

Developing evidence: the value of family health history

Lori A. Orlando, MD MHS

Family Health History

- Nominally "the first genetic test" (Francis Collins)
- Reflects both:
 - Shared environments
 - Shared genetics
- Imparts information only about risk
- Can (sometimes) be both more informative and more confusing than genetic/genomic results

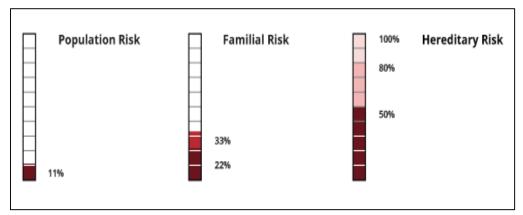




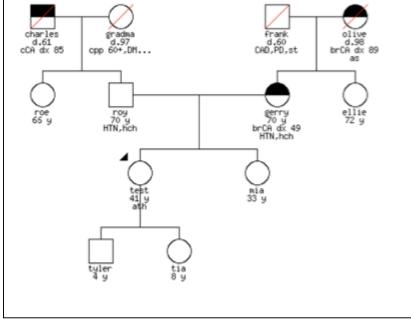
Shared Genes

FHH Data contributes to assessing genetic risk in 2 ways

Infer genetic risk



- Contextualize genetic results
- Assess co-inheritance







Evidence Summary

- Analytic validity
- Clinical validity

Clinical Utility



ANALYTIC VALIDITY





Systematic Review FHH Data

- 12 studies of community populations
- Good agreement between patiententered data and genetic counselor derived data

Public Health Genomics

Original Paper

Public Health Genomics 2009;12:73–83 DOI: 10.1159/000160667

Received: April 30, 2008 Accepted: July 17, 2008 Published online: October 2, 2008

Family History Questionnaires Designed for Clinical Use: A Systematic Review

G.T. Reid^a F.M. Walter^c J.M. Brisbane^b J.D. Emery^{a, c}

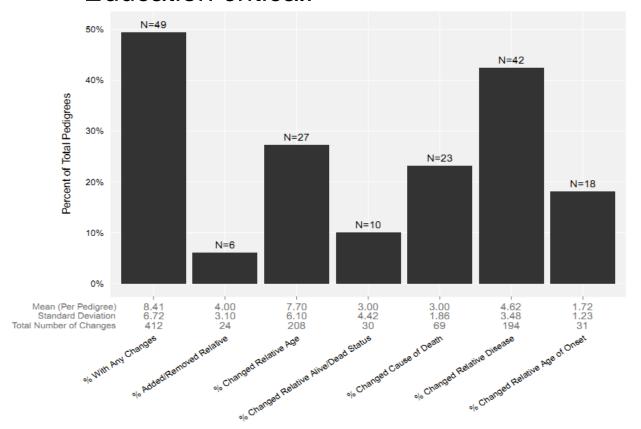
^aGeneral Practice, School of Primary Aboriginal and Rural Health Care, University of Western Australia, Claremont, W.A., and ^bOffice of Population Health Genomics, Health Department of Western Australia, Perth, W.A., Australia; ^cGeneral Practice and Primary Care Research Unit, Institute of Public Health, University of Cambridge, Cambridge, UK





Our Data

- Genetic counselor review of 3 generation pedigrees entered by primary care patients for 3 months- data correlation very high
- Education critical!



16% with changed recommendation

- 6% from high risk to population risk
- 10% from population risk to high risk



CLINICAL VALIDITY





Shared Genes: Infer Genetic Risk

- Alone
 - ▶ e.g. NCCN guidelines for HBOC testing

- In combination with other information
 - e.g. Dutch Lipid guidelines for familial hypercholesterolemia
 - ▶ BRCApro
 - ► MMRpro





Shared Genes: I

- Alone
 - ▶ e.g. NCCN guidelines for I

- In combination with oth
 - e.g. Dutch Lipid guidelines
 - ▶ BRCApro
 - ► MMRpro

Hereditary Breast & Ovarian Cancer Program

Genetic Red Flags Checklist



Genetic red flags are features of the personal or family medical history that suggest a higher than average genetic contribution to cancer. These are unusual presentations of cancer that are more likely when a genetic variant is present from birth. Use this checklist with the Risk Stratification tool.

+ or -	Red Flag	Explanation	Description
	Early age of onset	The average age for breast cancer diagnosis is > 50 yrs. Pre-menopausal breast cancer suggests an underlying susceptibility.	
	Bilateral disease/multiple primaries	Although a tumor may metastasize, it is rare to have more than one primary cancer. Bilateral breast cancer, or breast and ovarian cancer in the same person suggest a predisposition.	
	Male breast cancer	Breast cancer is rare in males, and when it occurs, suggests a hereditary susceptibility.	
	Ovarian cancer	Ovarian cancer is rare except with a hereditary predisposition. A history of ovarian cancer is alone indication for further evaluation for HBOC.	
	Multiple affected relatives	Two or more close relatives* with the same or related cancers* suggests a hereditary predisposition, especially when in consecutive generations.	
	Disease despite preventive measures	Some interventions like oophorectomy lower the risk for breast and ovarian cancer. If cancer occurs anyway, preexisting susceptibility is more likely.	
	Ashkenazi Jewish ancestry	1 in 40 individuals of Ashkenazi ancestry carries a mutation in either the BRCA1 or BRCA2 gene.	
	Other notable bistory	Unusual physical features, birth defects, intellectual disability or other notable family history may indicate a different genetic syndrome. Discuss these with a genetics professional.	

^{*}Close relatives include parents, children, siblings, grandparents, aunts/uncles and first cousins.



^{*}HBOC-related cancers include breast, ovarian, prostate, melanoma and pancreatic.

Shared Genes: Infer Genetic Risk

- Alone
 - ▶ e.g. NCCN guidelines for HBOC testing

- In combination with other information
 - e.g. Dutch Lipid guidelines for familial hypercholesterolemia
 - ▶ BRCApro
 - ► MMRpro





Shared Genes: I

Appendix 1: Dutch Lipid Clinic Network Criteria for making a diagnosis of Familial Hypercholesteroloemia (FH) in adults

Score

3-5

Alone

▶ e.g. NCCN guidelines for

- In combination with oth
 - e.g. Dutch Lipid guidelines

Possible FH

Unlikely FH

- ▶ BRCApro
- ► MMRpro

	Family history						
	women <60 years) or	nown premature coronary and/or vascular disease (men <55 years,	1				
	First-degree relative with K	nown LDL-cholesterol above the 95th percentile for age and sex					
	•	endinous xanthomata and/or arcus cornealis	2				
1	or Children aged less than 18 sex	years with LDL-cholesterol above the 95th percentile for age and					
	Clinical history						
	Patient with premature cor	ronary artery disease (ages as above)	2				
	Patient with premature cer	ebral or peripheral vascular disease (as above)	1				
	Physical examination						
1	Tendinous xanthomata		6				
3	Arcus cornealis prior to age 45 years						
٩	LDL-cholesterol (mmol/L)						
		LDL-C ≥8.5	8				
		LDL-C 6.5-8.4	5				
		LDL-C 5.0-6.4	3				
		LDL-C 4.0-4.9	1				
	DNA analysis: functional mutation in the LDLR, APOB or PCSK9 gene						
	STRATIFICATION						
	Definite FH		≥8				
	Probable FH		6–7				
- 1							



Shared Genes: Infer Genetic Risk

- Alone
 - ▶ e.g. NCCN guidelines for HBOC testing

- In combination with other information
 - e.g. Dutch Lipid guidelines for familial hypercholesterolemia
 - ▶ BRCApro
 - ► MMRpro





Important Considerations

- Guidelines developed based on evidence
 - What is family health history measuring?
 - What evidence links family history to the outcomes?
 - How was the evidence assessed?





Guideline Differences

TABLE V. Comparison of Genetic Counseling (GC) Referral Recommendations Between MeTree, and the NCCN's Colon and Breast Cancer Guidelines, and the Michigan Department of Community Health's Cancer Family History Guide (CFHG)

	MeTree G	MeTree GC referral	
	No, N (%)	Yes, N (%)	Total
CFHG GC re	eferral		
No	768 (64.9%)	94 (7.9%)	862 (72.8%)
Yes	86 (7.3%)	236 (19.9%)	322 (27.2%)
Total	854 (72.1%)	330 (27.9%)	1,184 (100%)
NCCN breast	cancer GC referral		
No	891 (75.3%)	12 (1.0%)	903 (76.2%)
Yes	114 (9.6%)	167 (14.1%)	281 (23.7%)
Total	1,005 (84.9%)	179 (15.1%)	1,184 (100%)
NCCN colon	cancer GC referral		
No	1,070 (90.4%)	103 (8.7%)	1,173 (99.1%)
Yes	0 (0%)	11 (0.9%)	11 (0.9%)
Total	1,070 (90.4%)	114 (9.6%)	1,184 (100%)

- Breast/ovarian cancer differences:
 - NCCN refers for any relative with ovarian cancer or breast cancer < age 45
- Colon cancer differences:

MeTree includes Bethesda criteria for any relative, NCCN only if the proband, FDR or SDR had colon cancer





What about common complex diseases?

FHH is better predictor the current genomic tests

- Coronary Artery Disease
 - Framingham risk score does not include FHH
 - Europeans multiple Framingham x 2.5 for FDR with premature CAD
 - Canadians multiple Framingham x 2 for FDR with premature CAD
- Diabetes risk
 - 3.2% without FDR to 14.3% (absolute risk) with FDR*
 - SNP OR varies ~2-3

*Annis AM, Caulder MS, Cook ML, Duqette D. Prev. Chronic Dis. 2005 2(2)





CLINICAL UTILITY





	Baseline FHH N=390 for all and 227 for deceased	MeTree N=1184 for all and 1179 for deceased
Quality Criterion		
 3 generations 	0 (0%)	1184 (100%)
 Relatives' lineage 	111 (28.4%)	1184 (100%)
 Relatives' gender 	356 (91.2%)	1184 (100%)
 Pertinent negatives 	173 (44.3%)	1184 (100%)
 Age of disease onset 	71 (18.2%)	854 (72.1%)
 Cause of death 	213 (98.1%)	695 (58.9%)
 Age of death 	172 (75.7%)	1156 (98.0%)

- 58.9% talked with their relatives
- Mean # of relatives talked to: 2.89 (SD 1.58)





	Baseline FHH N=390 for all and 227 for deceased	MeTree N=1184 for all and 1179 for deceased
Quality Criterion		
 3 generations 	0 (0%)	1184 (100%)
 Relatives' lineage 	111 (28.4%)	1184 (100%)
 Relatives' gender 	356 (91.2%)	1184 (100%)
 Pertinent negatives 	173 (44.3%)	1184 (100%)
 Age of disease onset 	71 (18.2%)	854 (72.1%)
 Cause of death 	213 (98.1%)	695 (58.9%)
 Age of death 	172 (75.7%)	1156 (98.0%)

- 58.9% talked with their relatives
- Mean # of relatives talked to: 2.89 (SD 1.58)







Baseline FHH N=390 for all and 227 for deceased MeTree N=1184 for all and 1179 for deceased			
• 3 generations 0 (0%) 1184 (100%) • Relatives' lineage 111 (28.4%) 1184 (100%) • Relatives' gender 356 (91.2%) 1184 (100%) • Pertinent negatives 173 (44.3%) 1184 (100%) • Age of disease onset 71 (18.2%) 854 (72.1%)		FHH N=390 for all and 227 for	N=1184 for all and 1179
 Relatives' lineage 111 (28.4%) 1184 (100%) Relatives' gender 356 (91.2%) 1184 (100%) Pertinent negatives 173 (44.3%) 1184 (100%) Age of disease onset 71 (18.2%) 854 (72.1%) 	Quality Criterion		
 Relatives' gender 356 (91.2%) 1184 (100%) Pertinent negatives 173 (44.3%) 1184 (100%) Age of disease onset 71 (18.2%) 854 (72.1%) 	 3 generations 	0 (0%)	1184 (100%)
 Pertinent negatives 173 (44.3%) 1184 (100%) Age of disease onset 71 (18.2%) 854 (72.1%) 	 Relatives' lineage 	111 (28.4%)	1184 (100%)
• Age of disease onset 71 (18.2%) 854 (72.1%)	 Relatives' gender 	356 (91.2%)	1184 (100%)
	 Pertinent negatives 	173 (44.3%)	1184 (100%)
• Cause of death 213 (98.1%) 695 (58.9%)	 Age of disease onset 	71 (18.2%)	854 (72.1%)
	 Cause of death 	213 (98.1%)	695 (58.9%)
• Age of death 172 (75.7%) 1156 (98.0%)	 Age of death 	172 (75.7%)	1156 (98.0%)

- 58.9% talked with their relatives
- Mean # of relatives talked to: 2.89 (SD 1.58)









	Baseline FHH N=390 for all and 227 for deceased	MeTree N=1184 for all and 1179 for deceased	 58.9% talked with their relatives Mean # of relatives talked to: 2.89 (SD
Quality Criterion			1.58)
 3 generations 	0 (0%)	1184 (100%)	
 Relatives' lineage 	111 (28.4%)	1184 (100%)	
 Relatives' gender 	356 (91.2%)	1184 (100%)	
 Pertinent negatives 	173 (44.3%)	1184 (100%)	
 Age of disease onset 	71 (18.2%)	854 (72.1%)	
 Cause of death 	213 (98.1%)	695 (58.9%)	
 Age of death 	172 (75.7%)	1156 (98.0%)	

- Pre-MeTree < 4% of FHHs were hih-quality (single relative)
- Post-MeTree 99% of FHHs were high-quality (single relative)





FHH-based Risks in General Population

TABLE IV. Frequency of Hereditary Syndrome Risk and Familial-Risk Recommendations for Each Clinical Decision Support Condition

Disease	Recommendation	Frequency among all participants (N ¼ 1,184), N (%)	Frequency among eligible participants ^a , N (%)
Hereditary syndrome risk	Genetic counselingb	308 (26.0%)	308/1,184 (26.0%)
Breast cancer	Breast MRI	10 (0.8%)	10/694 (1.4%)
	Chemoprophylaxis	58 (4.9%)	58/694 (8.3%)
Colon cancer	Start colon screening early	114 (9.6%)	114/1,178 (9.7%)
	More frequent colonoscopies	107 (9.0%)	107/1,178 (9.1%)
Ovarian cancer	Referral to gynecology	14 (1.2%)	14/694 (2.0%)
Thrombosis	Genetic testing ^b	42 (3.5%)	42/1,184 (3.5%)
	Genetic counseling ^b	29 (2.4%)	29/1,184 (2.4%)

The number of participants eligible for a recommendation in that disease category. Those with the disease are removed and for breast cancer and ovarian cancer, men are removed.





bThese recommendations make up the "hereditary syndrome risk" group, the others up the "familial-risk" group.

	Patients at Increased-Risk who Meet Criteria for Risk Management Strategy		D	nsed-Risk who iteria for t Strategy		
Risk Management Strategy	Total N	Before MeTree N (%)	After MeTree N (%)	Total N	Before MeTree N (%)	After Metree N (%)
Hereditary Cancer: Genetic Counseling	124	0 (0%)	18 (14.5 %)	364	0 (0%)	1 (0.2%)
Breast Cancer: MRI	4	1 (25%)	3 (75%)	280	5 (1.8%)	1 (0.4%)
Breast Cancer Chemoprevention	26	0 (0%)	0 (0%)	258	0 (0%)	0 (0%)
Ovarian Cancer: Gynecology	2	0 (0%)	1 (50%)	282	12 (4.2%)	9 (3.2%)
Thrombosis: Genetic Testing	11	1 (9.1%)	2 (18.1%)	477	0 (0%)	0 (0%)
Thrombosis: Genetic Counseling	7	0 (0%)	4 (57.1%)	481	0 (0%)	0 (0%)
Total	174	2 (1.1%)	28 (16.1%)	2,142	17 (0.8%)	11 (0.5%)

Decreasing Mismatch in Risk Level and Risk Services

- Pre-MeTree 2/19 (10%) undergoing increased risk management were at increased risk
- Post-MeTree 28/39 (72%) were at increased risk.





New Frontiers: contextualize genetics

■ PALB2*

- ▶ No FHH breast cancer risk 33% by age 70
- ▶ 2 or more FDRs with breast cancer risk 58% by age 70

BRCA

- ► Lifetime breast cancer risk 45-65%
- ▶ No FHH breast cancer?
 - + Counsyl tested 2500 women in San Diego for free
 - + 4.2% tested positive, half did not meet NCCN criteria
- Variants of Undetermined Significance





FHH – New Horizons

- FHH more informative than we think?
 - Social network analysis
 - Relationships between relatives
 - Estimate heritability
 - Disease clustering
- Differentiating Environmental from Heritable Risk
 - Environmental conditional risk
 - Estimate environmental relative risk



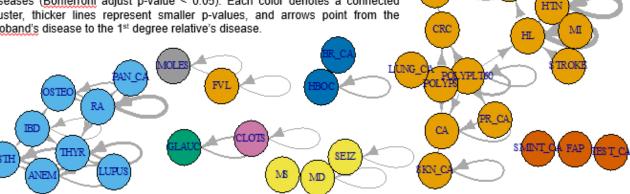


FHH – Nev

Genetic network and sub-networks of diseases

Fig 2. Network of diseases in 1st degree relatives

Diseases are nodes, conditional relative risks are the edges connecting the diseases (Bonferroni adjust p-value < 0.05). Each color denotes a connected cluster, thicker lines represent smaller p-values, and arrows point from the proband's disease to the 1st degree relative's disease.



Self

2nd Degre

st Degree

21

- FHH more infor
 - Social network
 - Relationships ł
 - Estimate herita
 - Disease cluste
- Differentiating E
 - Environmental
 - Estimate environment

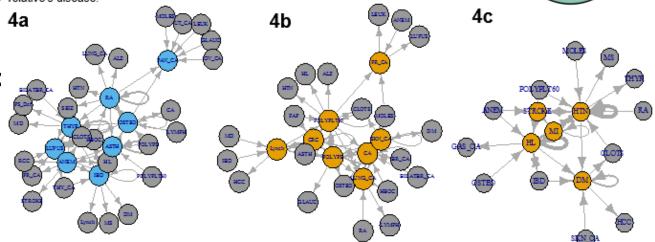
Fig 3. Consistency across relationship types

Overlap of disease pairs with Bonferroni adjusted p-values < 0.05 in all three relative types: self*, 1st, and 2nd degree relatives.

*Instances of disease A == disease B are omitted.

Fig 4a-c. Sub-networks of diseases in 1st degree relatives

Three sub-networks seeded using clusters identified in Figure 2, autoimmune (a), cancer (b), and metabolic syndromes (c). Included edges (disease pairs) contained a minimum of one disease from the clusters noted above with FDR adjusted q-value < 0.05. Thicker lines represent smaller p-values and arrows point from the proband's disease to the 1st degree relative's disease.





FHH – New Horizons

- FHH more informative than we think?
 - Social network analysis
 - Relationships between relatives
 - Estimate heritability
 - Disease clustering
- Differentiating Environmental from Heritable Risk
 - Environmental conditional risk
 - Estimate environmental relative risk





IMPLEMENTING IN CLINIC

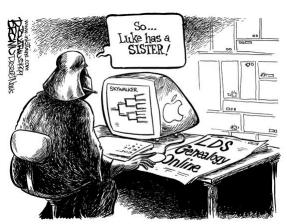




Barriers by Stakeholder

Patient

- Education
- Accuracy

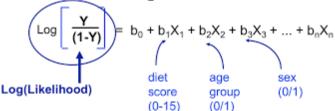


Provider

- Time
- Awareness
- Complexity



The Logistic Function



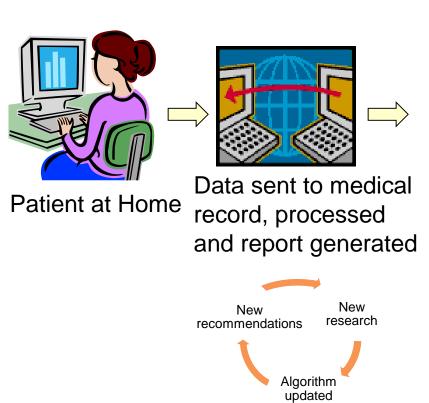
Health System

- Inadequate systems for data collection & providing actionable information
- Tools that interact with the EMR
- Awareness of population impact

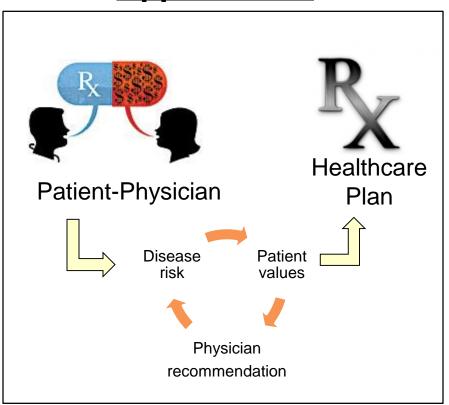




Ideal Flow of FHH Information



Appointment







Help is Available! FHH Tools

 Global Alliance for Genomics and Health has a catalogue of existing tools and their capabilities

https://genomicsandhealth.org/work-products-demonstrationprojects/catalogue-global-activities-family-history-tools

 Many are companies associated with genetic testing labs and very few provide clinical decision support





Program	Decision Support Diseases	Completed By	Publicly Available	Who Receives Output	Available at Point of Care	Action Oriented Recomm.					
MeTree [©]	colon, breast, and ovarian cancer; aortic aneurysm, heart disease, stroke, diabetes, hereditary cancer syndrome, hereditary cardiovascular syndrome, hereditary liver diseases	Patient online or physician's office	In future	Patient and physician	Yes	Yes					
Schroy et al.	colon cancer	Physician	Unknown	Physician	Yes	No					
GRACE	breast cancer	Patient in physician's office	Unknown	Patient, clinical nurse specialist, physician	Yes	No					
Family Healthware	coronary heart disease, diabetes, stroke, colon, breast, and ovarian cancer	Patient online	No	Patient	No	No					
Family HealthLink	coronary heart disease, cancer	Patient online	Yes	Patient	No	No					
CRIS	colon cancer	Patient in physician's office	No	Patient and physician	Yes	No					
MyGenerat ions	cancer	Patient online	Yes	Patient	No	No					
Hughes Risk Apps	breast and ovarian cancer, colon cancer, hereditary cancer risk	Patient – clinician can revise online or physician's office	Yes	Patient and physician	Yes	No					
Health Heritage.n et	87 diseases: multiple cancers, diabetes, neuromuscular diseases, and cardiovascular diseases	Patient online	In future	Patient	No	No					
Invitae	Cardiac disease, colon cancer, cmt, breast cancer, pancreatic cancer	Physician online	Yes	Patient and Physician	?	No					
MyFamily	Cancer, cardiology, GI- proprietary algorithms	Patient	In future	Physician	Yes	Yes					
Myriad	29 cancers	Patient	Yes	Patient	No	No					
Power Lineage	cancer	Patient and Physician	Yes	Physician	No	No					
				Ų	Duke M	APPLIED GENOMICS DukeMedicine & PRECISION MEDICINE					

MeTree

- Patient facing web-based software program
- Educates patients on what and how to collect FHH
- Gives patients time to collect FHH
- Easy to use graphical user interface
- Creates 3+ generation pedigree
- Generates risk scores and evidence-based risk stratified prevention recommendations for selected conditions
- Clinical decision support for patients and providers
- Evidence guidelines monitored with updating of rules





SMART-FHIR





What exactly is SMART-on-FHIR

SMART

- Substitutable medical apps, Reusable Technology
- Authentication through OAuth2
- HTML5 and Javascript permits views in an "app window"
- Microinteractions which allows wrapping of data into different "views"

FHIR

- Fast health interoperability resource
- ReSTful API (resource oriented)
 - Bi-directional data transfer
- FHIR profiles
 - include a growing list of defined resources
 - Permits plug and play interoperability
 - Leverages standardized nomenclatures (snomed, rxnorm, loinc, CVX, etc..)
- Extensions for data not already defined





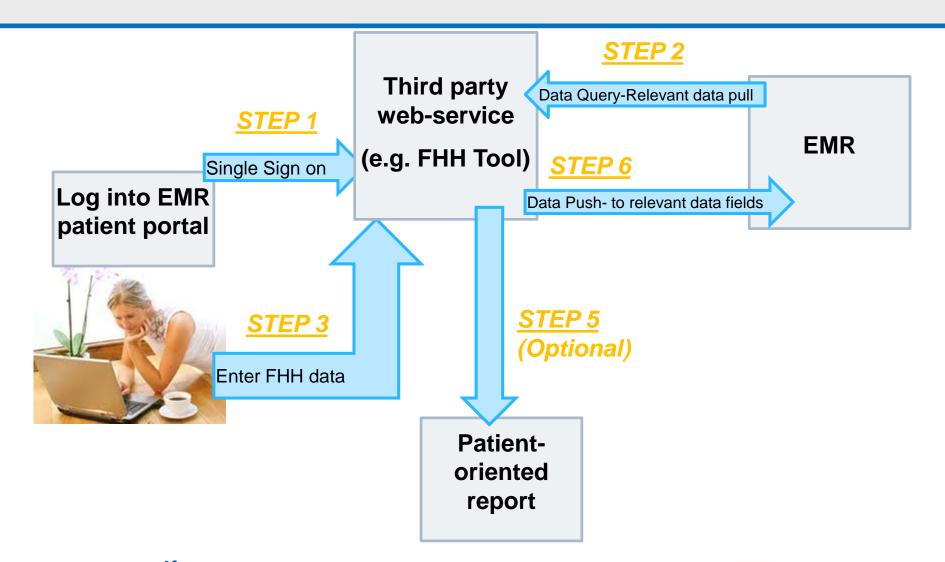
Key Features of SMART on FHIR

- Takes advantage of standards-based modern technology expanding accessibility, scalability, and interoperability.
 - HL7 now considers FHIR to be the next generation .api
 - These tools are already in use by systems like facebook and google so widely familiar to programmers outside the healthcare space
- SMART and FHIR combine authentication and data transmission in a single plug and play app
- Open source with no license fees
 - Prior to 2013 HL7 charged licensing fees and even now in some cases fees apply
- Narrowly defined data for plug and play capacity
 - The Argonaut project supported by all major stakeholders developed narrowly defined data to avoid the use of "optionality" as much as possible
 - Extension permit optionality when needed and once built by early adopters submitted to help establish a new data standard
- Widely supported by major EMR vendors





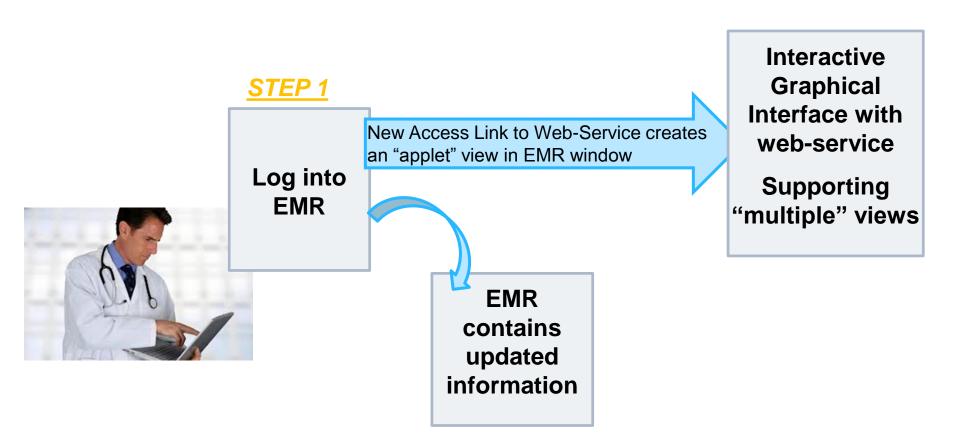
Patient Flow







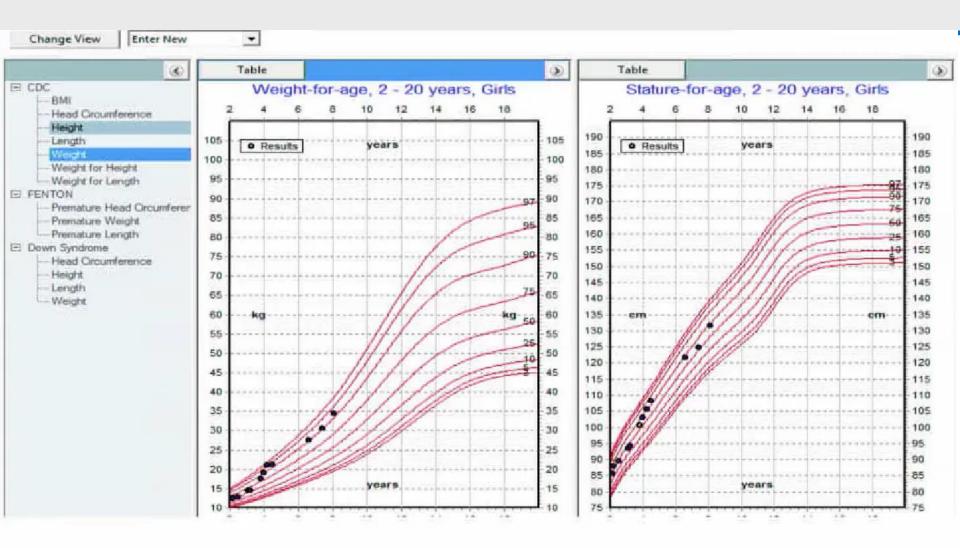
Provider Flow







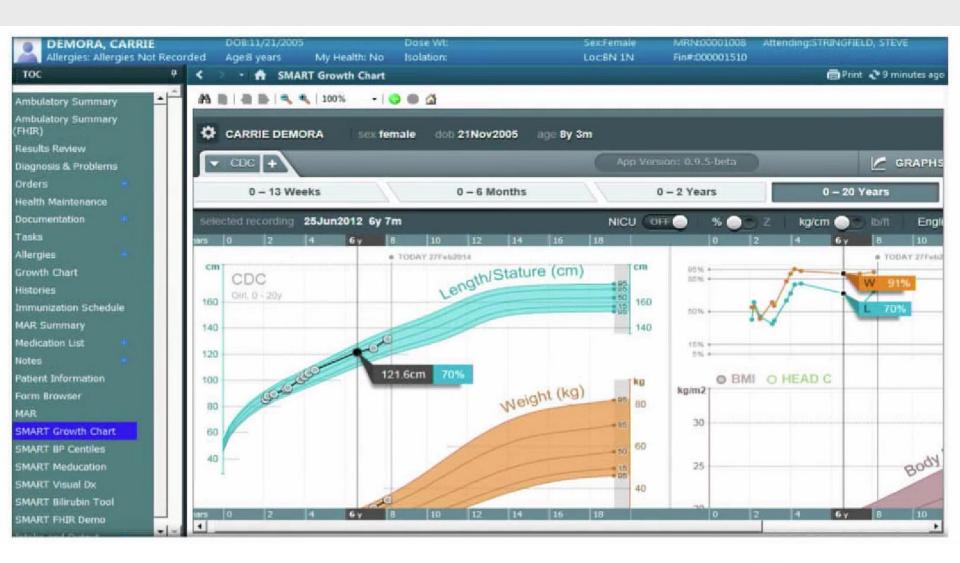
Example Provider View in Epic







Data Visualization with FHIR







Multiple Views: Patient-oriented







Questions?



