and the pathogen.

Using the model plant, *Arabidopsis thaliana*, has aided studies involving plant-microbe interactions. Its remarkably small genome has been completely sequenced thus allowing researchers to identify and perform functional analysis assays on little-known genes and proteins. It was with this information that a superfamily of transcription factors, encoded by WRKY genes, was discovered as major family of pathogen defense-response related genes in the Plant Kingdom.¹

This superfamily of around 72 genes², encode transcription factors that have zinc-finger motifs³ (Fig. 1) and bind to W-box elements (conserved sequence promoters) upstream of many defense-response genes. The up-regulation of WRKY gene transcription has been shown to occur during the onset of pathogen invasion and this up-regulation has the implication of WRKY gene-product involvement in pathogen defense-response.³

In addition to the complete understanding of the WRKY gene family's role as transcription factors another question that remains to be answered is whether the protein binding domain of the WRKY gene zinc-finger motifs leads to any specific interactions between WRKY and other proteins. The following project addresses this question by screening a cDNA library of the *Arabidopsis* genome in search of proteins that interact with specific WRKY genes.

Plant WRKY Transcription Factors

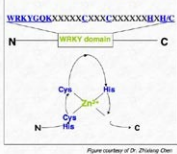


Figure courtesy of Dr. Zhixiang Chen

WRKY Gene Cloning

• WRKY genes of interest in this project are WRKY 6, 22, 25, 37, 55, and 64. These are amplified from a stock of previously purified DNA by using PCR. Table 1 is a list of primers used to amplify the individual gene sequences; Table 2 is the program used for amplification.

Table 1: Primers & restriction enzymes used to amplify the WRKY genes.

WRKY Gene	Primer Sequence/Restriction Sites	Restriction Enzymes
WRKY 6	2394: atggattctctgagagagatgactctg 2395: atccagggcgcctatgatattgctctg	BAMHI NOTI
WRKY 22	2439: acccagggcgcctatgatattgctctg 2442: atggcggcgcctatgatattgctctg	NOTI NOTI
WRKY 25	2396: atggattctctgagagatgactctg 2397: atccagggcgcctatgatattgctctg	BAMHI NOTI
WRKY 37	2398: atccagggcgcctatgatattgctctg 2399: atggcggcgcctatgatattgctctg	NOTI NOTI
WRKY 55	2449: acccagggcgcctatgatattgctctg 2450: atccagggcgcctatgatattgctctg	NOTI NOTI
WRKY 64	2441: atggcggcgcctatgatattgctctg 2442: atggcggcgcctatgatattgctctg	NOTI NOTI

Table 2: PCR Program

Time	Temperature
1) 64°	02:00 min
2) 94°	00:30 min
3) 55°	00:30 min
4) 72°	02:00 min
5) 72°	Repeat 25x
6) 72°	00:00 min
7) 4°	14:00 min
8) End	

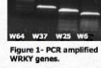


Figure 1: PCR amplified WRKY genes.

• Figure 1 shows the PCR amplified WRKY genes 6, 25, 37 and 64.

pSos Plasmid



Figure courtesy of Stratagene

Plasmid Vector Amplification

- The pSos Plasmid and appropriate WRKY genes were digested with the same restriction enzymes and ligated.
- After DNA isolation, a sample digestion was done to ensure that the pSos plasmid amplified in the *E. coli* contained the WRKY gene insert.
- *E. coli* containing the appropriate pSos plasmid and WRKY gene insert were then cultured overnight.
- The DNA from this stock was then used throughout the rest of the project.

Insert

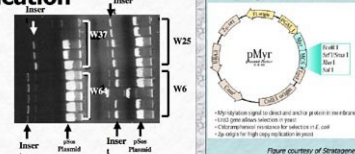


Figure courtesy of Stratagene

pMyr Plasmid



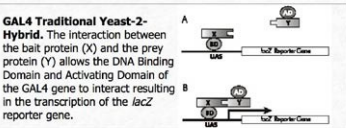
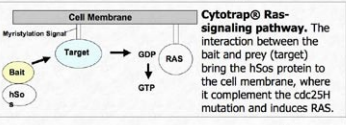
Figure courtesy of Stratagene

Cytotrap® Yeast-2-Hybrid vs. Conventional Yeast-2-Hybrid

	Cytotrap®	Conventional
Purpose	Detects protein-protein interactions in vivo by activating transcription of the <i>lacZ</i> reporter genes.	Detects protein-protein interactions in vivo by initiating transcription of the <i>lacZ</i> reporter genes.
Uses	Used for transcription activators or repressors, cytoplasmic post-translationally modified proteins, and proteins that are toxic to yeast.	Used to identify genes that encode for a protein that can interact with a given protein.
Yeast Strain	Temperature sensitive <i>cdc25H</i> containing the yeast homologue of the human <i>Sos</i> gene, which activates the Ras-signaling pathway.	The YRG-2 strain is a mutant in the production of <i>HIS3</i> and β -galactosidase (<i>lacZ</i>).
How it works	The <i>hSos</i> gene complements the <i>cdc25H</i> mutant at 37°, thus allowing growth at this selective temperature. The Ras-signaling pathway is induced when the <i>hSos</i> gene is localized to the plasma membrane via interaction between the bait fusion protein and the prey fusion protein. See Figure.	In the GAL4 system, expression of the reporter gene can only occur if both the DNA-binding domain (BD) and transcriptional activation domain (AD) of the GAL4 gene are interacting and localized to the UAS (yeast stream activating sequence) of the <i>lacZ</i> reporter gene. These interactions occur in the nucleus. See Figure.
Bait Protein	The bait protein is the protein of interest, expressed as a fusion protein with <i>hSos</i> via the <i>hSos</i> plasmid.	The bait protein is the protein of interest (X), expressed as a fusion protein with the GAL4 BD.
Prey Protein	The prey protein is a fusion protein between a myristoylation sequence and a cDNA library via the <i>pMyr</i> plasmid.	The prey protein is expressed as a library of proteins (Y) fused to the GAL4 AD.

To study the WRKY protein-protein interactions, the Cytotrap® Yeast-2-Hybrid assay was used because of its advantages over the conventional yeast-2-hybrid assay.

Figures courtesy of Stratagene



Yeast Transformation

- Bait Transformation:**
- The transformation of *cdc25H* temperature sensitive *Saccharomyces cerevisiae* strain with the bait construct was done according to the Cytotrap® protocol.
 - The transformed culture was then plated onto SD/Glucose (-Leucine) plates for 4-6 days at room temperature to select for yeast carrying the pSos plasmid vector.
- Prey Transformation:**
- The transformation of the *cdc25H* yeast cells with the prey construct was done via the 2-Hybrid TRAF® protocol for the maintenance of a plasmid.
 - The yeast culture was then plated onto SD/Glucose (-Leucine, -Uracil) agar and grown at room temperature.
 - After 48 hours, these plates were replicated onto SD/Galactose (-Leucine, -Uracil) and grown at 37°C for 6 days in order to complete the library screen.

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OpenEye Scientific Software

AFITT-Working with good chemistry

Thomas S. Peat, Jon Christopher, Kevin Schmidt, Brian Kelley, Matt Stahl, Geoff Skillman, Stan Wlodek & Anthony Nicholls

Abstract

AFITT is a new molecular graphics program developed by OpenEye Scientific Software for protein crystallographers. It runs on most operating systems, reads all common data formats, easily connects to databases and will generate good chemical structures from a SMILES string. In addition, it will create refinement dictionaries for ligands and other small molecules automatically.

Introduction

AFITT, a graphical tool for building macromolecules, was developed by OpenEye as a tool to help protein crystallographers create molecules with good chemistry and to promote better communication between chemists and crystallographers. To achieve this we have incorporated many functions that are found in modern software packages for both crystallographers and chemists. Python is used as the interpreter so scripting macros is straight-forward. Hooking AFITT to a database or chemical registry system to pull molecules into the program is a simple procedure of modifying three lines of code in a script available from OpenEye.

Rapid docking into electron density is fitted by OpenEye's Shape technology. To fit small molecules into density a new procedure has been developed which uses an MMFF force field potential and a Gaussian shape component.

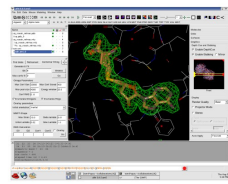


Figure 2: This snapshot shows the conformers generated from a SMILES string that have been docked into Fo-Fc density and refined using a combination of the MMFF force field and a Gaussian shape component. The input parameters are shown in the modeling window (left).

Once the molecule of interest has been fitted to density, one can simply click a menu item to output a refinement dictionary in either REFMAC or XPLOER format. Constraints for the refinement dictionaries are taken from the MMFF parameters where possible. The Ramachandran plot has incorporated the new Richardson⁴ parameters to give more accurate protein structures.

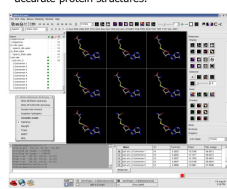


Figure 3: This figure shows the dictionary menu with options, the 3D, list and style windows. Shown are nine conformers of a single molecule in 'Brady Bunch' mode with the energy and tamano values in the spreadsheet below for each conformer. Note the options available for the aromatic model used for dictionary generation.

When refinement of a ligand structure inside a protein receptor is the primary objective, rather than complete protein-ligand structure refinement, we propose a simplified procedure of structure optimization in a force field potential perturbed by a Gaussian shape component:

$$V = V_{MMFF} + \lambda V_{shape}$$

where λ is a mixing term varied stepwise by small increments between successive optimizations (until either the maximum shape overlap or a specified maximum strain energy is achieved), V_{MMFF} is the Merck potential as described by Halgren¹, and V_{shape} determines the Gaussian molecular shape (Grant et al²).

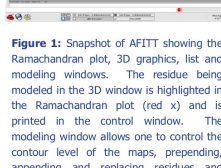


Figure 1: Snapshot of AFITT showing the Ramachandran plot, 3D graphics, list and modeling windows. The residue being modeled in the 3D window is highlighted in the Ramachandran plot (red x) and is printed in the contour window. The modeling window allows one to control the contour level of the maps, prepending, appending and replacing residues and changing angles all with icons and mouse clicks.

Protein	Ligand	Num.Corr.	Omega RMS	Strain	RMS
HR Protease	cyclohex	203	0.87	2.1	0.53
gR Kinase	gliclazide	22	0.83	1.29	0.55
Estrogen receptor/estradione		66	0.67	8.63	0.49
Thrombin	phenacetone	400	1.31	6.76(5)	2.46(5)
beta-lactamase	cefadroxil	238	1.1	4.75(45)	4.35(5)
T4 lysozyme	d-lysine	1	0.04	0.91	0.29
beta-lactamase	imipenem (covert)	146	0.56	0.46	1.18
beta-lactamase	albacicic inhibitor	66	0.62	1.74	0.92
PI3K nr	adenine diphosphate	400	1.71	12.30(29)	2.19(5)

Table 1: Shape strain energies (in kcal/mol) and RMS deviations (in Å) from published X-ray structures of several ligands in their protein receptors³. Five Gaussians per atom were used to represent each ligand atom. Values in brackets were obtained with Coulomb terms excluded from V_{MMFF} .

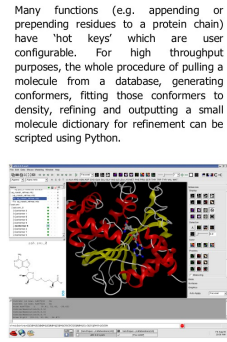


Figure 4: This figure shows the 2D window as well as the 3D, list and style windows. The text at the bottom of the window is the SMILES string of a cofactor. Shown is a ribbon diagram of the protein with a ball and stick model of the cofactor (courtesy of C. Gee & J. Martin). The buttons in the style window control the representations (ball and stick, ribbons, CPK, etc.) of the molecules.

Conclusion

AFITT is a new tool for protein crystallographers to easily build proteins and their associated ligands into electron density. It facilitates good chemistry and outputs refinement dictionaries to streamline the refinement process. It has many built-in tools for communication with chemists (SMILES interpreter, 2D graphics window, reads typical chemical formats, etc.). The user can also create high quality ribbon and surface representations (displaying properties such as electrostatics) of proteins. A 3D 'Brady Bunch' mode is available for viewing many objects simultaneously, such as a set of ligands for a given protein. Conformers can be sorted by energy, shape overlap, tamano, etc. using the spreadsheet function. Maps are generated 'on the fly' and secondary structure templates are available for building the protein molecule. Windows are detachable, and a user can set up a working environment and save it for later sessions. All in all, it is a tool you should try out!

Acknowledgments

We would like to thank the OpenEye development team for the OECHEM, Omega, Shape and Szybk libraries which make many of the functions provided in AFITT possible. We also thank our customers who have supported the development of this program and Christine Gee and Jenny Martin who provided maps and a model structure.

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School Library Websites and the Information Behaviors of Young Adults



Study funded by the 2005 AASL / Highsmith Research Grant

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BACKGROUND

The 21st century school library website, or virtual library, should have as broad an impact as its physical counterpart, expanding and reinterpreting service, meeting young users' needs where they live, play, and work--on the Web. These customized interfaces offer young people independence while they offer opportunities for professional intervention. They allow librarians and their partner educators to guide unlimited numbers of students anytime, any place. Through their websites teacher-librarians can extend their three roles as defined in *Information Power* (1998)—*learning and teaching, information access and delivery, and program administration.*

This poster describes the results of a mixed-method study examining the impact of school library websites on teen information-seeking behavior.

RESEARCH QUESTIONS

The disparity of school library website efforts, compounded by students' growing need for both online independence and intervention in the face of info-glut, suggests critical research questions:

- * Why, how, and when will high school students use school library websites?
- * How is student behavior affected by customized online resources, service, and guidance?
- * What common content and design elements do effective sites share?
- * How have they evolved since Anne Clyde's 1999 content analysis?
- * To what extent are these sites interfaces effective environments for: *learning and teaching, information access and delivery, and program administration?*

Research in this area should lead to the development of specific criteria for the evaluation of school library sites and to the development of replicable models for effective Web-based school library service and instruction.

EXAMPLES OF INTERFACES IN SAMPLE



METHODS

Selecting the Population

The study examines fully established sites and their impact on student use over time. High school seniors were selected for their long-term interaction with the sites. The researcher sought to examine exemplars of *best practice* by soliciting participation among high school sites selected for the IASL/Concord Award and as *School Library Journal's* Website of the Month.

Content Analysis

Using Anne Clyde's 1999 content analysis of 50 libraries as a baseline, the researcher conducted an updated analysis of 14 sites identified for study.

Web-based Survey of High School Seniors

An online survey of 1257 seniors in the 14 schools describes sections of the sites students most value, level of student use, and the influence of the sites on research behaviors. The instrument designed with QSurvey—a plug-in for the open source Zope package.

Focus Group Interviews

The researcher conducted four discussions with seniors at Springfield Township High School in Erdenheim, PA. Discussions were videotaped, transcribed, and coded using WEFT software.

CONTENT ANALYSIS

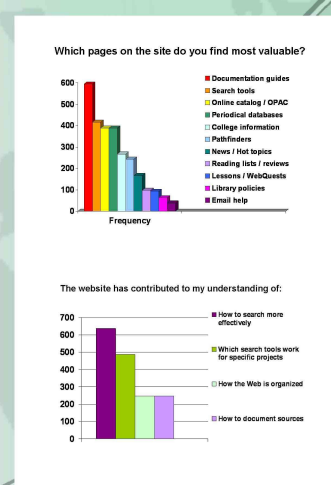
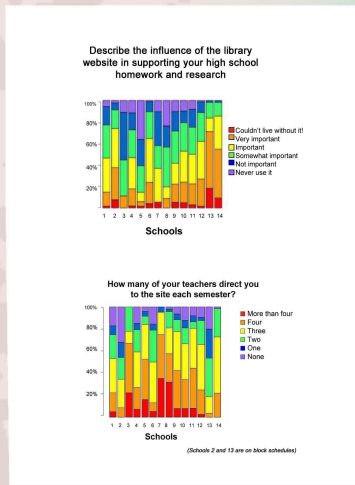
Comparison with Clyde (1999)

HOME PAGE FEATURE	# of 50	# of 14 (2005)
Name of school and library	41	14
Links to selected resources on the Internet	23	14
Information about the school library	29	13
Interactive email contact address	28	14
Link to a school home page	24	14
Date of the last update of the page	19	10
Links to Internet search engines	15	14
Research skills information or guides	6	14
Links to Internet resources for teachers	8	11
Librarians	8	9
Book reviews, lists of recommended books	7	12
Photograph of the school library	6	9
Information about citing Internet resources	6	14
Links to resources about the local area/region	5	11
News about the library or library activities	4	9
Information about the Internet for library users	4	13
Interest material	4	11
Online reference desk for email inquiries	3	10
Information about school library Internet use guidelines	3	9
The library rules	2	8
Electronic magazines	1	14

Suggested Additional Criteria For Websites

HOME PAGE FEATURE	NUMBER
Online Catalog/OPAC/Featured Search	14
Subscription Database	14
Staff Information	13
Pathfinders for Student Projects	12
Student Book Reviews & Recommendations	9
Online Password Lists (Protective)	9
Collaborative Lessons, WebQuests, MindMaps, Rubrics,	9
Mission	8
Teacher Support	8
Video Guidance or Virtual Tours	8
College and Career Information	8
Citation Generators	8
Presentations / PowerPoints	7
Podcasts (Academic Integrity, ASP, Selection, Video)	6
Support for Standardized Tests	6
Posters and Promotional Materials	5
Blogs	3
Library Newsletters	3
Book Club Information	3
Weekly Schedules or Calendars	3
Program Detection Tools (Turnitin)	3
Annual Reports	3

WEB-BASED SURVEY of 1257 Seniors



CONCLUSIONS

Focus Groups—4 groups of seniors, mixed ability levels

Representative response: "It'd be dumb not to use it." Did not stop at *satisficing*, sought scholarly materials. (Google not enough for academics research.) Believed interface helped them achieve better grades, meet teacher expectations, prepare for college. Appreciated databases, documentation advice, and pathfinders. Students had issues with selection of databases, losing passwords, query formation.

Content Analysis

Landscape much changed since Clyde's 1999 analysis. Addition of online catalogs & databases, collaborative lessons, presentations, blogs, interactive tools, media, pathfinders. Sites more interactive in approach and are moving towards translation of full program. **Web-based Survey of Seniors of 14 Sites Identified as *Best Practice*** Striking differences in data across schools. Students in some schools clearly value the websites. In others, the level of acceptance is generally positive, but moderate. Factor analysis revealed relationships between teacher recommendation and student acceptance. Usefulness factor connected to documentation guides, databases, online catalogs, and search tool options. Males scored significantly higher than females on usefulness.

Bottom Line: Effective school library websites are hybrid experiences: most effective when enhanced with face-to-face instruction and supported by faculty endorsement and whole-school programs.

QUESTIONS FOR FURTHER STUDY

- * Why are some library websites far more important to students than others?
- * Beyond design and content, what factors in school culture determine acceptance and use?
- * What role does faculty direction play in the acceptance of library websites?
- * How do librarians promote site use and acceptance into school culture?

RESULTS OF FORMATIVE RESEARCH FOR A FOOD STORE-BASED INTERVENTION IN BALTIMORE, MARYLAND

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Abstract



Obesity and obesity-related diseases in the United States disproportionately affect minorities and those living in urban centers. We conducted formative research aimed at understanding the role small and large food stores play in a low-income population's dietary behavior and other constraints to maintain a healthy diet in Baltimore, MD. The formative research involved in-depth interviews with storeowners and managers of large and small stores (n=17), a consumer survey in a representative sample of Baltimore residents (n=39), and an extensive food source survey in twelve randomly selected census tracts. People living in lower income census tracts had limited access to nutritious foods. Most small stores do not stock low fat products. In this setting, store environment can greatly influence consumer's choices and purchasing. For example, security devices can prevent customers from moving inside the store and reading nutrition labels. We are using these formative data to help us develop the Baltimore Healthy Stores program, which will target both large and small stores in the city with the aim of increasing healthier food options to inner city residents, and promoting them at the point of purchase. This study is supported by the Center for Livable Future, Johns Hopkins University.

Introduction

- Obesity and obesity-related diseases in the United States disproportionately affect minorities and those living in urban centers.
- Food stores can impact a community's ability to maintain an adequate and nutritious diet through the quality, price, and variety of food offered.
- Minorities living in inner cities face additional constraints to maintaining a varied diet, such as distance to supermarkets, inadequacy of public transportation, and lack of variety and fresh foods in smaller nearby neighborhood food stores (Ashman et al, 1993).

Study Setting: Baltimore City

- Baltimore City's poverty rate is 21%, compared to 7% in the rest of Maryland (Center for Poverty Solutions, 2002).
- Of all Maryland households that receive food stamps, 43% are located in Baltimore.
- Baltimore lost 15% of its supermarkets in the past two years.
- Local residents rely on corner and drug stores for their groceries (Klein, 2002), which tend to carry foods higher in sugar and fat, and few fruits and vegetables (Ashman 1993).
- Poor access to nutritious food by Baltimore's low-income population may contribute to the high rate of chronic diseases found in the city. 31% of adults in Baltimore are obese (BMI>30) (Clark, et al 2001). Death rates from heart disease increased 75% from 1990 to 1999 (BCHD, 1999).



Research Questions

- What are the sources of food available to Baltimore residents, and how do they vary by area?
- What is the organizational and environmental structure of corner stores?
- In what ways can available food sources influence purchasing behavior of residents?
- How do local residents make use of the food sources available to them?
- How do local residents cope with limited access to nutritious foods?
- How can the local food environment be improved?

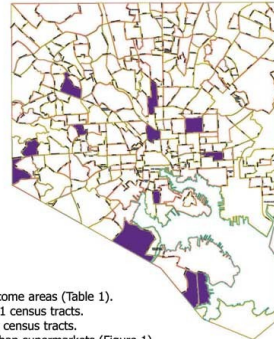
Methods

- Food Source Assessment** (n=164) in eleven randomly selected census tracts in Baltimore City to identify all food sources and determine availability of selected healthy foods.
- In-depth interviews** (n=19) conducted with store owners and managers of supermarkets and small stores.
- Consumer survey instrument** (n=39) to assess food purchasing patterns, use of local food sources, food preparation, food security and perceptions of healthy foods.

Results

Food Source Assessment

- Corner stores and carry-outs predominate in lower income areas (Table 1).
- We found a total of 164 food sources located in the 11 census tracts.
- Full-service restaurants predominate in higher income tracts.
- Eight times more small or medium-sized food stores than supermarkets (Figure 1).
- Eight times more carry-outs than supermarkets (Figure 1).
- Food is more expensive in census tracts with less availability of healthy foods (a gallon of milk is on average 18.6% more expensive) (Table 1).



Corner Stores in Baltimore

Physical layout of corner stores

- Customers separated from cashier and food by a Plexiglass wall or door.
- Money and purchases exchanged through a rotating window.
- Customers bunched inside if they wish to purchase larger items.

"We lose some business because customers can't come in to look and touch the food, but safety, safety." (Corner store manager)

Decision-making criteria for stocking and ordering

- Demand for product (main criteria)
- Store's physical structure (ex. capacity for refrigeration)
- Characteristics of the products (ex. perishable, price)
- Suppliers' procedures (ex. accept unsold products back)

"We don't buy what customers never buy, only buy popular product, otherwise sits there, gets bad, we don't want product to sit there, if not sell, try to avoid stock doesn't move." (Corner Store manager)

Main stocking and ordering methods

- Arrangements for regular delivery from suppliers
- Regular, direct purchases at wholesalers
- Purchases at major supermarket chains

Stocking and Promotion of healthier food

- Low stock of healthy foods**
 - Lack of demand for these products (main reason)
 - Inability to return unsold items
 - More expensive

Little promotion of healthier foods

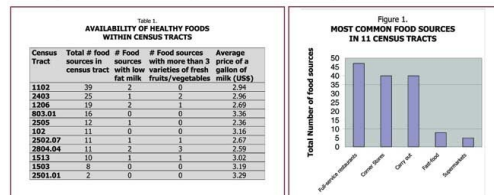
- Store setup (difficult to communicate)
- Lack of interest on the part of the customers.

"When I sold fruits, I was selling doughnuts at the same time. But if they had the same price, the customers always bought doughnuts, not fruits, not even bananas. When I asked them to try those foods, they didn't listen to me..." (Corner store manager)

Corner store and the community

- Security as number one problem for stores
- Friendships with some of their neighbors.
 - Pictures of neighborhood children and community recognition certificates pasted in store windows.
 - Efforts to help customers by supplying special items or carrying supplies to the home of elderly, and ill.

"Some customers are very nice. They are really close. Like friend...They're nice, friendly, smiling. Tell us their problem. They stop by every day. We see each other. We've been here twenty years. They were babies and we see them growing up." (Corner store manager)



Consumer Survey

- Female=55%, Male=45%
- African-Americans 72%, White 28%
- 18 % reported receiving one of the following assistance: Food Stamps, WIC, Commodity Food, Free/Reduced Price School Lunch
- 15% Food Insecure without hunger, 8% Food Insecure with Hunger (USDA Food Security Scale)
- Supermarkets were main location to buy food (Figure 2)
- Whole and 2% milk preferred over low-fat milk. Regular soda preferred over diet soda (Figure 3).
- Fruits and vegetables are bought frequently (Figure 4).



Successful Food-store Intervention: a Storeowner's perspective

- Changes in consumer behavior (consumer's interest in their own health).

"I always think that people here don't care about their health. That's why they become obese..." (Corner store manager)

- Combat crime and drug-related problems
- Media and TV commercials are a bad influence on customer's dietary habits.
- Work with food industry to decrease amount of sugar and fat.
- Improve profitability

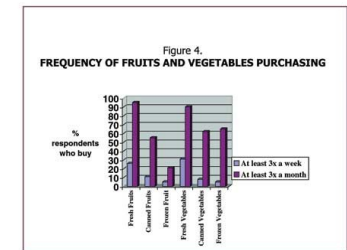
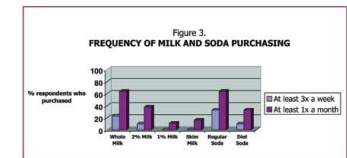
"I think you need to be financially sufficient to survive the negative profits, which may happen at the beginning. But, anyway, I don't think any health food promotion will work in this neighborhood unless you give things out for free." (Corner store manager)

Limitations

- Small sample size of census tracts, customers
- No interview with large supermarket managers

Conclusions

- Small corner stores are an important venue for nutrition interventions targeted at low-income areas of Baltimore.
- Small corner stores unlikely to close their doors to move to wealthier locations.
- Working with small as well as large stores has the potential to reach more people, and may be more sustainable in the long run.
- Intervention needs to combine changes in store environment concomitant with nutrition education for consumers.
- This information is being used to develop the Baltimore Health Stores program, which will target large and small stores in the city.





University of Ferrara
ITALY

Vascular Diseases Center

Background: Iron from red blood cells sequestered in the extra-cellular matrix in course of CVD is bound to ferritin and then to haemosiderin or up-taken by phagocytes. Such defensive mechanisms should avoid the generation of free iron and consequently of highly aggressive free radicals¹⁻³. It seems yet that the HFE mutations causes a less favourable management of the iron stored in the phagocytes (Fig1)⁴⁻⁶.

Aims: Chronic venous disease (CVD) represents the most common vascular disorder in Caucasians. Usually, is a minimally disabling disease, but in about 10 percent of cases it progresses towards chronic venous leg ulceration (CVU)⁷. The HFE gene mutations on chromosome 6 are the most common recognized genetic defects in iron metabolism of Northern European descents, and, usually, are asymptomatic conditions⁷. Since CVD leads to local iron overload in the affected legs, we investigated whether two common HFE mutations could increase the risk of CVU.

Results: Among patients affected by primary CVD, C282Y mutation increased the risk of developing CVU more than three times when compared to healthy controls (OR=3.24; CI 95% 1.45-7.23; P=0.005) and by almost five times when compared to patients with no skin lesions (OR=4.71; CI 95% 1.32-16.8, P=0.018).



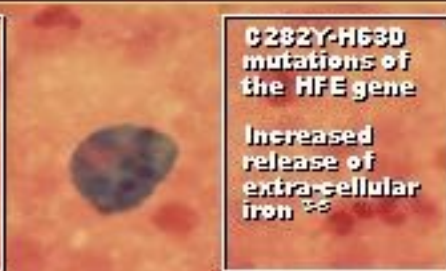
The Eclipse Effect In Ulcer Pathogenesis:

The Overlapping Of Primary CVD And The C282Y Gene Mutation

F. ZAMBONI, D. GEMMATI, S. TOGNAZZO, M. IZZO, P. MAZZA, S. CARANDINA, M. DE PALMA, L. FOGATO, P. FORTINI, A. LEGNARO, A. PALAZZO, F. PANCALDI, G.L. SCAPOLI, A. LIBONI.

Wild-type

Iron stored in ferritin-like structures, even for years

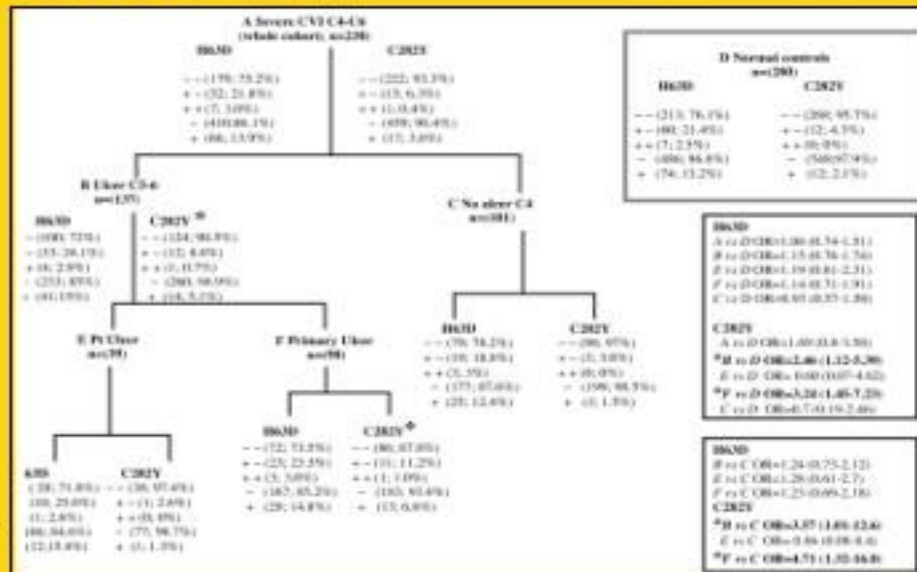


C282Y-H63D mutations of the HFE gene

Increased release of extra-cellular iron^{2,8}

Fig 1. A iron-laden macrophage in the ulcer bed (400X)

Methods: From a cohort of 980 consecutive patients affected by severe CVD (CEAP clinical class C4-6) referred to the Vascular Disease Center of the Ferrara University, we selected 238 cases with the exclusion of any other comorbidity factor potentially involved in wound aetiology (group A). They were subdivided in group B, including 137 patients with ulcer (class C5, C6 - 98 primary and 39 post-thrombotic cases), and group C with 101 cases with no skin lesions (class C4). They were completely matched for sex, age, and geographical origin with 280 healthy controls (group D). A total of 518 subjects were PCR-genotyped for HFE mutations (C282Y and H63D).



Conclusions: The coexistence of primary CVD with the common HFE C282Y mutation increases consistently the risk of developing venous leg ulceration. This finding paves the way for new strategies in terms of prevention and treatment. Of the many patients who suffer from varicose veins, only 10 percent develop venous ulcers. This high-risk minority could be identified in advance by means of a simple blood test that would act as a genetic screening device. Then, such preventive measures as elastic

stockings, superficial venous surgery, and avoidance of iron-rich foods and dietary supplements could be utilized in a targeted program of potentially great effectiveness.

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Evaluation of MUPUS data and the inverse heat conduction problem

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Abstract

Among the experiments selected for the Rosetta Lander of the ESA mission to comet 67P/Churyumov-Gerasimenko is the MUPUS package. One of the tasks of this package is a heat flow measurement at the surface of the nucleus of 67P/Churyumov-Gerasimenko. This is done by determining thermal parameters of the subsurface material (e.g. thermal conductivity, thermal diffusivity) and measuring the temperature profile below the surface by means of a penetrator. A distortion of the subsurface temperature field due to the measurement technique itself is inevitable. Both the shape of the lander and the thermal properties of the penetrator (which are different from those of the nucleus material) result in a significant perturbation of the subsurface temperature field. The first of these problems can be solved by using a deployment device which allows to position the penetrator at some distance from the lander. The perturbation of the temperature field can be reduced by solving the inverse heat conduction problem (IHCP). A method applicable for this transient case of the IHCP is presented. Using this method one can predict the temperature field in the surroundings of the penetrator and thereby obtain an undisturbed temperature profile for the subsurface material.

Deployment of Penetrator

Model calculations reveal that the measurement of the subsurface temperature profile should be made not directly below the lander, but at a distance of approximately half the lander diameter away in order to obtain a temperature profile undisturbed by the lander itself. These results are obtained using a two-dimensional, cylindrically symmetric model. The Penetrator (PEN) is modelled as a hollow tube of titanium (current design: fibre compound) and the surrounding nucleus material is assumed to be porous ice with heat factors ranging from 0.01 to 0.1 with a porosity ν of 0.5 and a pore radius of 0.5 mm. The contribution of water vapour to the heat transport is included in the effective thermal conductivity of the ambient material (Steiner et al., 1990), which results in an increase of the effective thermal conductivity with temperature (figure 2).

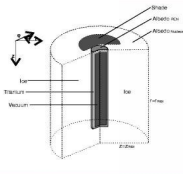


Fig. 1 Sketch of model geometry

The albedo of the nucleus surface is assumed to be 0.1 with free sublimation at the surface at a solar distance of 1 AU. As can be seen from figures 3 & 4, the temperature profile underneath the lander differs significantly from that of the surrounding half space. This is due to the fact that the diurnal heat wave cannot propagate below the lander. The effect is amplified if the lander has legs and does not prevent free sublimation of the surface ice (fig. 4).

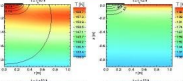


Fig. 2 Thermal conductivity of porous ice

These calculations demonstrate the need for a deployment device which is sketched in fig. 6.

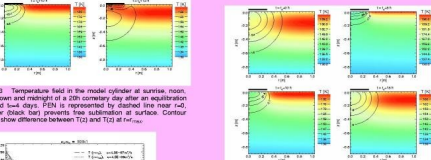


Fig. 3 Temperature field in the model cylinder at sunrise, noon, and sunset and at night at 20h. Contour lines show difference between T(x,z) and T(x,z) at full moon.

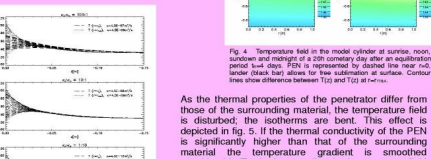


Fig. 4 Temperature field in the model cylinder at sunrise, noon, and sunset and at night at 20h. Contour lines show difference between T(x,z) and T(x,z) at full moon. Dashed lines show difference between T(x,z) and T(x,z) at full moon.

As the thermal properties of the penetrator differ from those of the surrounding material, the temperature field is disturbed; the isotherms are bent. This effect is depicted in fig. 5. If the thermal conductivity of the PEN is significantly higher than that of the surrounding material, the temperature gradient is smoothed considerably. To obtain an undisturbed temperature field the effect of the penetrator has to be reduced mathematically.

Fig. 5 Temperature profiles in and below the penetrator (dashed) and at the outer side of the model cylinder (solid) for various thermal diffusivity ratios of penetrator to nucleus (k_{pen}/k_{nuc}) and for various thermal conductivities of the penetrator (k_{pen}) at a penetration depth of z = 10 cm. The thermal conductivity of the nucleus is k_{nuc} = 0.01 W/mK. The thermal conductivity of the penetrator is k_{pen} = 0.1 W/mK. The thermal diffusivity of the penetrator is D_{pen} = 10⁻⁶ m²/s. The thermal diffusivity of the nucleus is D_{nuc} = 10⁻⁷ m²/s. The thermal conductivity of the penetrator is k_{pen} = 0.1 W/mK. The thermal conductivity of the nucleus is k_{nuc} = 0.01 W/mK. The thermal diffusivity of the penetrator is D_{pen} = 10⁻⁶ m²/s. The thermal diffusivity of the nucleus is D_{nuc} = 10⁻⁷ m²/s.



The inverse problem

Mathematical method
An undisturbed temperature profile can be obtained by calculating the ambient temperature field of the penetrator. This task involves solving the transient inverse heat conduction problem (IHCP) for the given geometry, i.e. estimate the temperature distribution within the model volume from temperature histories measured at discrete points (the sensors) and at discrete times. For simplicity the penetrator is modelled as a solid cylinder and thermal diffusivities are assumed to be constant. The heat conduction equation can be reformulated using dimensionless quantities ρ, c, α, r and Θ for radius, depth, thermal diffusivity, time and temperature respectively. The solution of the inverse problem then takes the form

$$\tilde{\theta}(r) = \sum_{k=1}^{\infty} \sum_{l=1}^{\infty} \tilde{v}_{kl} \tilde{w}_{kl}(r)$$

where $\tilde{\theta}(r)$ represents the k-th derivative of temperature response θ at the l-th sensor with respect to time, a method pointed out by Kupisz (1991). The \tilde{v}_{kl} Vectors are found by recursively solving an equation set including differential operator, known boundary conditions and sensor locations.

Errors

As the IHCP is an ill-posed problem small errors in the measurements result in large deviations of the solution. Special methods have to be used to calculate time derivatives. Derivatives show poorer convergence with higher order, therefore the series is truncated at k=2. In the calculations presented errors were assumed to be Gauss distributed with standard deviation 0.01.

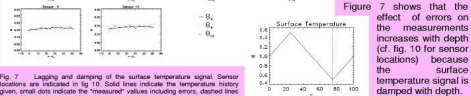


Fig. 7 Logging and damping of the surface temperature signal. Sensor locations are indicated by 1, 2, 3. Solid lines indicate the temperature signal, small circles indicate the 'measured' values including errors, dashed lines show history after smoothing.

Results

Stable solutions can be obtained even for high contrasts in thermal diffusivity between PEN and surrounding volume (Here: $\alpha_{pen} = 10, \alpha_{nuc} = 0.5$). The far temperature field can be estimated well and an undisturbed temperature profile is found.

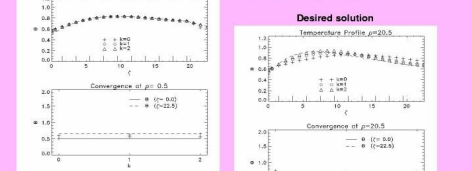


Fig. 8 & 9 Inverted temperature profiles of orders 0 to 2 in and below PEN (left) and at the outer border of the model cylinder (right). Dashed lines indicate the solution of the direct problem, vertical bars at bottom mark sensor locations. Lower plots show convergence of top and bottom node temperatures with increasing order. Small circles indicate the 'measured' values including errors.

The inversion algorithm is applicable to cases where the material surrounding the penetrator consists of layers of different thermal diffusivities (fig. 10).

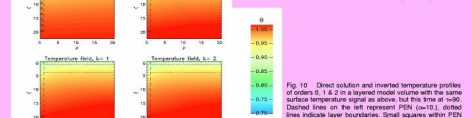


Fig. 10 Direct solution and inverted temperature profiles of orders 0, 1 & 2 in a layered model volume with the same surface temperature signal as in figure 7. Dashed lines on the left represent PEN ($\alpha = 10$), dotted lines indicate layer boundaries. Small squares within PEN (upper left) show sensor locations.

Conclusions

Methods have been found for removing the influence of both the lander and the penetrator itself on subsurface temperature measurements. The inversion of the measurements delivers stable results even in the presence of errors. It can be shown that the inversion algorithm can also handle a layered subsurface structure of the nucleus material.

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http://imgt.cines.fr

IMGT-ONTOLOGY and IMGT Scientific chart for the nomenclature of immunoglobulin and T cell receptor genes

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1 IMGT expertise

Experimental research
EMBL entries
IG and TR sequences
IMGT expertise
IMGT Scientific chart
IMGT Nomenclature
IMGT V-QUEST
IMGT data distribution
IMGT tools
IMGT LIGM-DB
IMGT Repertoire
IMGT V-QUEST

2 The 'CLASSIFICATION' concept of the IMGT-ONTOLOGY

IMGT-ONTOLOGY covers four main concepts: IDENTIFICATION, DESCRIPTION, CLASSIFICATION and ORIENTATION. The IG and TR nomenclature is based on the 'locus', 'group', 'subgroup', 'gene' and 'allele' concepts of the 'CLASSIFICATION' main concept. IMGT gene and allele names follow the nomenclature rules described in the IMGT Scientific chart (see IGLV2-11/91).

3 Genomic repertoire of the human IG and TR genes

IG: 339-354 genes	V	D	J	C	Number of genes
IGH at 14q32.33	233-129	27	9	11	170-176
IGK at 2p11.2	76	0	5	1	82
IGL at 22q11.2	73-74	0	7-11	7-11	87-96

TR: 228-234 genes	V	D	J	C	Number of genes
TRA at 14q11.2	54	0	61	1	116
TRB at 7q34	64-67	2	14	2	83-85
TRG at 7p14	12-15	0	5	2	19-22
TRD at 14q11.2	3	3	4	1	11

There are also 72 IG and TR exons and 1 IG processed gene.

4 IMGT resources

IMGT sequence databases
IMGT LIGM-DB
IMGT Repertoire
IMGT V-QUEST
IMGT Scientific chart
IMGT Nomenclature
IMGT V-QUEST

5 IMGT V-QUEST

Collier de Perles

6 IMGT LIGM-DB

IMGT LIGM-DB, a comprehensive database of 44564 IG and TR nucleotide sequences from human and from 124 other vertebrate species, with gene and allele identification and translation for fully annotated sequences.

IMGT Repertoire, the global Web resource in Immunogenetics for IG and TR of human and other vertebrates, with expertised data on genome, proteome, polymorphism and structure of the antigen receptors (Ig and TR). Genome data include chromosomal localizations, locus representations and germline gene tables. Proteome and polymorphism data are represented by protein displays, alignments of alleles and tables of alleles. These data are regularly published in the IMGT Locus in Focus section of Experimental and Clinical Immunogenetics. Structural data comprise 2D graphical representations designated as Collier de Perles and 3D representations of Ig and TR. The IMGT Repertoire is available via HTML pages (2780 documents, 3698 internal and external hyperlinks).

7 IMGT V-QUERY (V-Query and Standardization)

IMGT V-QUERY (V-Query and Standardization) is an integrated software which provides the identification of the germline V, D and J genes and alleles, involved in the IG and TR V-J and V-D-J rearrangements. IMGT V-QUERY also provides:

- analysis of the input IG or TR rearranged variable nucleotide sequences
- nucleotide alignments by comparison with the IMGT reference directory
- translation of the junction
- translation and Collier de Perles of the V coding regions.

IMGT V-QUEST is based on the IMGT unique numbering which has allowed the standardized description and analysis of the IG and TR genes whatever the antigen receptor (Ig or TR), the chain type or the species.

8 IMGT-ONTOLOGY

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10 Why an ontology for immunogenetics? Why a scientific chart?

- 1 Why an ontology for immunogenetics? Why a scientific chart?
- 2 On which concept and rules is based the IG and TR gene and allele nomenclature?
- 3 What can be expected from the IG and TR gene nomenclature in human?
- 4 What are the IMGT resources available using the standardized gene and allele nomenclature?
- 5 How to identify IG and TR genes from rearranged sequences?
- 6 How does the IMGT gene nomenclature facilitate interoperability?

Expertised data based on the IMGT-ONTOLOGY and on the IMGT Scientific chart are freely available in the IMGT/LIGM-DB database and in the IMGT Repertoire.