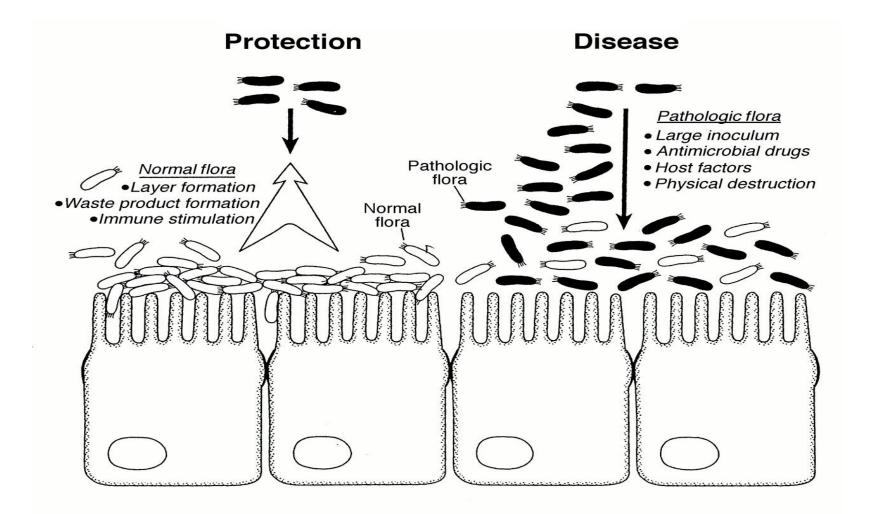
Bacterial Vaginosis: Pathogenesis, Presentation, and Diagnosis

Don Stalons, PhD, D(ABMM), MPH Dir., Clinical Laboratory, Diatherix

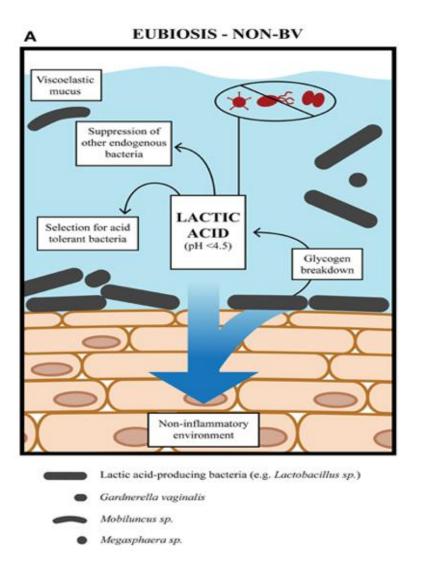


- Review the role of both pathogenic and commensal microbiota involved in urogenital infections
- Identify the methods to detect a broad range of vaginal microbiota from a single sample quickly, and cost effectively
- Discuss the practical application of the detection of a broad range of vaginal microbiota from a single sample

The Microflora of Mucosal Surfaces of the Human Body in Health and Disease



Eubiosis of the Female Vaginal Tract

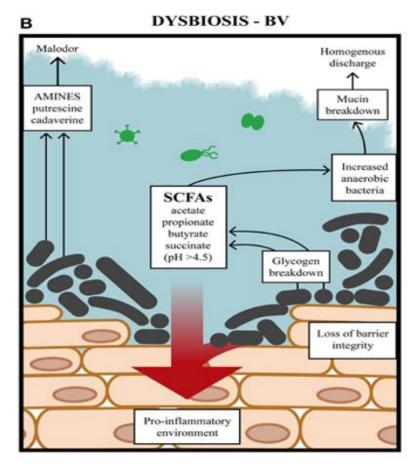


The Normal Microflora of the Vaginal Tract

- Predominant flora of lactobacilli species that colonize and secrete chemical products.
- An ecosystem that harbors a microbiota that protects it from invading pathogens including those that cause urinary tract infections and sexually transmitted diseases.
- Lactobacilli are dominant at concentrations of 10^7 to 10^8 CFU/g of vaginal fluid.
- Potential pathogens are kept at insignificant levels due to the production of large volumes of lactic acid and hydrogen peroxide

Aldunate et al. Antimicrobial and immune modulatory effects of lactic acid and short chain fatty acids produced by vaginal microbiota associated with eubiosis and bacterial vaginosis. Front. Physiol., June, 2015.

Dysbiosis of the Female Genital Tract



Prominent factors that may predispose patients to BV include:

- Recent antibiotic usage
- Decreased estrogen production of the patient
- Wearing an intrauterine device (IUD)
- Douching
- Sexual activity that could lead to transmission (e.g. having a new sexual partner or a recent increase in the number of sexual partners

- ★ Viral STI (e.g. HIV/HSV-2)
- Bacterial STI (e.g. Neisseria gonorrhoea, Chlamydia trachomatis)
- olarichomonas vaginalis

Aldunate et al. Antimicrobial and immune modulatory effects of lactic acid and short chain fatty acids produced by vaginal microbiota associated with eubiosis and bacterial vaginosis. Front. Physiol., June, 2015.

Prevotella sp. and Atopobium sp.

BV is one of the most widely studied obstetric/gynecologic infectious diseases and may affect 1/3 of women at some point in their lives

- Vaginal odor (the most common, and often initial, symptom of BV)
- Mild to moderate increase in vaginal discharge
- Vulvar irritation (not always present)
- Dysuria or dyspareunia are rare
- Disease is more prevalent in certain races and lower socioeconomic classes

These signs and symptoms were summarized by Amsel in 1983 and have become the clinical standard for BV diagnosis

- Vaginal pH > 4.5
- Presence of > 20% per HPF of "Clue cells" on wet mount examination
- Positive amine or "whiff test"
- Homogeneous, non-viscous, milky-white discharge adherent to the vaginal wall

Laboratory examination of vaginal smears and the determination of the Nugent Score

N Score = Sum of the scores for each bacterial morphotypes listed below (Note number of Organisms seen/100 X objective)

Lactobacilli	Score	Gardnerella, Bacteroides	Score	Curved Gram-negative bacilli	Score	Sum= Nugent Score	
30 or >	30 or > 0		0	0	0	0	
5-30	1	<1	1	<1	1	3	
1-4	2	1-4	2	1-4	1	5	
<1	3	5-30	3	5-30	2	8	
0	4 30 or >		4	30 or >	2	10	

Interpretation of Nugent Score

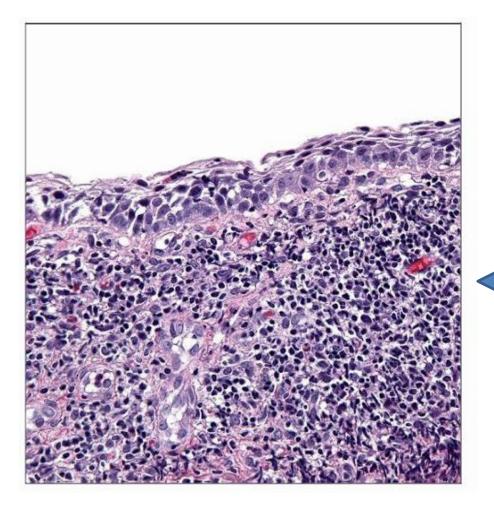
If N Score is:	AND:	Then Report				
0-3		Smear NOT consistent with BV				
4-6	Clue Cells NOT Present	Smear NOT consistent with BV				
4-6	Clue Cells ARE Present	Smear consistent with BV				
4-6		Smear consistent with BV				

Nugent RP, Krohn MA, Hillier SL. Reliability of diagnosing bacterial vaginosis is improved by a standardized method of gram stain interpretation. *J Clin Microbiol*. 1991 Feb. 29(2):297-301.

Aerobic Vaginitis

Distinguishing Features and Determination

Aerobic Vaginitis Differs from BV



- Discharge more colored and viscous
- Depletion of normal concentrations of Lactobacilli (very low numbers in more severe cases)
- Discharge is foul smelling (not the typical amine odor with BV)
- Histological appearance of desquamative inflammatory vaginitis (most severe form)
- Significant immune cytokine response (IL-1-β and IL-6)
- Cultures of often purulent discharge show Staph spp, Group B Strep, enterococci, and Gram neg bacilli (often E. coli and Klebsiella)

Nucci, M.R. Desquamative Inflammatory Vaginitis. Pathology & Laboratory Medicine. July, 2016

Presentation and Complications

- Patients complain of burning or painful sensation during intercourse
- Vulvar or vaginal itching
- Ulcerations often associated with moderate to severe case
- Aerobic vaginosis more likely associated with pregnancy complications
- Ascending chorioamnionitis
- Preterm rupture of the membranes
- Preterm delivery

Determination

- Yellow swab test
- Increased pH (> 6)
- Microscopy of wet mount
- Foul smell of discharge without application of KOH
- More esoteric tests include evaluation of cytokines (not feasible for routine practice)
- Other than those mentioned above, point of care testing is limited

The Need for Better Determination in Bacterial Vaginosis and 'Aerobic' Vaginitis

- Both disease entities often rely on subjective criteria of microscopic analysis
- Both diseases are associated with an increased risk of other sexually transmitted diseases
- These clinical entities cannot be treated and managed in the same way (see below)
- Both diseases can affect the outcome of pregnancy; often with severe consequences

Implicated Sexually Transmitted Diseases

- Chlamydia
- Gonorrhoeae
- Trichomonas
- Mycoplasma
- Ureaplasma
- HIV
- Herpes simplex I and II

Treatment Regimens

- Bacterial Vaginosis = Metronidazole or Clindamycin and restoration of Lactobacilli
- Aerobic Vaginosis = Kanamycin ovule, 2% Clindamycin topical, Ampicillin, Fluoroquinolones

Application and Unique Advantages of Molecular Technology

Identification of key organisms associated with vaginosis/vaginitis

Lactobacilli

Commensal organisms associated with colonization of the vaginal mucosal surface and are effective producers of H_2O_2 to suppress the growth of invading pathogens include:

- L. crispatus
- L. gasseri
- L. jensenii
- L. iners

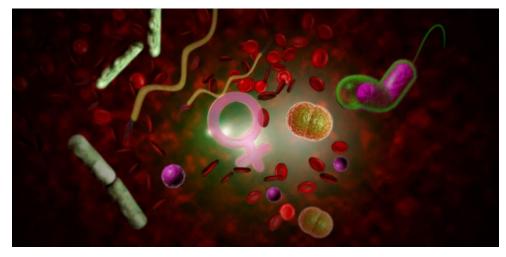
Organisms that are associated with both BV and Aerobic Vaginitis

- Clostridiales order (BVAB 1-3)
- Atopobium vaginae
- Gardnella vaginalis
- Sneathia/Leptotrichia
- Megasphaera types 1 and 2
- TM7 type bacteria

- Group B Strep
- Staph sp
 - E. coli
 - Enterococcus

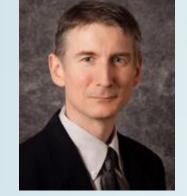
sp

- Traditional methods are subjective and lack sensitivity/specificity¹
- Reproducible molecular techniques are more empirical
- Panel-based or multiplex formats permit simultaneous detection of multiple targets associated with various conditions



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Vaginal Microbiota Testing using real-time PCR



Doug Rains, Chief Scientific Officer Quantigen

Introduction

• Main goals:

> To accurately ID pathogenic organism as quickly as possible.

- > To identify **co-infections** possibly requiring multiple drugs.
- > Ideally: identify any antibiotic resistance (future goal).

Finding a Better Approach

Ideal wish list for future infectious disease test:

- High level of specificity (preferably species-level information) and sensitivity.
- Broad coverage of the various microorganisms that can cause a similar presentation.
- A single, minimally invasive sample collection.
- Rapid turnaround times.
- Low cost per sample and easy workflow.

Panel Testing Using Real-Time PCR

- Many benefits:
 - **Specificity** Real-time PCR reports precisely which microorganism(s) are present.
 - Sensitivity Numerous CDC-acknowledged studies have demonstrated the improved detection rates of PCR-based methodologies over more traditional tests, especially for STIs.*

*Source: Morbidity and Mortality Weekly Report, Centers for Disease Control; March 14, 2014 / 63(RR02); 1-19.

Panel Testing Using Real-Time PCR

- Many benefits:
 - Broad coverage Real-time PCR comprehensive test covers 27 microorganisms from four major areas:
 - ✓ Sexually-transmitted infections (STIs)
 - ✓ Aerobic vaginitis (AV), including Group B Strep
 - ✓ Candidiasis
 - ✓ Bacterial vaginosis (details to follow)

Panel Testing Using Real-Time PCR

- Many benefits:
 - Flexibility One can choose which individual panel(s) to run, or perform a comprehensive screen in cases where either (a) presentation profile is vague or ambiguous, or (b) multiple infections are suspected.

Panel Testing Using Real-Time PCR

- Many benefits:
 - Single sample collection Panel-based real-time

PCR performs a fully comprehensive screen across all 27 organisms using a single vaginal swab.

Panel Testing Using Real-Time PCR

- Many benefits:
 - **Rapid turnaround** The ability to report full-panel

results within 12-24 hours of sample receipt.

Real-time PCR testing system

Utilizing Real-Time PCR System:

- Uses 5' nuclease chemistry (sensitive and specific).
- All assays on this panel were **pre-designed**.
- Low cost per data point / sample
- Easy workflow and quick TAT.
- Max. throughput: about 180 samples/8-hour shift.





Developing a real-time PCR bacterial vaginosis test

Studying Bacterial vaginosis: background

- A condition in which the vaginal microflora, normally dominated by lactobacillus spp., is overtaken by an array of anaerobic species.
- Often asymptomatic; when symptoms are present, most are non-specific (e.g., itching, discharge).

Developing a real-time PCR bacterial vaginosis test

Big challenges:

- No single microbe is exclusively associated with BV.
- Heavy reliance on presentation: Amsel criteria most common approach.
 - Questionable sensitivity, no accounting for lactobacilli.
- Alternatively, experienced labs can prepare a Gram-stained sample: Nugent testing.
 - Requires experience, can be time-sensitive, and is blind to species with no cell wall (e.g., mycoplasma).

Developing a real-time PCR bacterial vaginosis test

- > Better approach:
 - Characterize vaginal microflora using a highly specific and sensitive method, such as real-time PCR / 5' nuclease chemistry.
 - Survey a large collection of microbes known to associate with BV.
 - Determine which microbial signatures associate with BV (using Nugent scoring as the benchmark).
 - Develop an interpretive algorithm that is as independent
 - of sample collection technique as possible.

Microbes assessed

- Gardnerella vaginalis
- Atopobium vaginae
- Megasphera Type 1
- Megashphera Type 2
- Mycoplasma hominis
- Mobiluncus curtisii
- Mobiluncus mulieris
- Ureaplasma urealyticum

- BVAB2
- Prevotella bivia
- Lactobacillus iners
- Lactobacillus jensenii
- Lactobacillus gasseri
- Lactobcillus curtisii
- Broad-range 16s (for monitoring sample collection)

Real-time PCR BV Study Design

Phase 1a: algorithm training

- Collect 200 duplicate study swab samples one for Nugent, one for real-time PCR using large BV panel.
- Data → Bioinformatics partner for statistical analysis / development of a PCR-based interpretive algorithm that predicts BV status.

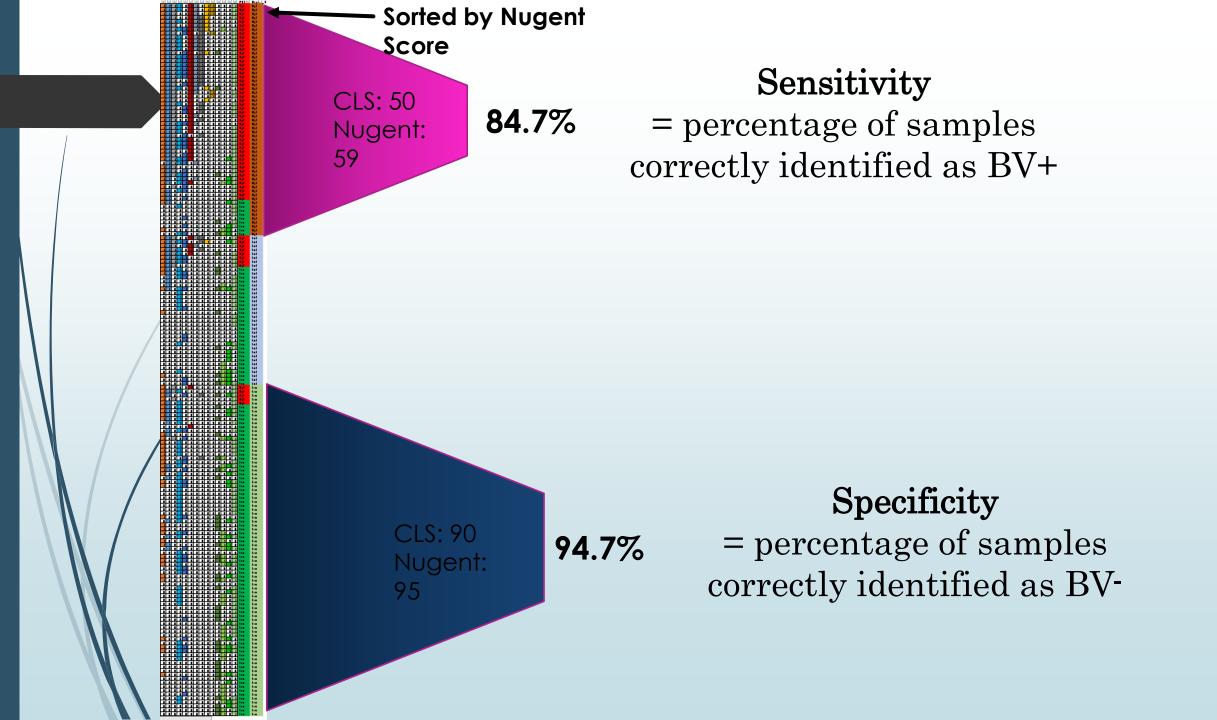
Real-time PCR BV Study Design

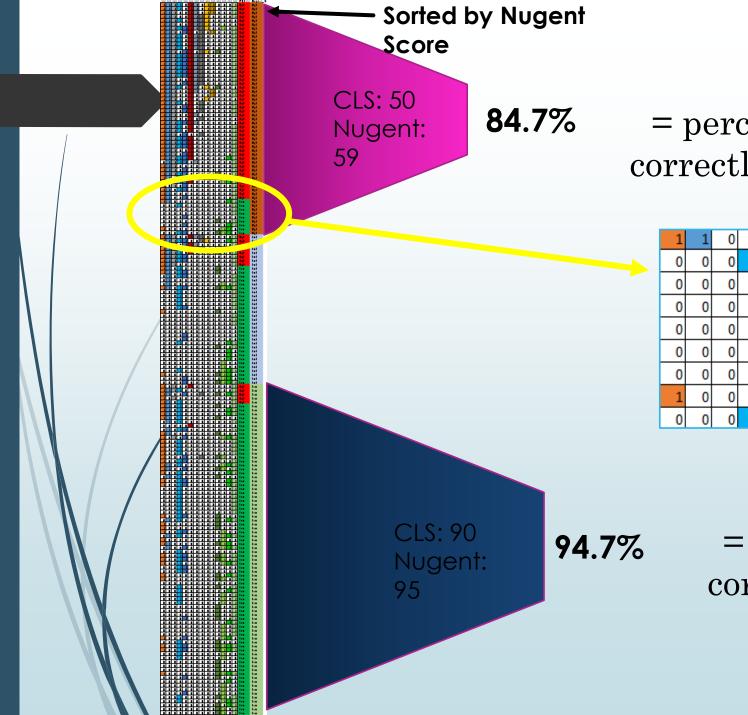
Phase 1b: algorithm validation

- Collect an additional 200 study samples for Nugent / real-time PCR.
- Apply algorithm developed in Phase 1a.
- Calculate specificity and sensitivity relative to Nugent scores.

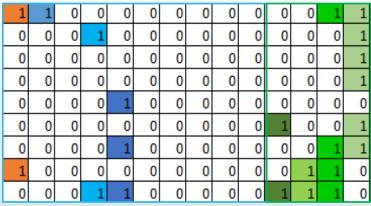
Example of Results

	.														
Nugent															
Score		G. vaginalis	A. vaginae	Megasph. 1	Megasph. 2	M. hominis	U. urealyt.	M. curtisii	BVAB2	M. mulieris	P. bivia	L. gasseri	L. iners	L. crisp.	L. jensenii
10	QG-1134-11														
8	QG-1189-2														
8	QG-1190-2														
9	QG-1197-2														
8	QG-1151-2														
8	QG-1152-2														
1	QG-1142-11														
1	QG-1133-11														
1	QG-1149-11														
1	QG-1150-21														
1	QG-1157-2														
1	QG-1158-2														
2	QG-1166-2														

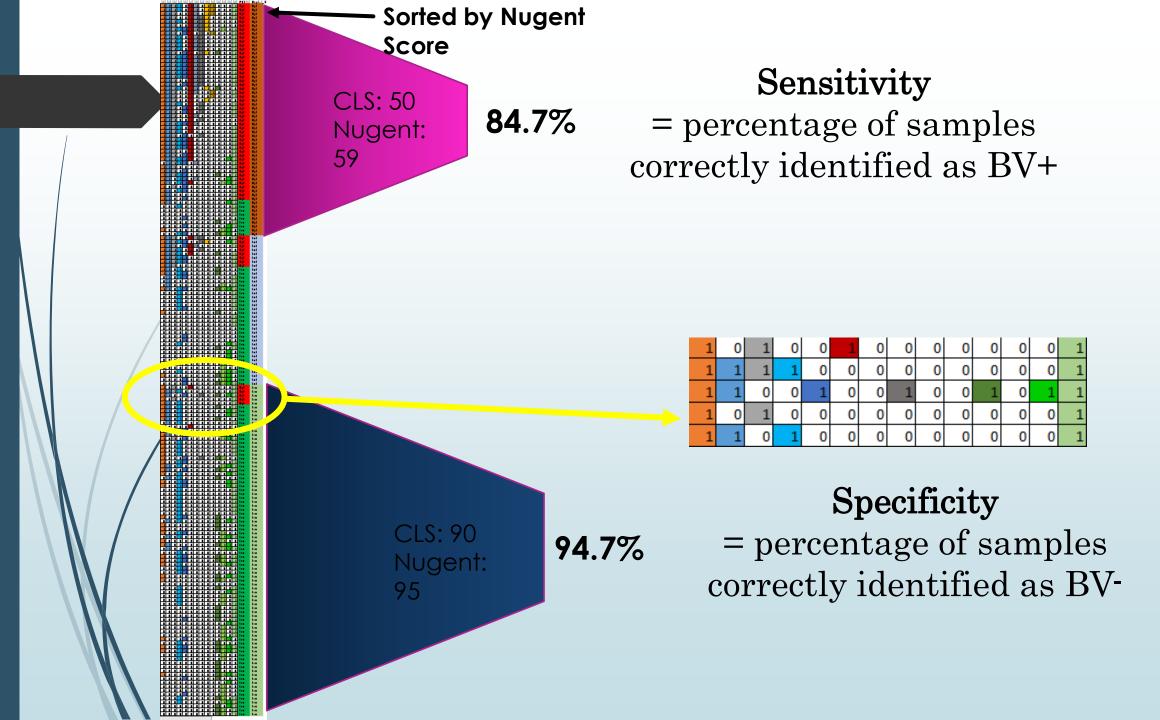




Sensitivity = percentage of samples correctly identified as BV+



Specificity = percentage of samples correctly identified as BV-



Real-time PCR BV Study: Phase 2

Phase 2 (ongoing)

- Collect an additional 200 study samples for Nugent / real-time PCR, including 50 negative subjects.
- In addition to Nugent scoring, attain putative BV status using both Amsel criteria and a secondary molecular method.
- Refine algorithm in an effort to achieve greater specificity and sensitivity.

Real-time PCR BV Study: Collaborators

A collaboration between Quantigen Laboratory in Fishers, IN, PrimeX Laboratories in Van Nuys, CA, and the Research and Development Institute (RDI) in Van Nuys, CA. Acknowledgments:

Erik Avaniss-Aghajani, PrimeX Laboratories Zohrab Bostanian, RDI Coriell Institute for Medical Research

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Developing a Molecular Assay Algorithm for Bacterial Vaginosis Determination

Jeffrey Shaman, PhD, Dir., Business Development, Coriell Life Sciences



<u>Data</u>

- Results from Real-time PCR Women's Health microorganism assay Infection Information
- Infection details and demographics from the Study

Report Requirements

- Results of assays
- Microorganism Details
- Interpretation
- Determination of BV

Coriell Life Sciences

- Borne from the 64 year old Coriell Institute for Medical Research
- Focused on empowering those who use genetics
- Support laboratories in their missions to deliver world-class molecular solutions
- Leader in Laboratory Reporting, Decision Support Tools, Medical Therapy Management, Medical Risk Reporting, Genetic Interpretation, and Pharmacogenomics

<u>Goal</u>

 Identify an Algorithm that can Recognize Patterns in the WH microorganism assay results from Real-time PCR

Success Metric

 The algorithm's output matches the Study's assessment of positive Bacterial Vaginosis

Report Requirements

- Results of assays
- Microorganism Details
- Interpretation
- Determination of BV



Report Requirements

- Results of assays
- Microorganism Details
- Interpretation
- Determination of BV

Algorithm Development Process

- Ingest raw data
 - 400 samples
- Convert raw data into usable form
 - Linearize Ct
- Apply statistical models to a training subset
 - (linear, logarithmic, orthogonal transformations, etc.)
- Evaluate wide variety of models- apply algorithm to validation set of data
- Choose model that meets success metrics

Algorithm Development Process Raw Data

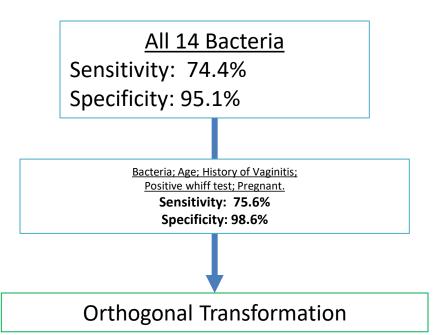
		c 1								· · ·				
	7_2016_VGL46													
-	* Experiment Name = VGL46													
-	* Experiment Run End Time = Not Started													
-	* Experiment Type = Gene Expression													
	* Instrument Name = 285880760													
	* Instrument Serial Number = 285880760													
.3 * Passive Reference =														
14 * Quantification Cycle Method = Ct														
15 * Signal Smoothing On = true														
16 * Stage/ Cycle where Analysis is performed = Stage 2, Step 3														
17 * User N	ame = NA													
18														
19 [Results]													
20 Well	Well Positic	on Omit	Sample Name	Target N	ame Task	Reporte	er Qu	encher	Ct Ct	Mear	1 Ct	SD	Amp Score	Cq
Conf CRI	AMPLITUDE	HIGHSD C	CRTNOISE RO	X Signal										
21 1 A1a1	false	QG-1001 AI	ICSW7C UNKNOWN	FAM NFQ-	MGB Unde	termined		0.000	0.000	Y	N	Y	6,882.794	
22 2 Ala2	false	QG-1001 AI	ICSW7C UNKNOWN	FAM NFQ-	MGB Unde	termined		0.000	0.000	Y	N	Y	5,844.265	
23 3 Ala3	false	QG-1001 AI	ICSW7C UNKNOWN	FAM NFQ-	MGB Unde	termined		0.000	0.000	Y	N	Y	5,817.441	
24 4 Ala4	false	QG-1001 AI	ID1VDK UNKNOWN	FAM NFQ-	MGB Unde	termined		0.000	0.000	Y	N	Y	5,667.353	
25 5 Ala5	false	QG-1001 AI	ID1VDK UNKNOWN	FAM NFQ-	MGB Unde	termined		0.000	0.000	Y	N	Y	5,684.471	
26 6 Ala6	false	QG-1001 AI	ID1VDK UNKNOWN	FAM NFQ-	MGB Unde	termined		0.000	0.000	Y	N	Y	5,204.382	
27 7 A1a7	false	OG-1001 AI	IN1GRC UNKNOWN	FAM NFO-	MGB Unde	termined		0.000	0.000	Y	N	Y	5,643.294	
28 8 Ala8	false		IN1GRC UNKNOWN					0.000	0.000	Y	N	Y	5,255.324	
29 9 A1b1			IN1GRC UNKNOWN					0.000	0.000	Y	N	Y	7,852.353	
30 10 A1b2	false		IQJCRB UNKNOWN	FAM NFO-	MGB Unde	termined		0.000	0.000	Y	N	Y	7,296.853	
31 11 A1b3			QJCRB UNKNOWN					0.692	0.000	Y	N	Y	6,611,441	
32 12 A1b4	false		IQJCRB UNKNOWN					0.000	0.000	Y	N	Y	6,273.706	
33 13 A1b5			IGJRP0 UNKNOWN				0.360	1.575	0.967	N	N	N	6,436.265	
34 14 A1b6			IGJRP0 UNKNOWN				0.360	1.599	0.980	N	N	N	6,607.941	
35 15 A1b7			IGJRP0 UNKNOWN				0.360	1.588	0.983	N	N	N	6,336.294	
36 16 A1b8			THSPV8 UNKNOWN					0.000	0.000	Y	N	Y	6,247.441	
37 17 A1c1			THSPV8 UNKNOWN					0.000	0.000	Ŷ	N	Ŷ	6,434.382	
38 18 A1c2			LHSPV8 UNKNOWN					0.548	0.000	Y	N	Y	6,021.059	
39 19 A1c3			101XJR UNKNOWN					0.674	0.000	Y	N	Y	5,976.471	
40 20 A1c4			101XJR UNKNOWN 101XJR UNKNOWN					0.000	0.000	Y	N	Y	5,604.529	
40 20 Ale4 41 21 Alc5			101XJR UNKNOWN 101XJR UNKNOWN					0.000	0.000	Y	N	Y	6,067.794	
41 21 Ales			IRSAXK UNKNOWN					0.781	0.000	Y	N	Y	5,869.029	
43 23 A1c7								0.000	0.000	Y	N	Y	5,888.941	
			IRSAXK UNKNOWN											
44 24 A1c8			IRSAXK UNKNOWN				0.000	0.000	0.000	Y	N	Y	5,675.529	
45 25 Ald1			IMSH8N UNKNOWN					1.591	0.964	N	N	N	6,407.441	
46 26 Ald2			IMSH8N UNKNOWN				0.262	1.591	0.958	N	N	N	6,139.412	
47 27 Ald3			IMSH8N UNKNOWN				0.262	1.590	0.971	N	N	N	5,955.941	
48 28 Ald4			II1NRX UNKNOWN					0.000	0.000	Y	N	Y	5,802.765	
49 29 Ald 5	false	QG-1001 AI	II1NRX UNKNOWN	FAM NFQ-	MGB Unde	termined		0.000	0.000	Y	N	Y	6,034.471	
rmal text file	~ ~				th:282171		1	: 149 Sel : 0				Wind	ows UTF-8	INS

Algorithm Development Process Raw Data

Evaluated 53 Distinct Models clustered the samples

wheat of	numbere	highlight about the feature subset				specificity	nan = max_neg. specificity	
subset of	number o	highlight about the feature subset	sensitivity	sensitivity	sensitivity			
			> 7 => BV+	> 6 => BV+	> 5 => BV+	< 4 => BV-	< 5 => BV-	
feature 🔻	num_fe 🔻	note_feature	sen_mip_ 👻	sen_mip_ 斗	sen_mip_ 👻	spe_man_ 🔻	spe_man_	
set16	30	pos_whiff, Pregnant; 14 bac log ^2, ^1	0.4634	0.6951	0.7439	0.8732	0.9789	
set18	31	History_of_Vaginitis_bin, pos_whiff, Pregnant; 14 bac	0.4634	0.6951	0.7439	0.8873	0.9859	
set13	30	Age, Pregnant; 14 bac log ^2, ^1	0.4878	0.6829	0.7439	0.8662	0.9859	
set15	29	Pregnant; 14 bac log ^2, ^1	0.4756	0.6829	0.7439	0.8662	0.9859	
set17	30	History_of_Vaginitis_bin, Pregnant; 14 bac log ^2, ^1	0.4634	0.6829	0.7317	0.8803	0.9859	
set19	32	Age, History_of_Vaginitis_bin, pos_whiff, Pregnant; 14	0.4512	0.6829	0.7439	0.8803	0.9859	
set20	28	12 bac log ^2, ^1; Age, History_of_Vaginitis_bin, pos_w	0.4878	0.6829	0.7561	0.8873	0.9859	
set23	26	pos_whiff, Pregnant; 12 bac log ^2, ^1	0.5	0.6829	0.7561	0.8803	0.9789	
set30	30	13 bac log ^2, ^1; Age, History_of_Vaginitis_bin, pos_w	0.4756	0.6829	0.7439	0.8803	0.9859	
set31	30	13 bac log ^2, ^1; Age, History_of_Vaginitis_bin, pos_w	0.4878	0.6829	0.7439	0.8873	0.9859	
set32	29	1 inter; 12 bac log ^2, ^1; Age, History_of_Vaginitis_bin	0.4634	0.6829	0.7561	0.8944	0.9859	
set01	29	14 bac log ^1; all others	0.4024	0.6707	0.7439	0.8591	0.9507	
set01	29	14 bac log ^1; all others	0.4024	0.6707	0.7439	0.8591	0.9507	
set04	33	9 bac log ^2, ^1; all others	0.5244	0.6707	0.7439	0.8451	0.9437	
set05	42	9 bac log ^3, ^2, ^1; all others	0.5244	0.6707	0.7439	0.8451	0.9437	
set06	44	1 inter; 14 bac log ^1, ^2; all others	0.4512	0.6707	0.7439	0.8662	0.9648	
set11	28	no others; 14 bac log ^2, ^1	0.4878	0.6707	0.7317	0.8732	0.9859	
set12	30	History_of_Vaginitis_bin, pos_whiff; 14 bac log ^2, ^1	0.4878	0.6707	0.7317	0.8732	0.9859	
set21	27	12 bac log ^2, ^1; History_of_Vaginitis_bin, pos_whiff,	0.4756	0.6707	0.7439	0.9014	0.9859	
set22	26	12 bac log ^2, ^1; History_of_Vaginitis_bin, Pregnant	0.4878	0.6707	0.7317	0.8873	0.9859	
set24	26	11 bac log ^2, ^1; Age, History_of_Vaginitis_bin, pos_w	0.4756	0.6707	0.7439	0.8944	0.9789	
set25	29	1 bac log^3, 12 bac log ^2, ^1; Age, History_of_Vaginitis	0.4878	0.6707	0.7561	0.8803	0.9789	
set26	26	11 bac log ^2, ^1; Age, History_of_Vaginitis_bin, pos_w	0.4878	0.6707	0.7561	0.8873	0.9859	
set27	24	10 bac log ^2, ^1; Age, History_of_Vaginitis_bin, pos_w	0.4878	0.6707	0.7439	0.8873	0.9789	
set28	29	1 bac log^3, 12 bac log ^2, ^1; Age, History_of_Vaginitis	0.4878	0.6707	0.7439	0.8873	0.9859	
set29	30	2 bac log^3, 12 bac log ^2, ^1; Age, History_of_Vaginitis	0.4878	0.6707	0.7439	0.8803	0.9789	
set33	29	1 inter; 12 bac log ^2, ^1; Age, History_of_Vaginitis_bin	0.4756	0.6707	0.7561	0.9014	0.9859	
set34	30	2 inter; 12 bac log ^2, ^1; Age, History_of_Vaginitis_bin	0.4634	0.6707	0.7561	0.8944	0.9859	
set01	29	14 bac log ^1; all others	0.4024	0.6585	0.7439	0.8591	0.9507	
set07	42	13.5 bac log ^2, ^1; all others	0.4634	0.6585	0.7439	0.8732	0.9648	
set08	41	13 bac log ^2, ^1; all others	0.4756	0.6585	0.7439	0.8732	0.9648	
set09	39	12 bac log ^2, ^1; all others	0.4878	0.6585	0.7439	0.8732	0.9648	
set14	29	Age; 14 bac log ^2, ^1	0.4878	0.6585	0.7317	0.8662	0.9859	
set02	43	14 bac log ^2, ^1; all others	0.4634	0.6463	0.7439	0.8732	0.9648	
set03		14 bac log ^3, ^2, ^1; all others	0.4634	0.6463	0.7195	0.8521	0.9437	
set10	39	no ethnicity; 14 bac log ^2, ^1; all others	0.4512	0.6463	0.7439	0.8662	0.9648	
set01		14 bac log ^1; all others	0.2979	0.5957	0.7447	0.7882	0.9059	

for the way they

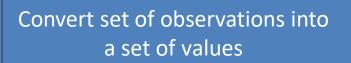


Algorithm Development Process Raw Data

Convert Data for Evaluation of Orthogonal Transformation Model

0 2 4.5442 1.5442 1.5442 1.5442 1.5442 1.5442 1.5442 1.5442 1.54444 1.54444	Pathogenic	Lactobacillus		
10 0.001 0 0 0 0 0 0 0.001 0.0	ID 🖃	Bacteria	Bacteria	
11 Gold 2018 G G G G G G G G G G G G G G G G G G G	QG-1003	0 0 0 1 0 0 0 0 0	0 0 0 1	
10 0.0184 1.175:0 0.464 0 0.186:0 0 0 7.355:0 0 0 10 0.0141 1.186:0 0 0 2.186:0 0 0 7.355:0 0 0 10 0.0141 1.186:0 0 0 2.186:0 0 0 1.186:0 0 0 2.186:0 0 </th <th>QG-1005</th> <th></th> <th>0 0 0 1</th>	QG-1005		0 0 0 1	
21 00-5140 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	QG-1006		0 0 0 0	
Image: State Stat	QG-1010		0 1 1 0	
$\begin{array}{c c c c c c c c c c c c c c c c c c c $				
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	QG-1012	0 1 1 1 1 0 1 0 0	0 0 0 1	
Control Definition	QG-1013		0 0 0 1	
All Gradienty Letter 0 Constrain Letter 0 Con	QG-1015		1 1 1 1	
2G-1022 1 1 0 0 0 0 0 1 0 0 2G-1025 1 0 0 0 0 0 0 0 1 0 0	QG-1017		0 1 1 0	
<u>2G-1026</u> 00000010010000000000000000000000000	QG-1018		1 1 0 0	
1G-1030 0 0 0 0 0 0 0 0 0 1 0 0	QG-1022		1 0 0 0	
QG-1031 1 0 1 0 0 0 0 0 1 0 1 1 QG-1034 1 1 1 0 1 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 1 0 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 1 0 0 0 1 0 0 0 0 1 0				
QG-1037 1 1 0 1 1 1 0 1 </td <td>QG-1025</td> <td></td> <td>1 0 0 0</td>	QG-1025		1 0 0 0	
QG-1043 0 1 0 0 1 0 0 1 0 QG-1045 0 0 0 0 0 0 0 0 0 0	QG-1026	0 0 0 1 1 0 0 0 0	0 0 0 0	
2G-1046 1 0 1 0 0 1 </td <td>QG-1029</td> <td></td> <td>0 0 0 1</td>	QG-1029		0 0 0 1	
2G-1051 0 1 0 0 0 0 0 0 1 0 2G-1052 1 0 0 0 1 0 0 0 0 0 1 0	QG-1030	0 0 0 0 0 0 0 0 0	1 0 0 0	
1G-1053 1 1 1 0 0 0 0 0 1 0 1 0	QG-1031		0 1 1 1	
LG-1056 1 0 1 0 0 0 0 0 0 1 0 1 0				
QG-1057 1 1 0 0 1 0 0 1 </td <td>QG-1034</td> <td></td> <td>0 0 0 1</td>	QG-1034		0 0 0 1	
QG-1061 1 1 0 0 1 0 0 1 1 0 QG-1063 1 1 1 0 0 0 1 1 0 0 1 0 <	QG-1037		0 0 0 1	
2G-1065 1 0 0 0 1 1 1 1 2G-1067 0 0 0 0 1 0 0 0 1 1 1	QG-1041		0 1 0 0	
QG-1068 1 0 0 0 1 0 1 </td <td>QG-1043</td> <td>0 1 0 1 1 0 0 0 0</td> <td>0 0 0 1</td>	QG-1043	0 1 0 1 1 0 0 0 0	0 0 0 1	
<u>26-1070</u> 0 0 0 0 0 0 0 0 0 0 1 1 0	QG-1045		0 0 0 0	
2G-1074 1 1 1 0 1 1 0 1 1 0 0	QG-1046		0 0 0 1	
	QG-1049		0 0 0 1	
	QG-1051	0 1 0 0 0 0 0 0 0	0 0 0 1	
	QG-1052		0 0 0 1	
	OG-1053			

	Pathogenic											Lactobacillus				
ID 🖃		Bacteria											Bacteria			
QG-1003	0	0	0	1	0	0	0	0	0	C	0	0	0	1		
QG-1005	1	1	1	1	0	1	0	1	0	C	0	0	0	1		
QG-1006	1	1	1	1	1	1	1	0	0	C	0	0	0	0		
QG-1010	1	0	0	0	1	0	0	0	0	C	0	1	1	0		
QG-1012	0	1	1	1	1	0	1	0	0	C	0	0	0	1		
QG-1013	1	1	1	0	1	1	0	0	0	C	0	0	0	1		
QG-1015	1	1	0	1	1	0	0	0	0	C	1	1	1	1		
QG-1017	0	0	0	1	0	0	0	0	0	C	0	1	1	0		
QG-1018	0	0	0	0	1	0	0	0	0	C	1	1	0	0		
QG-1022	1	1	0	0	0	0	0	0	0	C	1	0	0	0		
QG-1025	1	0	0	0	0	0	0	0	0	C	1	0	0	0		
QG-1026	0	0	0	1	1	0	0	0	0	C	0	0	0	0		
QG-1029	1	1	1	1	1	1	0	0	0	C	0	0	0	1		
QG-1030	0	0	0	0	0	0	0	0	0	C	1	0	0	0		
QG-1031	1	0	1	0	1	0	0	0	0	C	0	1	1	1		
QG-1034	1	1	1	0	0	1	1	0	0	C	0	0	0	1		
QG-1037	1	1	1	1	1	1	1	1	0	C	0	0	0	1		
QG-1041	1	0	0	1	1	0	0	0	0	C	0	1	0	0		
QG-1043	0	1	0	1	1	0	0	0	0	C	0	0	0	1		
QG-1045	0	0	0	0	1	0	0	0	0	C	0	0	0	0		
QG-1046	1	0	1	0	0	1	0	0	0	C	0	0	0	1		
QG-1049	1	1	1	1	0	1	1	0	1	1	0	0	0	1		
QG-1051	0	1	0	0	0	0	0	0	0	(0	0	0	1		
QG-1052	1	0	0	1	0	0	0	0	0	(0	0	0	1		
OG-1053		4	- 1	0	- 1	0	0	0	0			0	0	4		



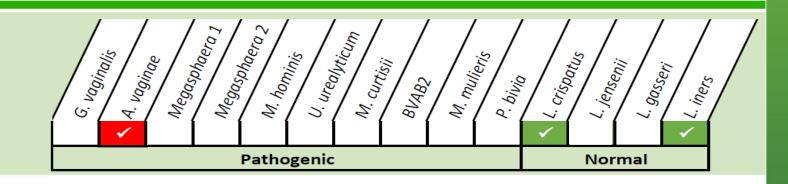
CLS1 Score 0.812002 -3.65964 -3.33897 1.374516 -1.92621 -2.43526 0.689537 1.862487 1.926656 0.103814 0.861521 1.052761 -2.51703 1.464104 0.183106 -3.49796 -4.65665 0.879888 0.087137 1.134531 -1.7104 -6.36313 0.136064 0.209419

CLS1 Algorithm sensibly groups specimens according to bacterial presence

- The CLS1 High group contains only 5% of Nugent Lows; those 5 samples "look" pathogenic
 – CLS1 High = BV+
- The CLS1 Lows are Nugent Lows with a mix of additional Nugent categories (Intermediates, Highs)
 – CLS1 Low = Not conclusive for Bacterial Vaginosis
- "Exceptions" to the CLS1 Algorithm make biological sense

CLS1 Algorithm Result = LOW

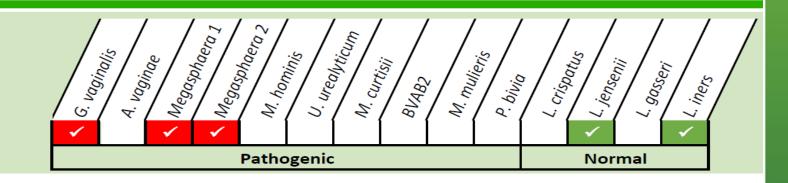




• Investigation outcomes: The pattern of pathogenic and normal bacterial flora does not suggests bacterial vaginosis.

CLS1 Algorithm Result = HIGH

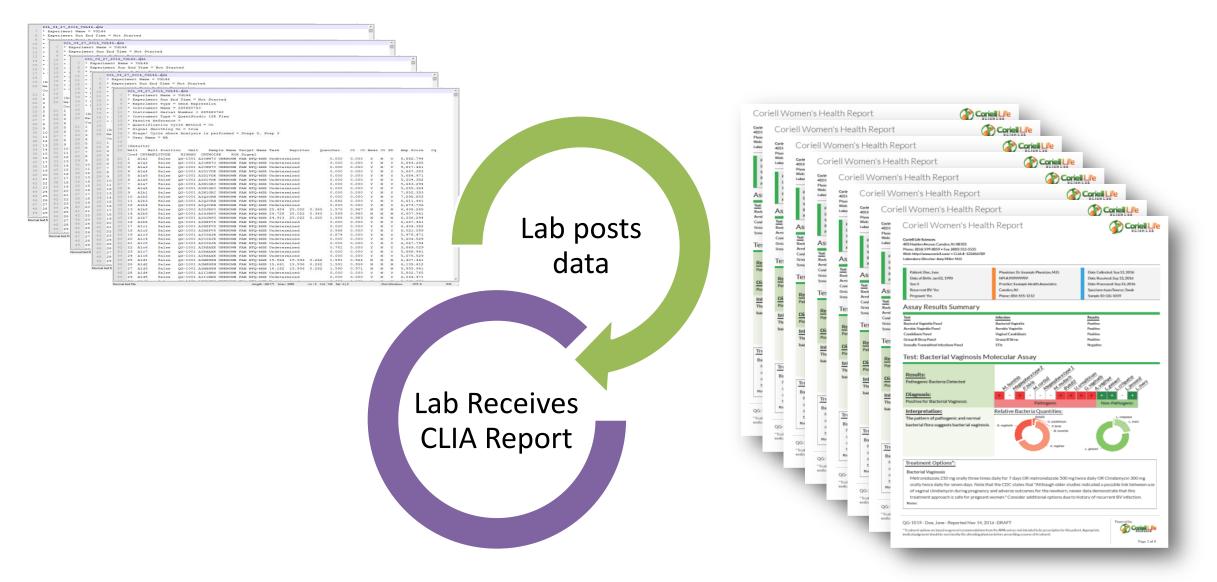




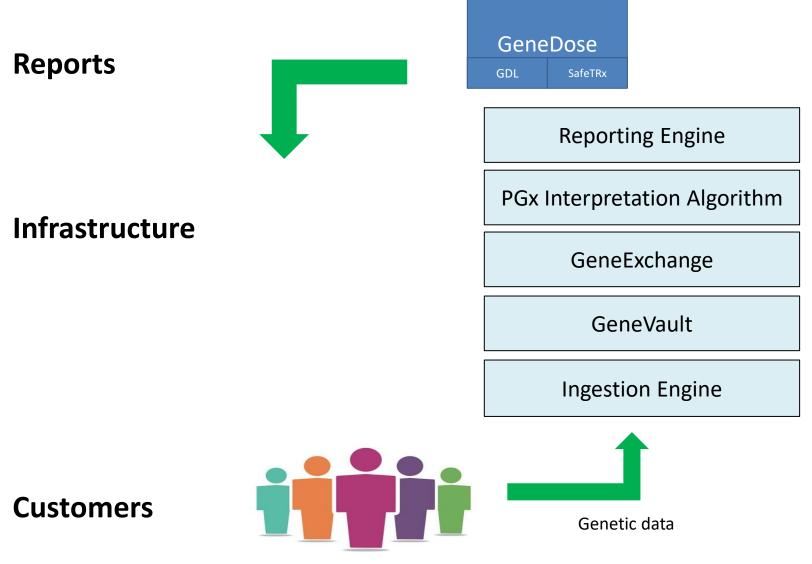
• Interpretation: The pattern of pathogenic and normal bacterial flora suggests bacterial vaginosis.

CLS REPORTING SOLUTIONS -EXAMPLES

Simple Reporting Process

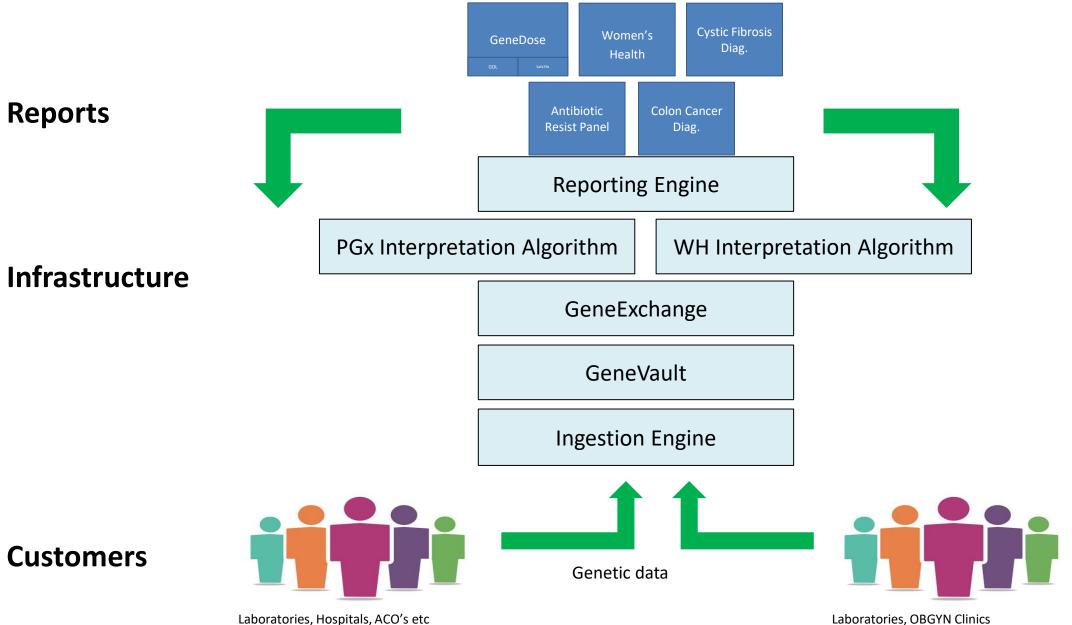


Process and Architecture

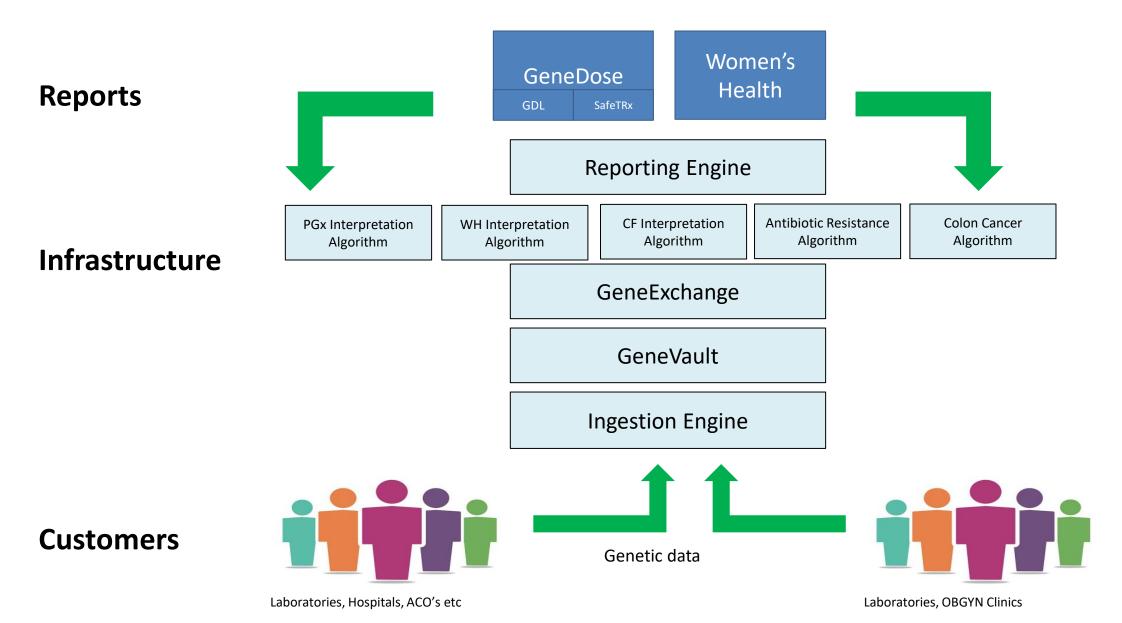


Laboratories, Hospitals, ACO's etc

Process and Architecture



Process and Architecture



- Support laboratories in their missions to deliver world-class diagnostic solutions
- Complete Decision Support
- Actionable based on Study with Quantigen and ThermoFisher Scientific
- Customizable reports logos, branding, and panels