

Custom Software Development for Clinical and Basic Research

When Your Needs Go Beyond Standard Tools

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Open Source Team Lead

Research IT Services Overview

(<http://bmi.cchmc.org>)

- System Administrators (Windows, Linux, Mac)
- Storage Administrators
- Database Administrators (Oracle, MSSQL, MySQL, PostgreSQL)
- Help Desk
- Application Developers (.NET, Sharepoint, Open Source Expertise)
- Data Services
- Work very closely with CCHMC Information Services.

Research IT - Application Developers

- Open Source – Andrew Rupert
 - Uses open source languages such as PHP, Perl, Python for their applications. Many projects focus on applications that interface with the computational cluster.
- .NET – John Stullenberger
 - Uses the Microsoft .NET Framework for their projects. Also involved with developing custom Sharepoint tools.
- Data Services – Ron Bryson
 - Focuses on data extracts from Epic and Clarity.

What do the Research IT Application Development groups do?

- We develop custom software to make your life easier!
- This can range from large scale stand alone software packages to modifications of existing open source tools to suite your needs.
- If you have ideas, contact us! Our projects often come from casual chats.

help@bmi.cchmc.org

Types of Applications

- Web Applications / Services
- Desktop Applications
- Mobile Device Development

Uses of our Applications

- Electronic Data Capture
- Data Reporting
- Interactive Systems
- Collaboration Systems
- Alert / Notification Applications
- Utility / Automation

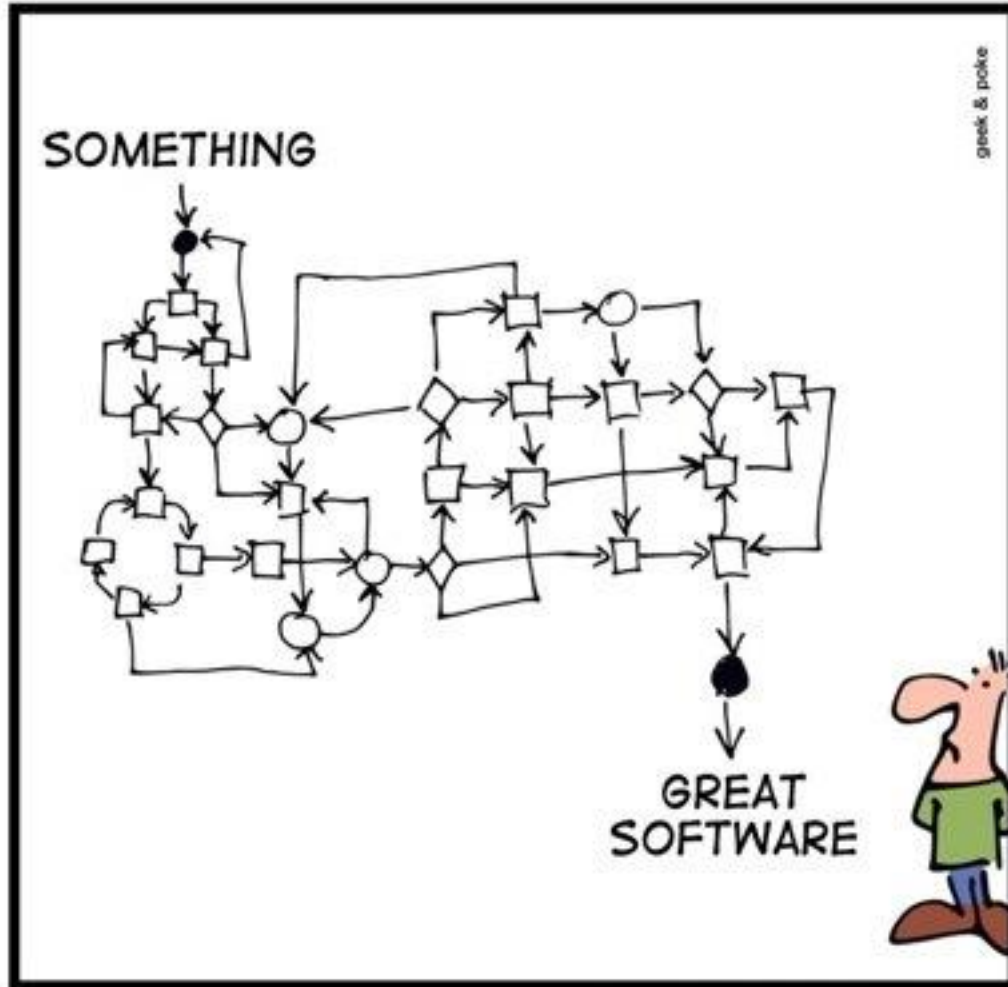
Custom Development vs Out of Box Key Differences

- ***Cost**
- ***Time**
- ***Functionality**
- Flexibility
- Security
- Accessibility

Custom Development vs Out of Box

- Out the Box
 - Pros
 - Less Expensive
 - Faster to Implement
 - Cons
 - Limited Functionality
 - Limited Customization

SIMPLY EXPLAINED



DEVELOPMENT PROCESS

Research IT - Application Developers

- Work with a wide variety of divisions
 - Pediatric Neuroimaging Research Consortium
 - Sports Medicine
 - Rheumatology
 - Psychology
 - Anderson Center
 - Etc.
- Along with a variety of research cores
 - Flow Cytometry Core
 - Confocal Microscopy Core

Research IT - Application Developers

- We work on larger grant funded projects when a PI needs entire custom applications developed.
- We also help with smaller “one-off” tasks that are made easier with simple scripts or programs.
- Most applications are now web based. Can access them from anywhere. No need to install software on every computer!

Research IT - Application Developers

- We follow best practices in terms of programming structure and security, e.g. role based access and federation.
- We can help with integrating existing systems into your projects, e.g. TimeTracker – CORES, Active Directory authentication, etc.
- If you think you have a problem that we can help with, please don't hesitate to contact us!

help@bmi.cchmc.org

WHEN YOU HEAR THIS:



*YOU KNOW YOU'RE IN A
SOFTWARE PROJECT*

High Performance Computing Overview - Hardware



- ~1000 compute cores in 100 servers in production
- ~600 cores in 160 servers in development
- Intel / AMD processors
- Up to 24 cores
- Up to 256GB memory
- NVIDIA GPUs

Features

- Available for all CCHMC and collaborating external researchers on request.
- 10Gig Ethernet backend network.
- Direct connection to clustered High Performance storage servers.
- Consistent mount points for home directories and data directories across the HPC and all of the Linux systems.
- Command line and graphical interface.

Applications

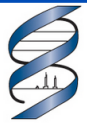
- Whole-genome / exome analysis
- Microbial ecology
- Protein docking, folding and structure prediction
- Natural language processing
- Functional neuroimaging

LONI Pipeline

- Provides a graphical workflow builder that interfaces with the computation cluster through LSF.
- Allows investigators and researchers to easily change parameters without the need to edit code and shell scripts.
- Able to interface with web applications using Java Web Start.

LONI Pipeline

Logged in as Andrew Rupert (rup8bo) [Logout]



CASSI

Tools **Upload VCFs** Manage Cohorts Administration

- Query
- Download File
- Delete File
- Trio Analysis**
- Singleton
- Add to Cohort
- Custom pipe

Trio sequencing analysis for potentially pathogenic variants

Click on LONI icon after selecting desired trios

[More Info](#)

Trios

<input type="checkbox"/>	Child Name	Family Name	Mother Name	Father Name	cohorts	files
<input checked="" type="checkbox"/>	1220.1	EE_1220	1220.2	1220.3	andytest	F.vcf
<input checked="" type="checkbox"/>	1352.1	EE_1352	1352.2	1352.3	andytest	F.vcf
<input checked="" type="checkbox"/>	1354.1	EE_1354	1354.2	1354.3	andytest	F.vcf
<input type="checkbox"/>	1511.1	EE_1511	1511.2	1511.3	andytest	F.vcf
<input type="checkbox"/>		EE_1579	1579.2	1579.3	andytest	F.vcf
<input type="checkbox"/>		EE_788	788.2	788.3	andytest	F.vcf



Project Name:

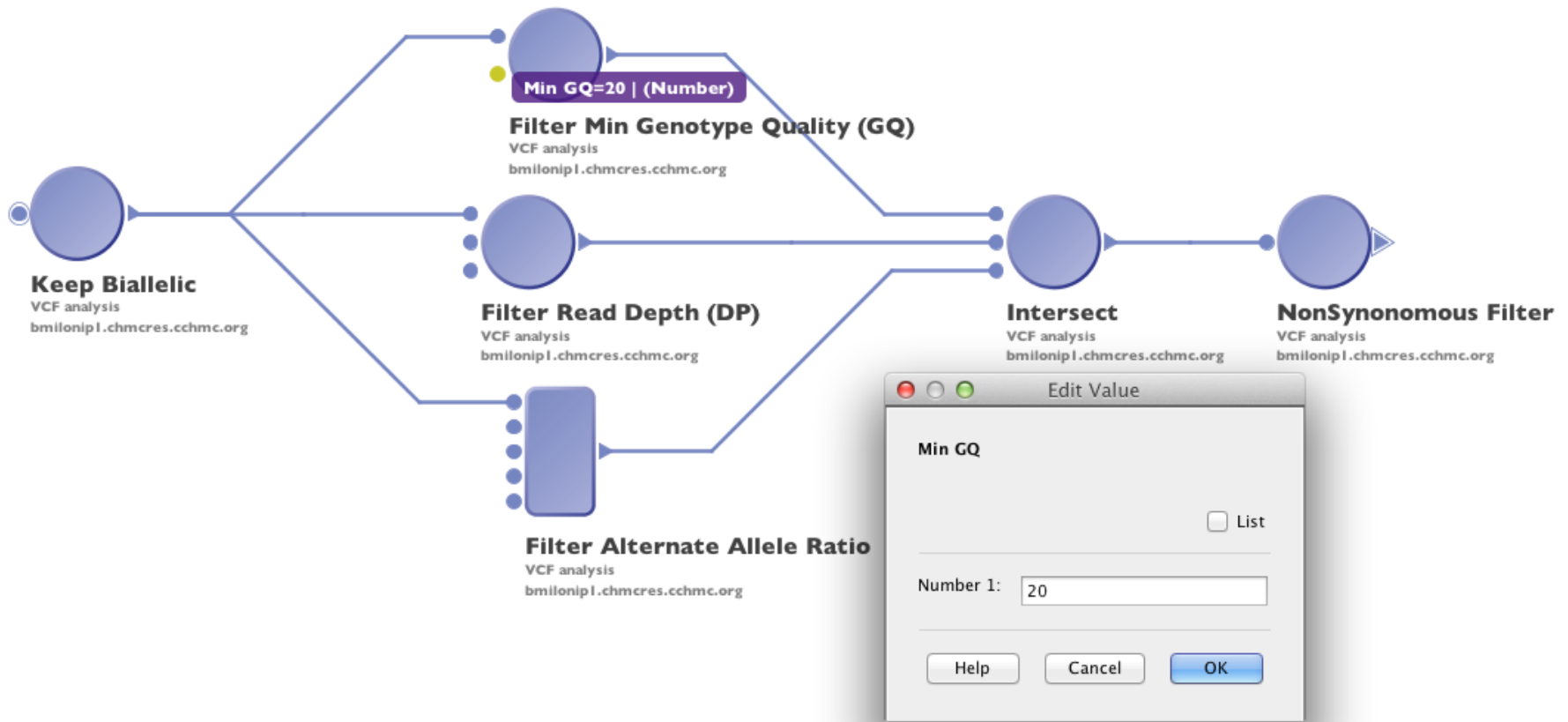


LONI Pipeline

The screenshot displays the LONI Pipeline software interface. The window title is "LONI Pipeline" and the active pipeline file is "0a5e9f32.pipe". The interface is divided into several sections:

- Server Library:** A tree view on the left showing a hierarchy of folders: "Server Library" > "b milionid1" > "Modules". Under "Modules", there are folders for "AFNI", "BrainSuite09", "C-MIND", "FSL", "FSL 3.3", "LONI", and "VCF-Tools". The "VCF-Tools" folder is expanded, showing several filter modules: "Intersect on Sites", "Keep Mendel Errors", "Max Alt Reads(AD) Filter", "Min Alt Reads(AD) Filter", "Min Genotype Quality (GQ) Filter", and "Min Read Depth (DP) Filter". There are also "Workflows" and another "b milionid1" folder at the bottom of the tree.
- Module Groupings:** A dropdown menu at the top of the main workspace is set to "allFiltersV4".
- Workflow Diagram:** A central workspace showing a flowchart of the pipeline. It starts with three input nodes: "Output Directory", "Trio Samples", and "Source Names". These feed into a sequence of processing modules: "Extract Trio", "QC Filters" (VCF analysis), and "Analysis Models" (VCF analysis). The output of "Analysis Models" branches into two paths: one leading to "Annotation" (VCF analysis) and another leading to "Rename and Store". Both "Annotation" and "Rename and Store" feed into the final "Summarize" module. The URL "b milionip1 .chmores .cdhmc.org" is visible below each module name.
- Bottom Bar:** Contains navigation buttons (back, forward, refresh) and a status indicator showing "1 Connection" and "1%".

LONI Pipeline



Open Source Project Examples - Demos

- CASSI – Cincinnati Analytical Suite for Sequencing Informatics
 - John Harley, Ken Kaufman, Leah Kottyan, Sue Thompson
 - Repository and processing pipelines for Next-Generation Sequencing data.
- X-Ray Study Web Portal
 - Greg Myer (PI)
 - Surgeons will answer questions about an X-Ray Image
 - Measurements are made in browser about various lesions.

Add an Image

ID:

Single Image: No file chosen

Full Image: No file chosen

Visible? Yes
 No



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3333 Burnet Avenue, Cincinnati, Ohio 45229-3039
Code Version:

Image Management

[+ Add Image](#)

























































Id	Single	Full	ID OK?	Visible?	Actions
A					Update Delete
AY986079					Update Delete
B					Update Delete
BN836497					Update Delete
BN836497L					Update Delete
BN836497R					Update Delete
BR661041					Update Delete
BW					Update Delete
BW11110437					Update Delete
C					Update Delete
CA1113687					Update Delete
CG650043					Update Delete
CH1270139					Update Delete
CH1270139L					Update Delete

Image Classification

0

Total Number Completed: 0

30



A.) Standing AP

 Not Visible

Width of OCD lesion:

Measure the `Width of OCD lesion` by clicking on the image to start the line and clicking to end the line. , Must be less than 86.0

Open Source Project Examples - Demos

- CpG Processing Pipeline and Variant Knowledge Base
 - Pete White and John Harley
 - Unified data intake, processing pipeline, and variant database for CCHMC next-generation sequencing data.
 - Allows for custom CCHMC annotations and queries.
 - Full permission system to allow sharing of data with collaborators.
 - Dashboard to allow researchers to view where their samples are in the pipeline.

Super Awesome Samples

Permissions

PI: [Super Man](#), Business: [Batman](#), Type: [Public Queryable](#)

Lorem ipsum dolor sit amet, consectetur adipiscing elit. Quisque suscipit ante metus, non pulvinar dui rhoncus et. Vivamus vitae nisi a lacus accumsan pretium. Duis id neque ut lectus lacinia aliquet. Pellentesque a sodales eros. Donec suscipit tincidunt est, aliquet imperdiet ante faucibus id. Sed ornare dolor lorem. Phasellus et mi nisi. Suspendisse sed orci in eros finibus dictum. In eleifend vel tellus in scelerisque. Sed gravida, ex dignissim rhoncus aliquam, quam libero malesuada ex, non blandit dolor nunc sit amet mi. Nunc tortor augue, pulvinar vitae risus quis, feugiat malesuada lacus. Integer nec urna consequat, efficitur ipsum ac, semper turpis.

* Click the status icon to see QC metrics

Sample	Status	Progress	Variants
▼ S1		In Process	65197

Show Files

Sample Info

Specimen Info

Type: Human
Assay: Whole Exome

Study Group: g2
Cell Line: 2
Individuals: 4
Race: Caucasian
Gender: M
Ethnicity: Non-Hispanic



Super Awesome Samp

PI: Super Man, Business: Batman, Ty

Lorem ipsum dolor sit amet, consectetur adipisc
Vivamus vitae nisi a lacus accumsan pretium. D
Donec suscipit tincidunt est, aliquet imperdiet a
Suspendisse sed orci in eros finibus dictum. In e
aliquam, quam libero malesuada ex, non blandit
feugiat malesuada lacus. Integer nec urna conse

Sample

▼ S1

Sample Info

Type: Human
Assay: Whole Exome

Specimen Info

Study Group: g2
Cell Line: 2
Individuals: 4
Race: Caucasian
Gender: M
Ethnicity: Non-Hispanic



Super Awesome Permissions ✕

Global Project Permission

Public: No Download ▼

Name	Download & View	Upload	Admin
✖ Phillip Dexheimer	✔	✖	✖
✖ Nick Felicelli	✔	✔	✔
✖ Mojtaba Kohram	✔	✔	✖
✖ Andy Rupert	✔	✔	✔
✖ David Van Horn	✔	✖	✖

Select a user ▼
Add User
Done

* Click the status icon to see QC metrics

Variants

65197

example searches: 1-1000-100000, OR4F5

Region chromosome 1 / 66000 - 75000

Variant (@chrom:pos/REF>ALT)	dbSNP	Alternate count	Allele frequencies	Gene
@chr1:66162/A>T		3/20		
@chr1:66176/T>A		3/20		
@chr1:66331/A>C		2/20		
@chr1:66442/T>A		1/20		
@chr1:66457/T>A		1/20		
@chr1:66507/T>A		4/20		
@chr1:67179/C>G		1/20		
@chr1:67181/A>G		2/20		
@chr1:69511/A>G	rs75062661	14/20	Exac - 0.894 1000G - 0.652 ESP - 0.544	OR4F5 (gene card)
@chr1:73841/C>T		3/20		

« »



example searches: 1-1000-100000, OR4F5

Variant @chr1:69511/A>G

DBNSFP_variant	
ESP6500_EA_AF	0.887429
fold-degenerate	0
PROVEAN_score	.;1.54
phastCons100way_vert...	0.05858
ExAC_AF	8.938e-01
GERP++_RS	1.15
Uniprot_aapos	141
ExAC_AC	75589
aaref	T

AVGPOST	0.7173
ASN_AF	0.87
AA	null
THETA	0.0052
SNPSOURCE	LOWCOV
VT	SNP
LDAF	0.6051
ERATE	0.0237
AC	1424
AFR_AF	0.33



Project Examples - Demos, Cont.

- Instrument Time Tracker
 - Andrew Rupert, Michael Wagner
 - Transparently tracks real time lab instrument usage for the Flow Cytometry and Confocal Microscopy cores.
- Scheduling Calendars
 - Sort Scheduler, MRBS, etc.



Please Log In	
Logon name	<input type="text"/>
Password	<input type="password"/>
Language	English US (Default) ▾
Keep me logged in (requires cookies)	<input type="checkbox"/>
<input type="button" value="Log In"/>	

[View Schedule](#) | [Help](#)

phpScheduleIt v1.2.11

Administrator



Welcome Back, Andrew
Log Out | My Control Panel

Wednesday, November 11, 2015
Help

> My Quick Links ?

- » Bookings
- » My Calendar
- » Schedule Calendar
- » Email Preferences
- » Email Administrator
- » Log Out

- System Administration**
- » Manage Schedules
- » Manage Blackout Times
- » Manage Resources
- » Manage Announcements

- » Manage Groups
- » Manage Users
- » Manage Reservations
- » Approve Reservations

- » Mass Email Users
- » Search Reservations
- » Export Database Content
- » View System Stats

> My Announcements ?

Announcements as of 11/11/2015
• There are no announcements.

> My Reservations ?

Start Date	End Date	Resource	Start Time	End Time	Created
You do not have any reservations scheduled.					



My Reservations	My Past Reservations	My Participation	My Past Participation	Other Reservations	Other Past Reservations	Pending Approval	Blacked Out Time
-----------------	----------------------	------------------	-----------------------	--------------------	-------------------------	------------------	------------------

Monday, 10/12/2015	7:30am	8:00am	9:00am	10:00am	11:00am	12:00pm	1:00pm	2:00pm	3:00pm	4:00pm	5:00pm	6:00pm	7:00pm
4-Laser Ariel	Startup			Javid Mohammed				Jose Javier 70 µm		Jonathan Schick	Shutdown		
5-laser Arnie	Startup			Yutaka Maeda 100 µm		Luis Queme 100 µm	Javid Mohammed			Shutdown			
MoFlo XDP	Startup			Ramesh Nayak 100 µm			Sarah Potter 100 µm		Shutdown				

Tuesday, 10/13/2015	7:30am	8:00am	9:00am	10:00am	11:00am	12:00pm	1:00pm	2:00pm	3:00pm	4:00pm	5:00pm	6:00pm	7:00pm
4-Laser Ariel	Startup			Heping Xu 70 µm				Sachin Kumar 100 µm		Damien Reynaud		Shutdown	
5-laser Arnie	Startup			Megha Desai 70 µm			Carine Bouffi 70 µm	Rajeswari Jayavaradhan				Shutdown	
MoFlo XDP	Startup			Sara Meyer 100 µm		Xian Li 100 µm	Sarah Potter 100 µm		Shutdown				

Wednesday, 10/14/2015	7:30am	8:00am	9:00am	10:00am	11:00am	12:00pm	1:00pm	2:00pm	3:00pm	4:00pm	5:00pm	6:00pm	7:00pm	
4-Laser Ariel	Startup			Jing Fang 100 µm			Ashwini Hinge 70 µm		Monica DeLay		Shutdown			
5-laser Arnie	Startup			David Muench 100 µm		Oded Volovelsky 70 µm	Mei Wang 70 µm				Jonathan Schick	Shutdown		
MoFlo XDP	Startup			Javid Mohammed									Shutdown	

Thursday, 10/15/2015	7:30am	8:00am	9:00am	10:00am	11:00am	12:00pm	1:00pm	2:00pm	3:00pm	4:00pm	5:00pm	6:00pm	7:00pm	
4-Laser Ariel	Startup		Staff Meeting	Maha Almanan 70 µm							Shutdown			
5-laser Arnie	Startup		Staff Meeting	Tim Hubbell		Heping Xu 70 µm				Shutdown				
MoFlo XDP	Startup			David Muench 100 µm		Xiaomeng Ren 100 µm		Takuji Suzuki		Andre Olsson 100 µm		Shutdown		

You are **modifying** an existing reservation.

Basic

Location	R5001
Phone	636-2770
Notes	BL2 or BL2+

Please change the starting and ending times:

Start	End
10/16/2015	10/16/2015
10:00am	2:00pm

Will be reserved for:

Name	
Phone	
Email	
PI	

Created	09/18/2015 @ 03:48:08 PM
Last Modified	N/A

Notes

TMH, YFP+, APcy7+, APc-,

Reminder -- Never --
before reservation

Delete?

Sort Set Up

Type of Cells/Study	m BM		
Have you done this sort with us before?	<input checked="" type="radio"/> Yes <input type="radio"/> No		
BSL Level/Agent	2 retro and lenti >48hrs		
Cell Size (μ m)			
Number of Samples	3		
Starting Cell Number	<5 e6 each		
Number of Cells Needed			
% of Target Cells Expected			
Nozzle Size	<input checked="" type="radio"/> 70 μ m <input type="radio"/> 85 μ m <input type="radio"/> 100 μ m <input type="radio"/> 130 μ m		
ND Filter	<input type="radio"/> 1.0 <input checked="" type="radio"/> 1.5 <input type="radio"/> 2.0		
Purpose of Sort	<input type="radio"/> RNA <input type="radio"/> Transplant <input checked="" type="radio"/> Culture <input type="radio"/> Other		
Populations Collected	YFP+	APcy7+	
	AP		
Sample Tube	<input type="radio"/> 1ml <input checked="" type="radio"/> 5ml <input type="radio"/> 15ml Conical		
Sort Type	<input checked="" type="radio"/> 1-way <input type="radio"/> 2-way <input type="radio"/> 3-way <input type="radio"/> 4-way		
Collection Tube	<input type="radio"/> Eppendorf <input checked="" type="radio"/> FACS Tubes <input type="radio"/> 15ml <input type="radio"/> ACDU		
Sample Temp ($^{\circ}$ C)	4		
Collection Temp ($^{\circ}$ C)	4		
Colors Used	YFP	7AAD	APC Cy7
	APC		

Save

Cancel

Check Availability

Project Examples - Demos, Cont.

- ADHD Team
 - Tanya Froehlich and Leanne Tamm
 - Mobile App (iOS and Android)
 - Daily SMS reminders to complete survey
 - Also accessible via a web browser
 - Current survey asks questions regarding ADHD (but can be extended/reused)

Admin Control Panel

[Add Subject](#)[Update Subject](#)

Add Subject

Subject ID**Password****Re-enter Password****User's Cell Phone
Number****Projected Start Date**

Start date of Assessment (A1)

Projected End Date

End date of Assessment (A1)

Time for Reminders[Continue](#)



Login

Username

Password

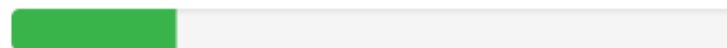
Login

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Medical Center



EMA Ratings - TEAM Study

Please fill in the information below



EMA Ratings for Wednesday, November 11, 2015

7. Loses things necessary for tasks or
activities (school assignments,
pencils, or books)

- Never
- Occasionally
- Often
- Very Often
- Skip Question

Project Examples - Demos, Cont.

- C-MIND - Cincinnati MR Imaging of NeuroDevelopment
 - Jennifer Vannest (Co-PI), Scott Holland (Co-PI)
 - Fully custom longitudinal data entry, querying, and processing application for fMRI images.
 - Demographic and behavioral data collected for healthy children.

If you need assistance with the development of custom software tools or help configuring existing software packages, please contact us!

help@bmi.cchmc.org

Andrew.Rupert@cchmc.org