



Expert Models for Decision Makers™

Molecular-based Surveillance in Food
Manufacturing Facilities Using Next Generation
Sequencing Techniques and Software

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IAFP Europe 2016

BACKGROUND

Background

Phylogenetic Profiles of In-House Microflora in Drains at a Food Production Facility: Comparison and Biocontrol Implications of *Listeria*-Positive and - Negative Bacterial Populations

Edward Fox, Katie Solomon, John Moore, Patrick Wall
and **Séamus Fanning**

Applied and Environmental Microbiology, **2014**,
80(11):3369

Study

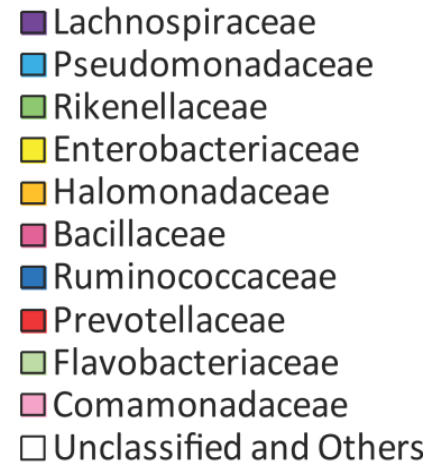
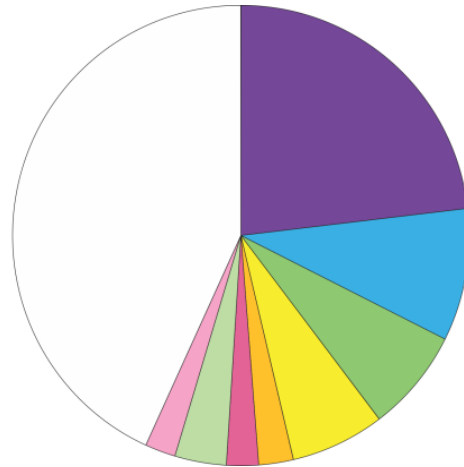
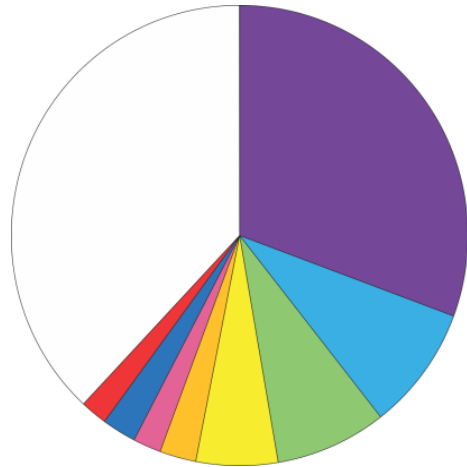
- Examined interaction between *Listeria* species and other microorganisms
- Data gathered from drains in a meat production facility
- Four drains examined – two *Listeria* positive, two *Listeria* negative
- Microbiome of drains examined, and overall diversity analysed



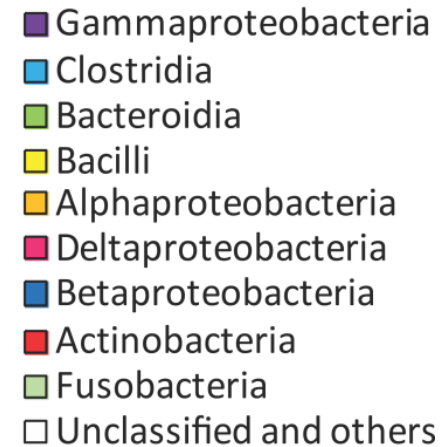
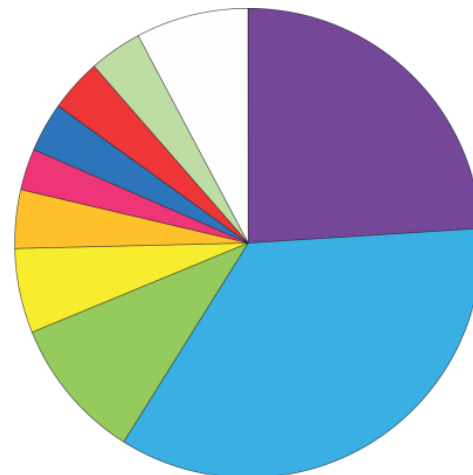
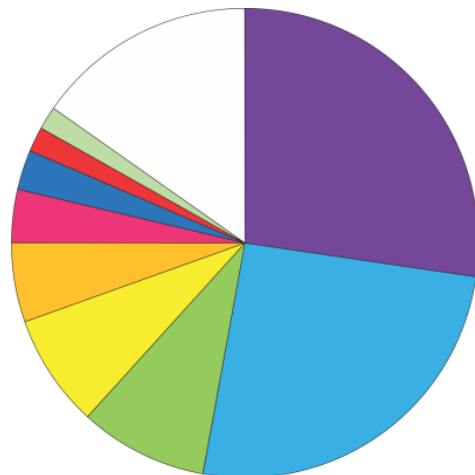
Microbiome Analysis

Negative

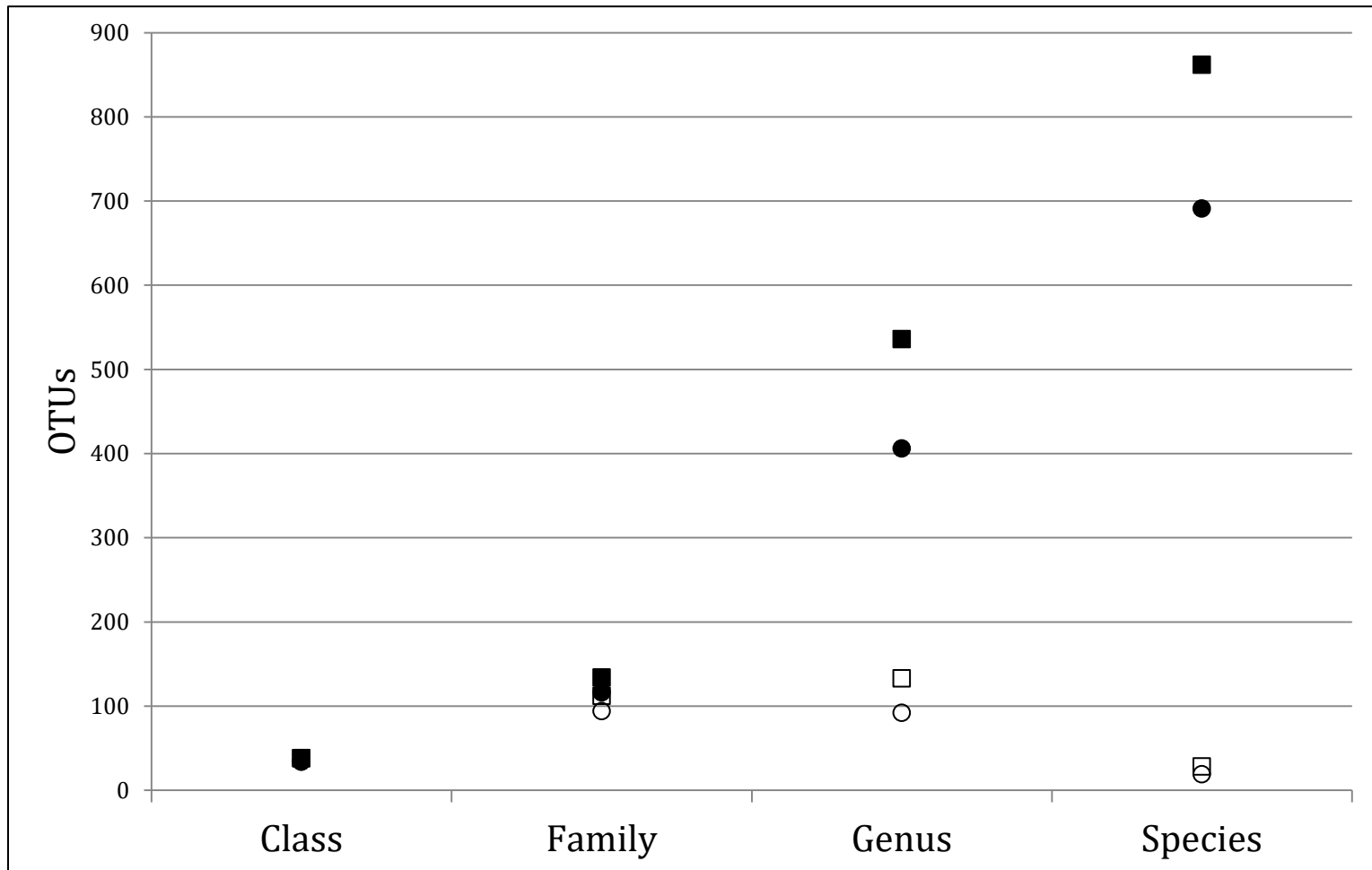
Positive



Classes



Families



●: *Listeria*-negative drains, overall diversity; ○: *Listeria*-negative drains, classified OTUs only; ■: *Listeria*-positive drains, overall diversity; □: *Listeria*-positive drains, classified OTUs only.

Results

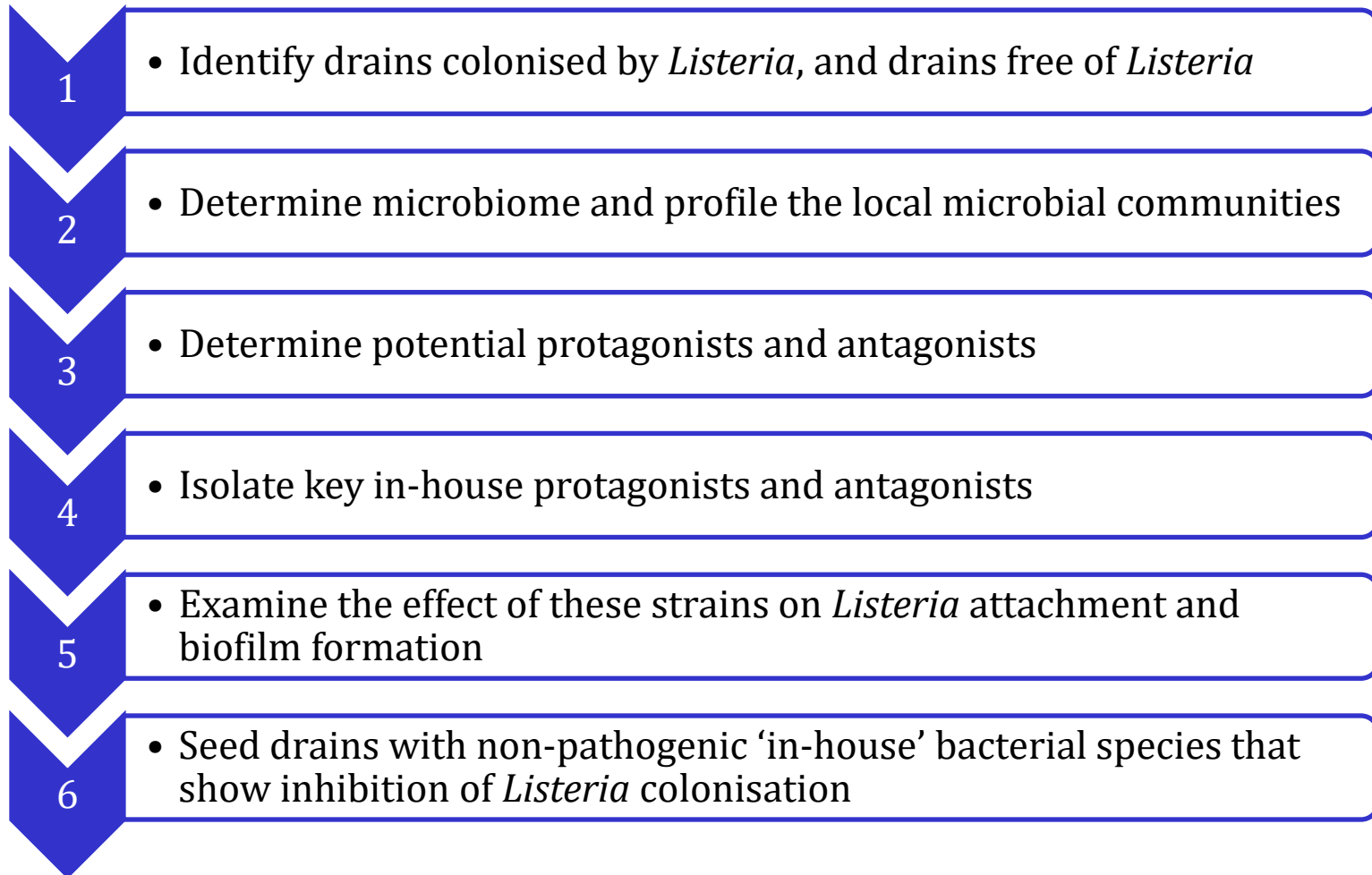
Microbiome

- 21 families found *only* in Listeria positive drains
- Janthinobacterium, Prevotella, and Pseudomonas all associated with higher abundance in Listeria-negative drains

Co-Culturing

- Presence of *J. Lividum* reduced the attachment and biofilm growth of *L. monocytogenes*
- *E. Gallinarum* caused significant increase in *L. monocytogenes* attachment and biofilm formation

Suggested Control Strategy



Questions

- Can we quantify the relationship between the microbiome of a manufacturing facility and specific bacteria of interest?
- Can we quantify/predict what would be an effective biocontrol strategy?
- Can we examine specific bacteria using WGS in parallel with the microbiome?
- What traits can be identified using WGS and monitored over time and space?

THE S.A.F.E. PROJECT

The SAFE Project

- Sequencing Alliance for Food Environments
- Three year project in collaboration with:
 - University College Dublin Centre for Food Safety (UCD-CFS)
 - Five postdoctoral researchers
 - Creme Global
 - Six industry partners

Project Goals

Develop a pipeline of data using genome-based technology (WGS & WMS)

Develop mathematical models of safety and quality

Link gene-based information to phenotype for tracking/tracing of bacteria of interest

Use phenotypic data to highlight potential solution strategies to food safety and quality

Provide software tools to improve food safety & quality decision making steps

Tasks

Task 1

- Sampling plan design

Task 2

- Whole Genome Sequencing
- Microbiome Characterisation

Task 3

- Bioinformatic analysis

Task 4

- Production solution scenarios

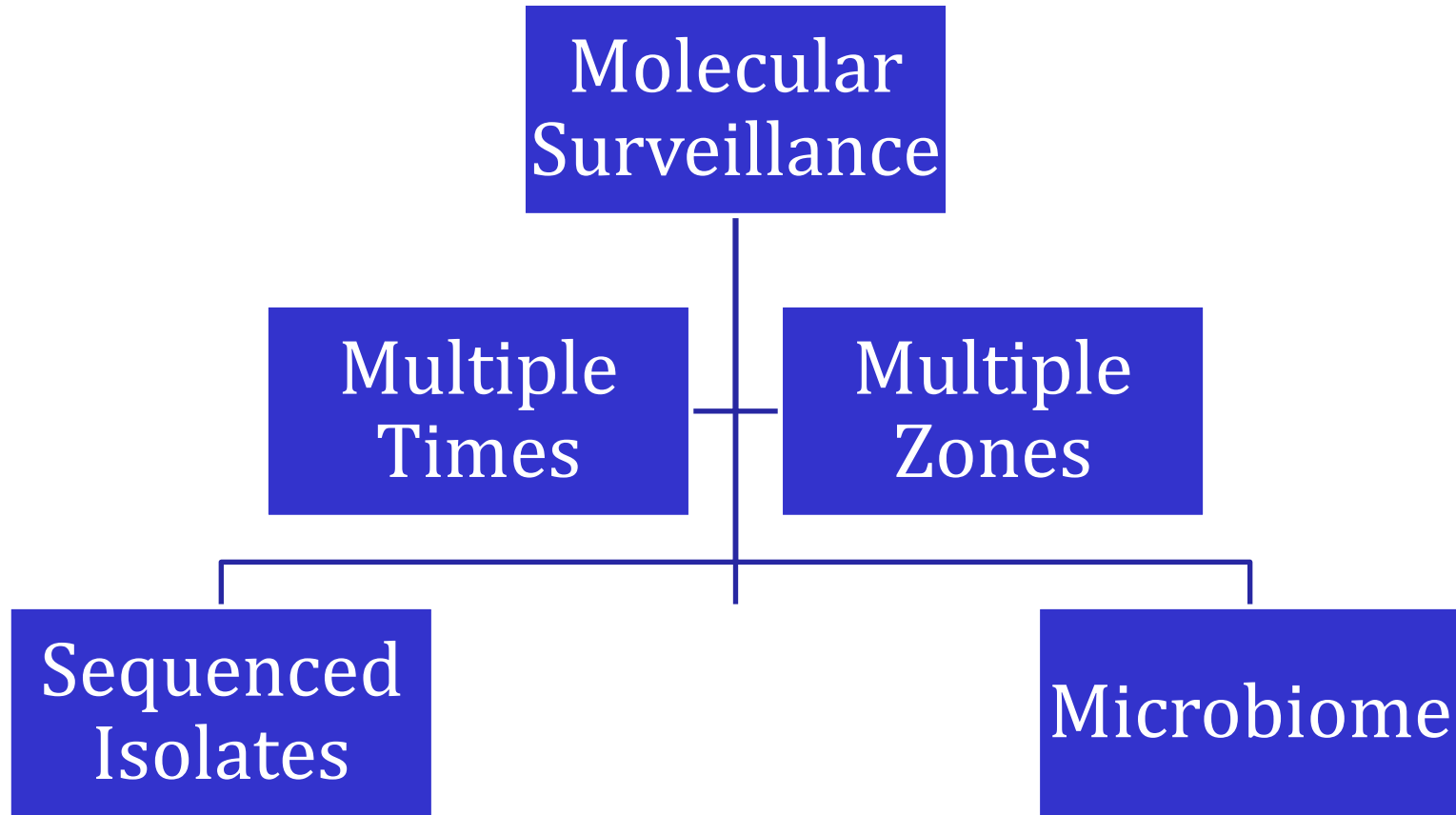
Task 5

- Modelling and Software

Industry Partners

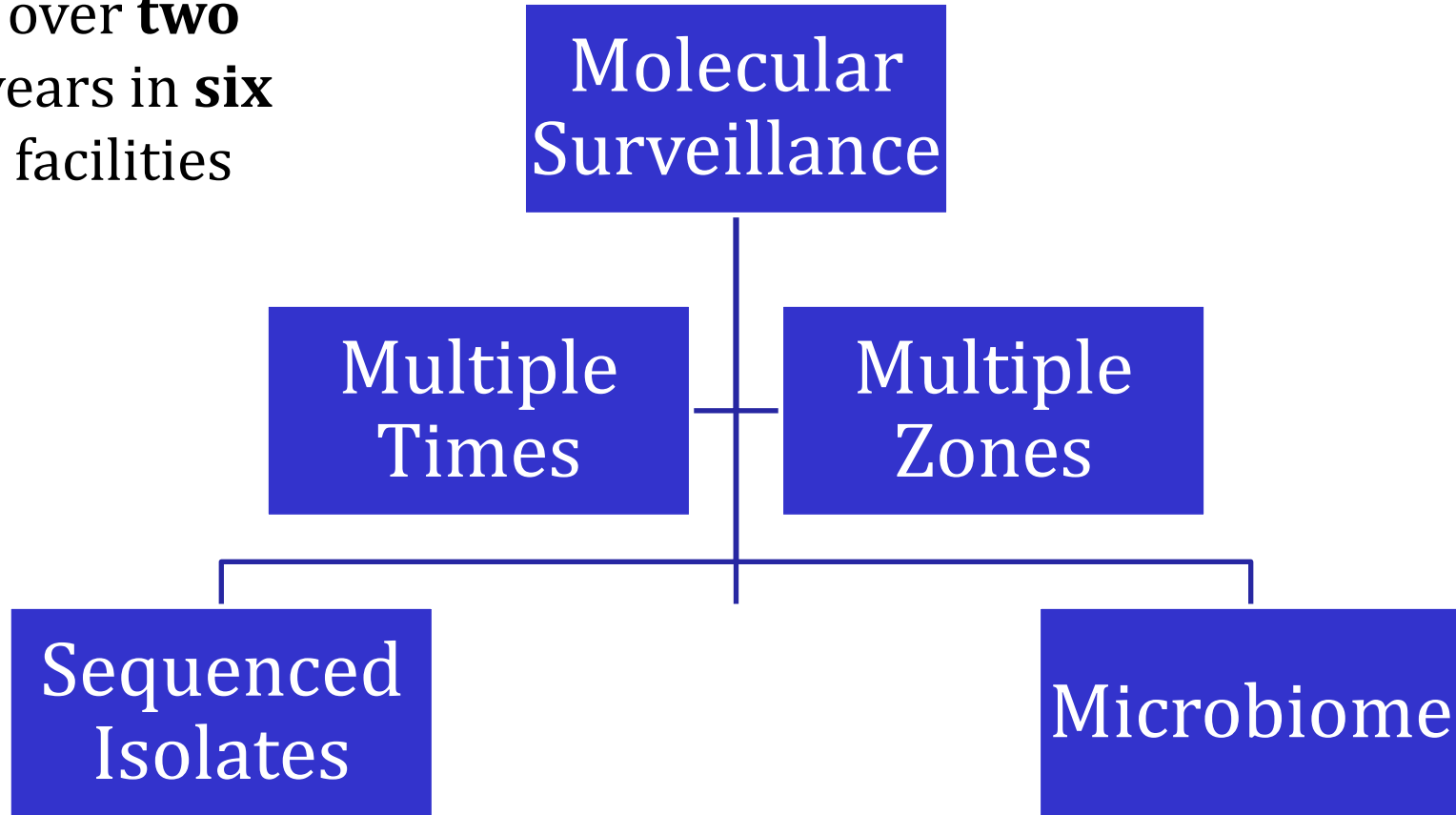


Sampling Plan



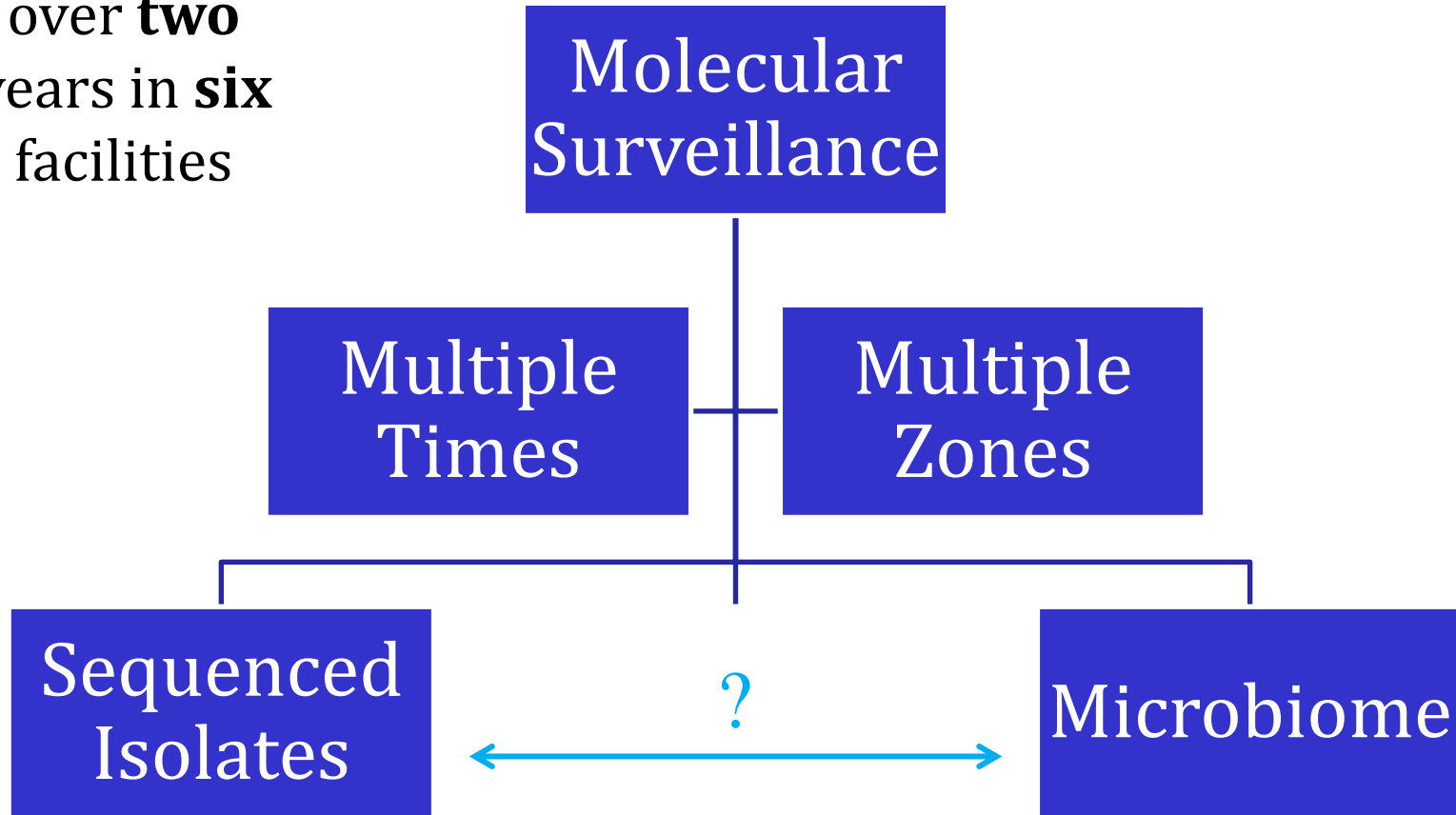
Sampling Plan

Monitored
over **two**
years in **six**
facilities

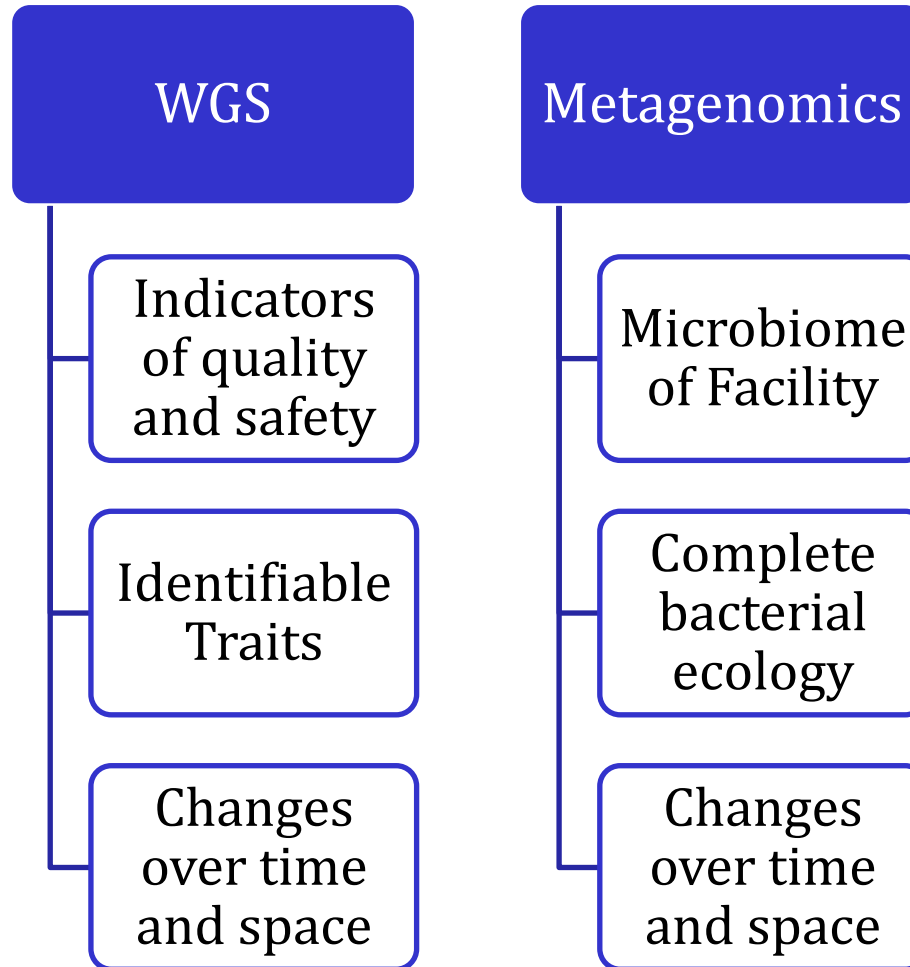


Sampling Plan

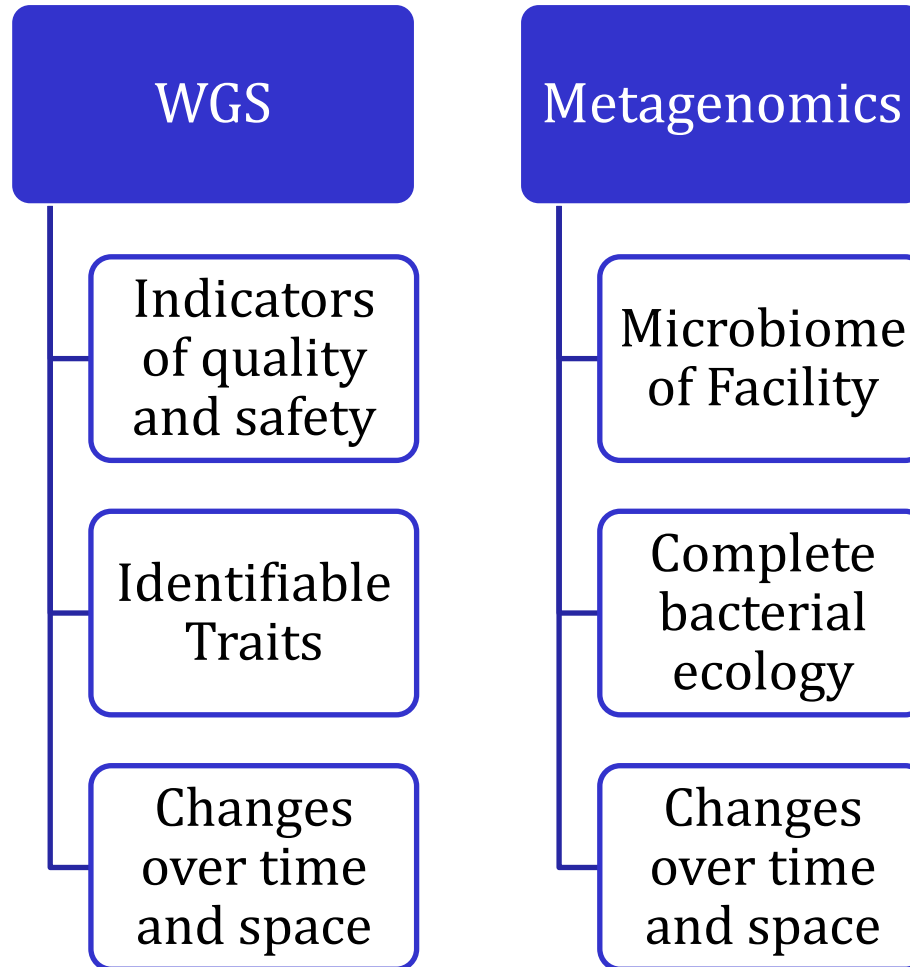
Monitored
over **two**
years in **six**
facilities



Sampling Data

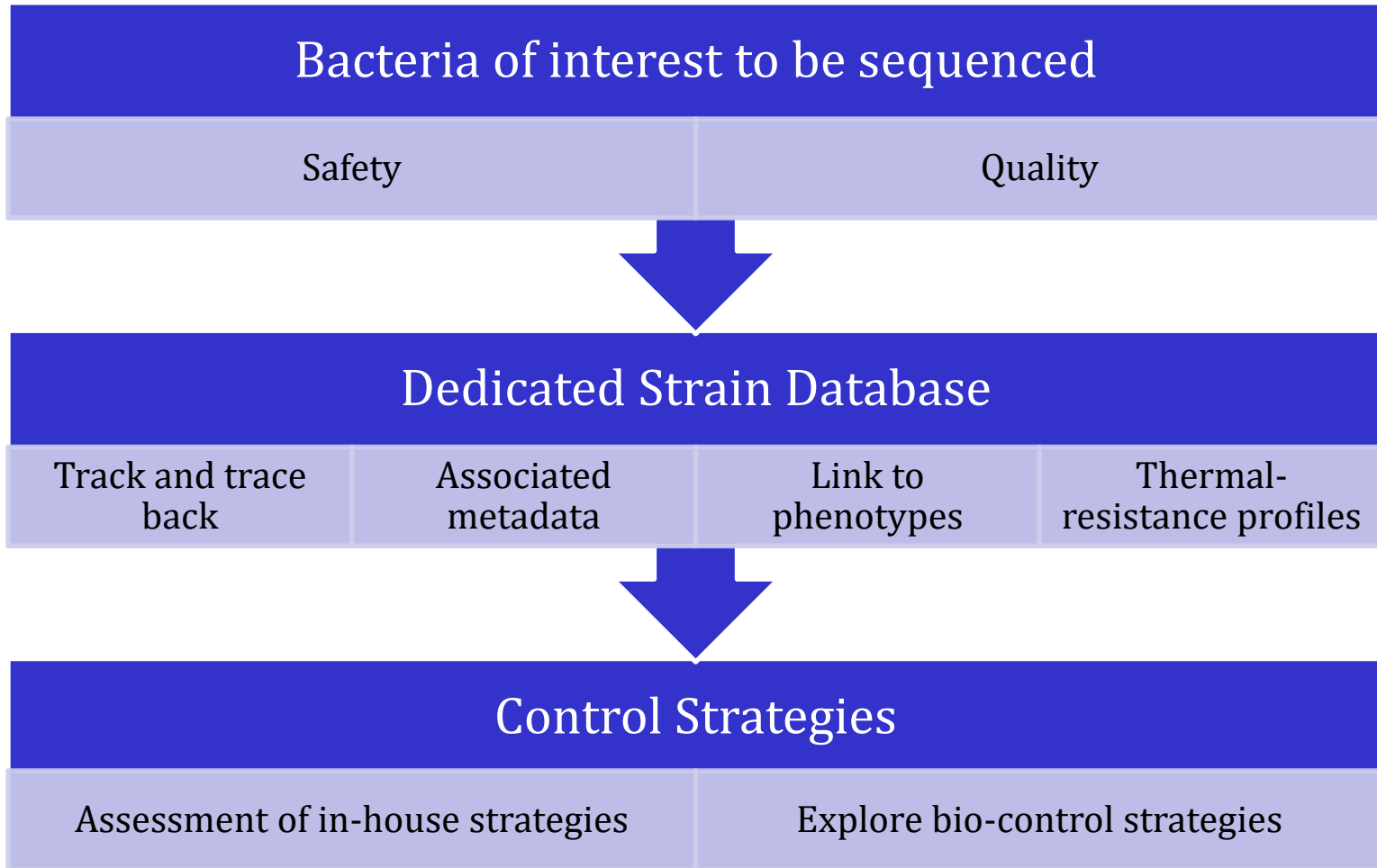


Sampling Data

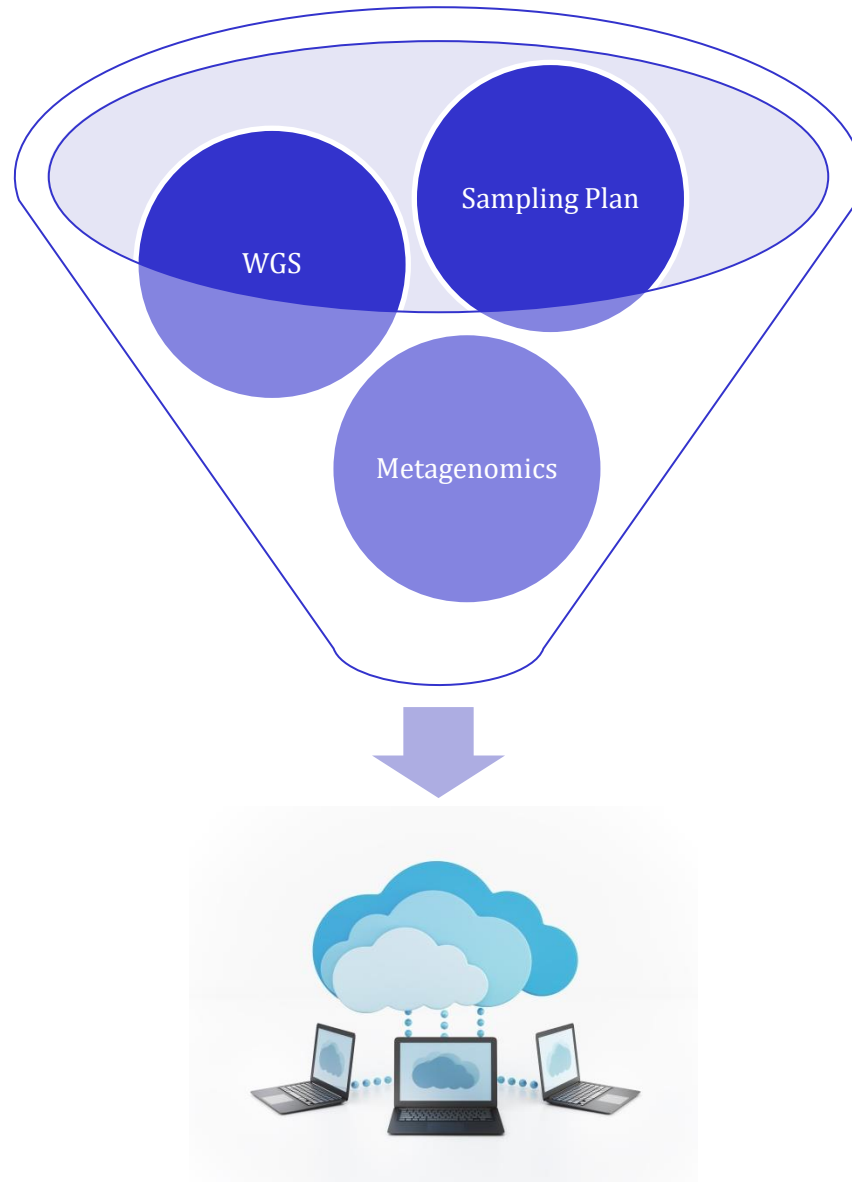


Analysed separately and in parallel

Whole Genome Sequencing



Final Output



SOFTWARE PLATFORM

SAFE

EMAIL

PASSWORD

LOGIN

Data > 2017 > Samples

Samples

Year	Month	Area	Sample Number
2017	Feb	Dry room	12345
2017	Feb	Wet room	22345
2017	Mar	Wet room	32345

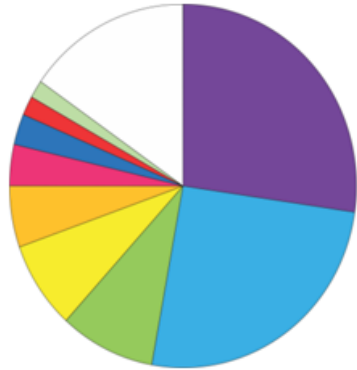
Data > 2017 > Samples

WGS Analysis

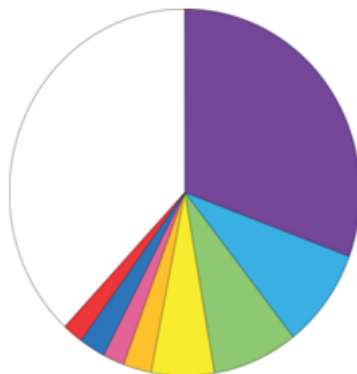
Isolate ID	Date	Location	AM Resistance	Virulence	Thermal Resistance	Biofilm Formation	Biocide
10-00001	Feb-17	Dry Zone, High Risk	Green	Green	Green	Green	Orange
10-00002	Feb-17	Wet Zone, Low Risk	Red	Green	Green	Green	Green
10-00008	Feb-17	Dry Zone, High Risk	Green	Green	Green	Orange	Green
10-00009	Feb-17	Wet Zone, Low Risk	Green	Orange	Green	Green	Orange
10-00017	Feb-17	Dry Zone, High Risk	Orange	Green	Red	Green	Green
11-00005	Jun-17	Wet Zone, Low Risk	Green	Green	Green	Orange	Green
11-00537	Jun-17	Wet Zone, Low Risk	Green	Orange	Green	Green	Green
11-00538	Jun-17	Wet Zone, Low Risk	Green	Green	Green	Orange	Green
11-01558	Jun-17	Wet Zone, Low Risk	Green	Green	Green	Green	Orange
11-01559	Jun-17	Wet Zone, Low Risk	Green	Green	Green	Green	Green

Data > 2017 > Metagenomic Analysis

Sample 123



- Gammaproteobacteria
- Clostridia
- Bacteroidia
- Bacilli
- Alphaproteobacteria
- Deltaproteobacteria
- Betaproteobacteria
- Actinobacteria
- Fusobacteria
- Unclassified and others



- Lachnospiraceae
- Pseudomonadaceae
- Rikenellaceae
- Enterobacteriaceae
- Halomonadaceae
- Bacillaceae
- Ruminococcaceae
- Prevotellaceae
- Flavobacteriaceae
- Comamonadaceae
- Unclassified and Others



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Thank You

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