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Paving the Way for Future Emerging DNA-based Technologies: Computer-Aided Design and Manufacturing of DNA libraries

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[2] i.e. name of the person(s) responsible for the preparation of the document

[3] Short name of partner(s) responsible for the deliverable

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Abstract

The 24 Month Meeting of the project CADMAD took place at the Weizmann Institute of Science on March 19 and 20, 2013. It consisted of individual Working meetings of each Work Package on the first day and on the second day review of the work done over the second year and future plans for the next 6 months.

CADMAD 24M Meeting

March 19 morning - Mini Symposium on Synthetic Biology
March 19 & 20, 2013 - 24 Month Project Meeting

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GENERAL

1. In the framework of the 24 Month Meeting, a Mini Symposium on Synthetic Biology was organized by the Mathematics and Computer Sciences Faculty of the Weizmann Institute on March 19 in the morning.

The speakers were 3 members of the CADMAD consortium
Frank Edenhofer - *'Programming transcriptional networks for reprogramming cells'*
Natalio Krasnogor – *'Computational tools for rapid model prototyping in synthetic biology'*
Udi Shapiro and Tuval Ben Yehezkel – 'Computer aided design and manufacturing of DNA for synthetic biology'

and one speaker outside CADMAD consortium:
Ido Bachelet, Bar-Ilan University– '*Natural user interfaces for controlling molecular machines*'

Invitations to this Symposium were sent to the scientific community in Weizmann with special emphasis to the biological departments, and to the other Universities in Israel.

2. Following the 24M Meeting, the 2nd Review meeting took place in the presence of the project Office Teresa de Martino and four reviewers. Status of the research work and achievements was reported to the PO and Reviewers who will send soon their review Report.

Internal work package discussions and plan for future work

WP1	Name: Developing textual and graphical tools for computer-aided DNA library specification
WP Leader	UNOTT
Participants	WEIZ, UKB

Main Objectives

WP objectives (remaining)
O1 Define a core programming language for DNA libraries with a visual counterpart
O2 Extend core with dialects specific to library requirements of varied biotechnological applications
O3 Deliver a polished graphical user interface for specification and management of libraries
O4 Develop reverse parsing algorithms for extracting libraries from sequences

The main objectives of the internal WP1 discussions were to:

- present work done since the 18M meeting in Venice to all CADMAD partners in advance of review
- recap DNALD language, GUI and datamodel improvements
- demonstrate new graph view of library outputs, how graph was obtained from datamodel, and show that it could be used for new library construction planning algorithm (WP2)
- preview review slides for inclusion in WP2 (mispriming) and WP5 (PqsR library) for feedback
- present work plan for next 6 months and refine in accordance with WP1 partners input

The following points were gathered from the WP1 round table presentation and discussion with all CADMAD partners on March 19th – 21st 2013 and in separate discussions between partners in WP1 (UNOTT: Jon, Natalio), WP2 (WEIZ: Ofir, Udi, Tuval, Tzipi), and WP5 (UKB: Sandra, UH: Adrian, Constantine, UNOTT: Miguel, Stephan).

Discussion - Summary
WP1 and WP2 collaboration yielded new approach to library construction planning which was accepted by PI.
Graph-based visualization approved by WP5 partners – want release with this functionality improved.
PqsR library requires several features that are relevant to other WP5 partners: efficient representation and sampling of back-translations, one-pot assembly using ambiguous primers, delivery in specific plasmids.
Work is good but must be published and presented to have wider impact. 3 specific dissemination outputs were identified: 1. conference paper at Fifth International Workshop on Biological Design Automation on DNA reuse datamodel and construction planning algorithms based on it 2. journal paper for DNALD language and software with biological examples from CADMAD partners 3. workshop at Nottingham for potential consumers of combinatorial DNA libraries, demonstrating our approach and tools.

Conclusions
✓ Language and GUI are sufficient for specifying simple combinatorial DNA libraries, but more work is needed on both to facilitate, use and display biologically relevant annotations and constraints.
✓ Graph-based approach has a sound computer science foundation and is a step in the right direction to communicating degrees of freedom in library, but more work is needed to improve representation of DNA reuse and scalability of visualization.
✓ Reverse parsing to be addressed using combination of graph-based data structures from stringology and evolutionary algorithms literature: DAWGS, LCS, suffix arrays, genetic programming by grammatical evolution.

Action items	Person responsible	Deadline
✓ Submit abstract for talk at IWBDA 2013 (SB6.0 London) on combinatorial DNA library construction planning with DNA reuse	Jonathan Blakes and Ofir Raz	April 2013
✓ Improve functionality for handling protein sequences for UNOTT and UH libraries.	Jonathan Blakes	May 2013
✓ Add biological annotations and constraints to language.	Jonathan Blakes	June 2013
✓ Present at IWBDA	Jonathan Blakes and Ofir Raz	July 2013
✓ Submit paper based on IWBDA talk to ACS Synthetic Biology	Jonathan Blakes	August 2013
✓ Add sequence view with translation frames	Jonathan Blakes	September 2013
✓ Submit paper on combinatorial DNA library specification using DNALD and DNA Library Designer with examples from WP5 partners to Nature Methods.	Jonathan Blakes	October 2013
✓ Address reverse parsing of unstructured sequences into reasonable DNALD.	Jonathan Blakes	November 2013
✓ Coordinate workshop on combinatorial DNA library design with DNALD and DNA Library Designer, open to CADMAD partners and colleagues of their institutions. Aim would be to disseminate CADMAD, teach synthetic biologists how to design combinatorial DNA libraries with our software and gather broader feedback for its future improvement.	Jonathan Blakes	December 2013

Assigned internal deliverables

From		To		Deliverable description	Purpose	Due Date
WP1	UNOTT	WP5	UKB	Choose subset of sequences from azurin library to be obtained by traditional synthesis methods, and send to Sandra Meyer at UKB.	1. facilitate biological investigation of post-transcriptional regulation of azurin by UNOTT 2. subsequences can be reused by CADMAD to construct the remaining sequences of library 3. get discount from synthesis company by ordering many library subsets together	April 2013 (delivered)
WP5	UH	WP1	UNOTT	Hypothetical DNA library designs for separated and mixed large-scale protein libraries.	Drive addition of relevant features to language and GUI, provide material for journal paper.	May 2013
WP1	UNOTT	WP5	All	DNALD releases	Deliver requested features to users	May, June, September 2013

Foreseen Internal Meetings

NONE

WP2	Name: Developing biochemistry and algorithms for a computer-aided DNA design based on DNA reuse
WP Leader	WEIZMANN
Participants	UNOTT, UKB, RUB, ETHZ, FMI, UH, OSM

Main objectives

- Developing and optimizing the biochemistry of DNA processing based on DNA reuse
- Algorithms for planning the DNA processing and library construction

Discussion - Summary

During the internal meeting WEIZMANN presented its results with regards to:

1. Progress with existing libraries (intronome).
2. The integration and optimization of Gibson assembly
3. Development of IPA method
4. Development of microfluidics-based methods for primer quality prediction.
5. Computational methods for construction planning

Conclusions

We had good progress in all projects and all deliverables were accepted.
During the meeting, after results were presented, we discussed how we move forward in each one of the WP projects.
Specifically:

Action items

Item	Person responsible	Deadline
Further development of the computational system for construction planning using novel algorithms	WEIZMANN	M30
Analysis of microfluidic primer miss-priming experiments using machine learning	WEIZMANN, UNOTT	M36
The IPA protocol will be further validated.	WEIZMANN	M36

Assigned Internal deliverables

From		To		Deliverable description	Purpose	Due Date
WP3	ALL, WEIZ	WP3	ALL, WEIZ	Weizmann and ALL will work to publish the work on EWOD and smPCR.	Publication	M36
WP2	UNOTT, WEIZ	WP2	UNOTT WEIZ	Weizmann and UNOTT will work to publish the work on primer predictions	Publication	M36
WP1	UNOTT, WEIZ	WP1	UNOTT WEIZ	Presenting algorithms for DNA assembly in IWBD	Publication	M36

Foreseen Internal Meetings

NONE

WP3	Name: Automation of DNA processing based on DNA reuse
WP Leader	John McCaskill, Patrick Wagler (RUB)
Participants	RUB, UKB, ETH, ALL, UH

Main Objectives

- Automation of DNA processing biochemistry using current available robotic technology
- Develop an open-source robot programming language
- Introducing next generation Micro-fluidic technology to DNA processing

Discussion - Summary

Summary of CADMAD internal WP3 meeting on Tuesday, March 19, 2013:

Patrick Wagler (RUB) led the presentation and the discussion at the CADMAD internal WP3 meeting, since John McCaskill's (WP leader) flight was delayed substantially.

Task 3.1: This task was finished officially in year 1. However, in addition to the R&S work reported in year 1 by WEIZ and RUB, WEIZ led a new activity in year 2 involving millifluidic integration using electrowetting cartridges. WEIZ and ALL developed requirements and specifications for implementing Y-operations as well as Gibson assembly steps on existing ALL cartridges. Based on discussions with WEIZ and CADMAD advisor TECAN, RUB developed open design custom electrowetting cartridges, that could serve as a basis for testing interfacing integration with full microfluidics (sub nl scale). RUB presented modified overall integration concept in WP3.

Task 3.2: Automation of DNA processing biochemistry using currently available technologies (Leader: WEIZ): partner WEIZ has developed and tested all the scripts required for DNA editing using the Y operation. Additionally, WEIZ has developed automation for a new assembly reaction, namely the Gibson operation.
Task 3.3: Develop RoboEase, an open-source robot programming language (Leader: ETHZ): Partner ETHZ concluded their CADMAD task on RoboEase for year 2 with work on quality control and making the library usable as a tool within other software, as well as with experiments run in the lab. Further collaborations with Weizmann are planned.
Task 3.4: RUB highlighted the progress in the next generation microfluidic technology for DNA processing. In the first project year RUB developed an electronic DNA processing chip that integrates droplet based I/O´s with on chip reaction, electronic separation & sample transfer. The main two topics in year 2 were: (i) the development of a custom EWOD interface system to allow connection of microfluidics with combinatorial preprocessing millifluidics as well as a concept of an example application of an Y operation in two successive rounds of PCR, ss-digestion and separation followed by ds completion of hybrid products were shown and (ii) the development of a combinatorial droplet generator chip capable of producing thousands of 10-100 pl droplets with different content from millifluidic droplets in the 100nl plus range. RUB performed first experimental tests for an alternating droplet formation in the droplet modules (cf. D3.9). RUB also reported on the successful demonstration of the three basic microfluidic operations for on-chip processing in year 2 of the CADMAD project: (i) DNA extraction from droplet into on-chip separation gel (ii) DNA separation and transport to desired injection point and (iii) DNA injection into new droplet. In particular, product separation of short DNA (24-45nt) was improved by feedback wave electrophoresis.

Current activities were discussed, which involve experiments programmable on-chip separation of longer DNA (1000bp) for DNA synthesis prepared by WEIZ and delivered to RUB. Additional discussion involved the allocation of results (Task 3.2 or Task 3.4) regarding the demonstrating full cycles of DNA synthesis (Gibson assembly) on ALL cartridges in view of CADMAD review reporting. Planning discussions between ALL and WEIZ on an extension application were held.

Conclusions

- ✓ Good progress in microfluidic integration (RUB, DNA editing core functions of the chip at sub nl scale were tested)
- ✓ A new custom EWOD pre-processor PCBs was designed for the interface to microwell plates (RUB)
- ✓ A sub nl combinatorial droplet generator chip was fabricated & alternating droplet generation was demonstrated (RUB)
- ✓ Proof-of-concept for performing DNA assembly on ALL's (300nl scale) EWOD system at WEIZ
- ✓ Automation of scripts and Gibson reaction using liquid handling robots (ETH, WEIZ)
- ✓ All reporting and deliverable responsibilities were addressed (all partners)

Action items	Person responsible	Deadline
✓ WEIZ will attempt to develop smPCR for EWOD	Tuval	?
✓ WEIZ will complete analysis of IPA on EWOD	Tuval	?
✓ RUB and WEIZ will specify microfluidic application	John,Tuval, Udi	M28

Foreseen Internal Meetings

Participants		Purpose	Date	Place
McCaskill, Wagler, Tangen, Minero, Ben-Yehezkel, Udi Shapiro	RUB WEIZ	DNA library synthesis in microfluidics	15/04/13	skype
McCaskill, Tangen, Minero Ben-Yehezkel	RUB WEIZ	DNA library synthesis in microfluidics	22/04/13	skype
		Further skype meetings between partners will be held in the spring and summer 2013		

WP4	Multi-layer system integration and the development of faults detection, isolation and correction methodologies
WP Leader	WEIZMANN
Participants	UNOTT, UKB, RUB, ETHZ, FMI, UH, OSM

Main objectives

• Integration of the system
• Developing methodology for fault detection, isolation and correction

Discussion - summary

During the internal meeting WEIZMANN presented its results with regards to:
1. The integration of the CADMAD technology multi-component system.
2. Development of a dedicated system for the quality monitoring and analysis of robotic scripts from the CADMAD production systems.

Conclusions

We had very good progress on all the WP projects and all deliverables were accepted. We also discussed how to move forward in all fronts.

Action items

Item	Person responsible	Deadline
Final testing of the integrated system (Weizmann)	WEIZMANN	M36
Re-writing the automation system in Python.		M36
Further improvement of the automated fault detection system (Weizmann).	WEIZMANN	M36
Presentation of the automated robotic QC system at IWBDA.	WEIZMANN	M36
Weizmann will work to publish the robotic QC work.	WEIZMANN	M36
The integration work will be published in a book chapter on synthetic biology	WEIZMANN	M36

Foreseen Internal Meetings

NONE

WP5	End users' applications: Directing system development and potency validation
WP Leader	UKB
Participants	WEIZMANN, UNOTT, ETHZ, FMI, UH

Main Objectives

(1) to focus and direct the development of the CADMAD platform to current and future DNA programming requirements,
(2) to validate the produced libraries and
(3) to compare the CADMAD libraries against libraries made by existing technologies. There was one deliverable in the second year of the project, namely the high level description of application libraries (D5.4). To fulfill this deliverable the end users re-designed six DNA libraries using the newest version of DNA library designer (DNALD) software. Furthermore, preparations were started to achieve the third main objective, the comparison of CADMAD libraries against libraries made by existing technologies.

Discussion - Summary

The re-designed libraries were presented and it was decided that the end users will define subsets of these libraries that will be produced by conventional DNA synthesis. It was proposed to order sub-libraries either a GeneArt (0.32 € per bp for fragments up to 3 kb) or at IDT (89 € for fragments up to 500 bp).

It was agreed upon that the sub-libraries will be defined and ordered until end of April 2013. If possible the fragments should be ordered as IDT GeneBlocks with subsequent Gibson assembly (when necessary) performed by each partner. It is planned to use the ordered GeneBlocks not only for the generation of the sub-libraries bu also as starting material for the generation of libraries by CADMAD technology.

To confer about the end users' experiences in designing the libraries using DNALD and the generation of the sub libraries as well as to discuss first biological results achieved using the sub-libraries an internal WP5 meetinç should take place at the end of 2013.

Conclusions

- ✓ Sub-libraries should be designed using DNALD until end of April 2013 and files send to UKB and UNOTT
- ✓ DNA-fragments of sub-libraries should be ordered at IDT until end of April 2013
- ✓ IDT-fragments should be used to generate sub-libraries by Gibson assembly
- ✓ Each partner should perform downstream processing of the sub-library as defined in D5.4

Action items	Person responsible	Deadline
✓ Design of sub-libraries using DNALD	WP5 members	April 2013
✓ Ordering of sub-libraries (generation by conventional DNA-synthesis	WP5 members	April 2013
✓ Generation of sub-libraries by Gibson assembly	WP5 members	August 2013

✓ Start of downstream processing of generated sub-libraries	WP5 members	November 2013

Assigned internal deliverables

From		To		Deliverable description	Purpose	Due Date
WP5	All	WP5	UKB	Design of sub-libraries using DNALD	Preparation for generation of DNA-libraries made by conventional DNA-synthesis	April 2013
WP5	UKB	WP1	UNOT	Design of sub-libraries using DNALD	Preparation for generation of DNA-libraries made by conventional DNA-synthesis	May 2013
WP5	All	WP5	ALL	Ordering of sub-libraries	Preparation for generation of DNA-libraries made by conventional DNA-synthesis	April 2013
WP5	ALL	WP5	ALL	Generation of sub-libraries by Gibson assembly	Preparation for generation of DNA-libraries made by conventional DNA-synthesis	Aug 2013
WP5	ALL	WP5	ALL	Downstream processing of sub-libraries	Evaluation of libraries made by conventional DNA-synthesis	Nov 2013

Foreseen Internal Meetings

Participants	Purpose	Date	Place
WP5	Workshop/webconference on sub-libraries and their biological applications.	Dec 2013	UKB

12M Meeting Minutes – Follow up

WP1

Action items	Person responsible	Deadline	Status
Create private repository with existing WP5 libraries and other from past WEIZ synthesis projects for software testing and tutorials.	Jonathan Blakes	June 2012	
Sharing code for generator data structure and DNA sequence ambiguation algorithms with WEIZ.	Jonathan Blakes	August 2012	
Release new version of DNA Library Designer, with robust evaluation scheme but no new language features, to partners for testing.	Jonathan Blakes	July 2012	
In parallel with their testing we will add read/write support for SBOL and ApE formats, connectivity to one or two sequence databases, improved visualization with the possibility of zooming in/out of the graphical representation of the libraries with labeled sequence fragments (as in the WIS web-based original version), to be delivered incrementally through point releases.	Jonathan Blakes	November 2012	
Prototyping "pipes/flows" visual interface, secondary structure detection/filtering, functional annotations, more databases connections, read/writing GENOCAD and GeneDesigner formats, and other WP5 requested features. Time permitting and automatic updates functionality	Jonathan Blakes	2nd annual review in 2013	

Assigned internal deliverables

From		To		Deliverable description	Purpose	Due Date	Status
WP4	WEIZ	WP1	UNOTT	Original DNApl language interpreter implementation (archive of Yair Mazor's files)	Identify undocumented language features and disambiguate intentions of ++ operator	April 2012	
WP2	WEIZ	WP1	UNOTT	DNApl files for intronome and translation libraries	Enlarge set of libraries for testing software	April 2012	

WP1	UNOTT	WP4	WEIZ	Code for sequence generators (and their sampling in the case of backtranslation) and DNA sequence ambiguation	Defer potentially expensive operations to backend	August 2012	
WP5	UKB	WP1	UNOTT	Lists of sequence DBs, software, organisms and UI sketches provided by partners and prioritized by number of partners that provide them	Obtain and prioritize features to be developed	July 2012	
WP1	UNOTT	WP5	all	Rolling software releases	Incremental development and feedback	July 2012 onwards	

Foreseen Internal Meetings

Participants		**Purpose**	**Date**	**Place**	**Status**
Name	Institute				
Jonathan Blakes	UNOTT	Integration of computed DNA library specifications (WP1) with construction planning algorithm inputs (WP5) and communication of planning failures to IDE.	July 2012	Nottingham, UK or Weizmann Institute, Israel	
Ofir Raz	WEIZ				
Jonathan Blakes	UNOTT	Discuss WP5 partners additional library requirements (language features), graphical user interface storyboards (IDE features for deliverable 1.3) and tutoring in use of the software (to guide suitable end-user documentation).	July	Bonn, Germany or Nottingham, UK	
Sandra Meyer	UKB				

WP2

Action items	Person responsible	Deadline	Status
Commence primer design project	Tuval		Accomplished
Develop a shared fragment interface	Blakes & Raz		Accomplished
Devise reaction conditions for HT synthesis	Tuval		Accomplished
Design and implement the design -> planning interface	Blakes		Accomplished
Extend planning algorithm with degeneracy support	Ofir Raz		Accomplished

Assigned internal deliverables

From		To		Deliverable description	Purpose	Due Date	Status
WP 1	UNOTT	WP2	Weizmann	Library description Interface	Integration		Accomplished
WP 2	Weizmann	WP1	UNOTT	Library validation	Integration		Accomplished

Foreseen Internal Meetings

Participants		Purpose	Date	Place	Status
Name	Institute				
Jonathan Blakes	UNNOT	Defining the design->planning interface.	August	Nottingham	Accomplished
Ofir Raz	Weizmann				

WP3

Action items	Person	Deadline	Status
Test of EWOD millifluidics at Tecan lab in San Jose	McCaskill, Tuval b. E.	31.7.2012 (Month 18)	Activity shifted to new project partner ALL
Collect information on robotic platforms	Panke	31.8.2012 (Month 19)	Ongoing, in synchrony with requirements for Roboease
Transfer Roboease for biochem assay to partners	Panke	28.2.2013 (Month 25)	Currently being implemented with DHAP assay
Transfer of RoboEase programmer documentation from ETHZ to RUB (+1month)	Stelling	31.5.2012 (Month 16)	ETHZ provided RUB with internal access to documentation

Assigned internal deliverables

From		To		Deliverable description	Purpose	Due Date	Status
WP#	Partner	WP#	Partner				
3	RUB	3	Weizmann	Amplification samples	Sequencing test of products	Several times over next 6 months	Volumes too small to carry out. Procedure under review
3	Weizmann	3	RUB	Sequencing results	Sequencing test of products	Several times over next 6 months	See comment above
3	ETHZ	3	UKB	Roboease file	Implement assay on robot	28.2.2013	Cancelled due to lack of relevance
			FMI	See above	See above	See above	
			UEVE	See above	See above	See above	
			UH	See above	See above	See above	

Foreseen Internal Meetings

Participants		Purpose	Date	Place	Status
Name	Institute				
Ellis Whitehead	ETHZ	Database work	August 2012	Rehovot	Rescheduled for July 2013 with intention of collaboration

					on joint publication
Ofir Raz	WEIZ	Production System integration	December 2012	Basel	Occurred with Ehud Magal in February 2013
Tuval, Shapiro McCaskill	WEIZ, RUB	Test of EWOD millifluidics for Y operation	May-June 2012	San Jose	See action item above

WP4

Action items	Person responsible	Deadline	Status
Integrate DNALD with the planning module	Blakes&Raz	o	Accomplished
Integrate planning module's I/O with the database	Ofir Raz	o	Accomplished
Integrate automation module's I/O with the database	Ofir Raz	o	Accomplished
Integrate Roboease's I/O with the database	Whitehead&Raz	o	Accomplished
Implement DB-bound lab-work protocols	Ofir Raz	o	Accomplished

Assigned internal deliverables

From		To		Deliverable description	Purpose	Due Date	Status
WP4	Weizmann	WP3	ETHZ	Reagents database model	Handling production reagents		Accomplished

Foreseen Internal Meetings

Participants		Purpose	Date	Place	Status
Name	Institute				
Jonathan Blakes	UNOTT	Integrating WP1 by defining the design->planning interface.	August	Nottingham	Accomplished
Ofir Raz	Weizmann				
Ellis Whitehead	ETHZ	Integrating the Database model with the Roboease WP	August	Basel	Accomplished
Ehud Magal	Weizmann				

WP5

Action items	Person	Deadline	Status
First re-design of present DNA libraries	WP5 members	May 2012	Accomplished
Search for already existing programmes that feature desired applications and send to UKB	WP5 members	May 2012	Accomplished
Send a compiled list of programmes/desired applications to UNOTT	UKB	June 2012	Accomplished
Second re-design of present DNA libraries	WP5 members	Aug 2012	Accomplished
Finish end user's more complex library drafts	WP5 members	Dec 2012	Accomplished

Assigned internal deliverables

From		To		Deliverable description	Purpose	Due Date	Status
WP 5	All	W P5	UKB	Re-design of present libraries using advanced version of DNald and presentation of visual output	Test and challenge advanced version of DNald and define further end users' requirements	Sep 2012	Accomplished
WP 5	UK B	W P1	UNO TT	Re-design of present libraries using advanced version of DNald and presentation of visual output	Test and challenge advanced version of DNald and define further end users' requirements	Oct 2012	Accomplished
WP 5	All	W P5	UKB	High level description of application libraries	Demonstrate that CADMAD is able to address multiple parameters of diverse end users' needs	Dec 2012	Accomplished
WP 5	UK B	W P1	UNO TT	High level description of application libraries	Demonstrate that CADMAD is able to address multiple parameters of diverse end users' needs	Jan 2013	Accomplished

Foreseen Internal Meetings

Participants		Purpose	Date	Place	Status
UKB	UEVE	Discussion about definition of requirements and specifications for DNApl and vDNApl	13th Feb 2012	UEVE	Accomplished
UKB	UNOTT	Discussion about implementation of further functions in DNald and providing feedback concerning the usability of the programming language	July 2012	UNOTT or UKB	Accomplished,via email
FMI	UKB	Discussion about DNA libraries and definition of further requirements and specifications for DNApl and vDNApl	Sep/Oct 2012	UKB	Accomplished, at FMI, Nov 2012

Meeting Agenda

Noon

Tuesday, March 19, 2013 Morning Mini Symposium on Synthetic Biology Sponsored by CADMAD, a FET-Open Consortium, The Weizmann Institute of Science Faculty of Mathematics and Computer Science Location : Botnar Auditorium, in Belfer Building	
9:00 – 9:15	Welcome and Opening remarks Zvi Livneh, Dean of the Faculty of Biochemistry
9:15 – 10:00	**Frank Edenhofer** - *'Programming transcriptional networks for reprogramming cells'* Stem Cell Engineering Group, Institute of Reconstructive Neurobiology University of Bonn - Medical Center
10:00 – 10:45	**Natalio Krasnogor** – *'Computational tools for rapid model prototyping in synthetic biology'* Applied Interdisciplinary Computing, School of Computer Science University of Nottingham
10:45 – 11:00	**Coffee Break**
11:00 – 11:45	**Ido Bachelet** – '*Natural user interfaces for controlling molecular machines'* Institute of Nanotechnology & Advanced Materials Bar-Ilan University
11:45 – 12:30	**Udi Shapiro and Tuval Ben Yehezkel** – 'Computer aided design and manufacturing of DNA for synthetic biology' Depts. of Applied Math and Computer Science and Biological Chemistry Weizmann Institute of Science

24 Month Project Meeting (Day I)			
Time	***Title***	***Responsible person***	***Location***
12:45	Registration in the lobby of Ziskind Building Welcome reception & lunch– in the Faculty Lounge,#141, ground floor	Ehud Shapiro And staff	Zisking Building, Faculty Lounge #141, ground floor
Work Packages specific workgroups			
13:45 – 14:45	**WP1** Developing textual and graphical tools for computer-aided DNA library specification	UNOTT	Room 261, 2nd floor
14:45 – 15:45	**WP2** Developing biochemistry and algorithms for a computer-aided DNA design based on DNA reuse	WEIZMANN	Room 261, 2nd floor
15:45– 16:00	**Break**		
16:00 – 17:00	**WP3** Automation of DNA processing based on DNA reuse	RUB	Room 261, 2nd floor
17:00 – 18:00	**WP4** Multi-layer system integration and the development of faults detection, isolation and correction methodologies	WEIZMANN	Room 261, 2nd floor
18:00 – 19:00	**WP5** End users' applications: Directing system development and potency validation	UKB	Room 261, 2nd floor
	Evening at leisure		

Wednesday, March 20 ***24 Month Project Meeting (Day II)***			
Time	***Title***	***Responsible person***	***Location***
9:00	Opening of the Meeting	Ehud Shapiro - WEIZMANN	Ziskind Building Room #1
Topics to be covered in blue			
9:00 – 9:25	**Coordinator General Overview on the project** - project objectives, team and responsibilities - How the project has taken into account the reviewers' recommendation listed in the first review report. WP Leaders are requested to give input to the coordinator on this - specific objectives planned for the period to be reviewed - overview of achieved objectives (in terms of deliverables and milestones) - deviations from original plans	WEIZMANN – Prof. Udi Shapiro	Ziskind Building Room #1
Work Packages Review of the work done over the second year ***(presentations: 20 min - discussion/questions 20 min)*** - planned objectives (generally and for period under review) - achieved objectives (in terms of deliverables and milestones) - future work and anticipated deliverables			
9:25 – 10:05	**WP1** Developing textual and graphical tools for computer-aided DNA library specification	UNOTT – Prof. Natalio Krasnogor	Ziskind Building Room #1
10:05 – 10:45	**WP2** Developing biochemistry and algorithms for a computer-aided DNA	WEIZMANN –	Ziskind Building

	design based on DNA reuse	Dr. Tuval Ben-Yehezkel	Room #1
10:45 – 11:00	**Break**		
11:00 – 11:40	**WP3** Automation of DNA processing based on DNA reuse	RUB – Prof. John McCaskill	Ziskind Building Room #1
11:40 – 12:20	**WP4** Multi-layer system integration and the development of faults detection, isolation and correction methodologies	WEIZMANN – Dr. Tuval Ben-Yehezkel	Ziskind Building Room #1
12:20 – 13:00	**WP5** End users' applications: Directing system development and potency validation	UKB – Dr. Sandra Meyer	Ziskind Building Room #1
13:00 – 13:45	**Lunch break**		Ziskind Building, faculty lounge #141
13:45 – 14:00	**WP6** Dissemination and Exploitation	OSM - Pnina Dan	Ziskind Building Room #1
14:00 – 14:15	**WP7** Management and Technical Coordination • Review project administrative , financial and reporting procedures • Website management	Pnina Dan Tuval Ben-Yehezkel	Ziskind Building Room #1
14:15 – 15:15	Discussion, conclusions	All Partners Moderator: Udi/Tuval	Ziskind Building Room #1
15:15	Fixing next meeting location and date Closing the Meeting	Ehud Shapiro	Ziskind Building Room #1
	Afternoon and evening at leisure		

List of Participants

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WP6	Dissemination, Exploitation, training and Education
WP Leader	OSM
Participants	All Partners

Discussion - Summary

Dissemination activities were discussed to include:

1. Publishing in peer review journals
2. Participation in conferences
3. Website
4. Workshop – Internal
5. B.Sc. and M. Sc. Courses

Publishing in peer reviews journals: 15 articles were published
Participation in conferences: 33 publications in conferences throughout Europe
Website: the project website is maintained by WEIZMANN

2nd year Workshop:

In the framework of the 24 Month Meeting, a Mini Symposium on Synthetic Biology was organized by the Mathematics and Computer Sciences Faculty of the Weizmann Institute on March 19 in the morning.
The speakers were 3 members of the CADMAD consortium
Frank Edenhofer - *'Programming transcriptional networks for reprogramming cells'*
Natalio Krasnogor – *'Computational tools for rapid model prototyping in synthetic biology'*
Udi Shapiro and Tuval Ben Yehezkel – 'Computer aided design and manufacturing of DNA for synthetic biology' and one speaker outside CADMAD consortium:
Ido Bachelet, Bar-Ilan University– '*Natural user interfaces for controlling molecular machines'*
Invitations to this Symposium were sent to the scientific community in Weizmann with special emphasis to the biological departments, and to the other Universities in Israel.

Conclusions

Dissemination activities should be encouraged: Teresa de Martino recommends CADMAD to publish and disseminate their intermediate results by acknowledging the project.

WP7	Management and Technical Coordination
WP Leader	OSM
Participants	WEIZMANN

Summary

The following items were covered:

Deliverables

Editing, approving and delivering 32 deliverables to the EC

- WP1 – 1 deliverables
- WP2 - 5 deliverables
- WP3 – 5 deliverables
- WP4 - 4 deliverables
- WP5 - 1 deliverable
- WP7 – D7.2(2) is being delivered with preparation of the present minutes.

Milestones

All 24 Month milestones were achieved

Administrative and financial Co-ordination

Financial management

- Revise the periodic partners' financial reports

Preparation of P2 reports

- Providing templates
- Collecting and reviewing the technical and financial data
- Sending the P2 Periodic report to the project officer and the reviewers before the 2nd Review Meeting

Maintaining the Consortium Agreement and the Grant Agreement:

GA Amendments

Addition of a new partner: Advanced Liquid Logic France – ALL
Extension of the project duration to M45

The Advisor Board

Two members of the Advisory Board attended the meetings :

Dr. Zohar Yakhini - Agilent Co.& Technion, Israel and Dr. Marc Feiglin - Tecan Group , Switzerland

Internal meetings and Deliverables

- Eight Internal deliverables were exchanged between the partners
- 12 Internal meetings were held

Financial

What should be reported here????