CLAIMS

1. A computer-implemented method for source attribution of a contaminant at a site, the method comprising

storing an electronic representation of the site in electronic memory, the representation comprising respective location information about one or more surfaces within the site,

receiving in the electronic memory contamination status information about a surface of the one or more surfaces,

modifying the representation to associate the location information with the contamination status information of the corresponding surface,

repeating the receiving and modifying steps to generate a data set comprising a plurality of associated contamination status information and location information, and

analysing the data set to attribute the source of the contaminant to at or near a surface of the one or more surfaces,

wherein the contamination status information comprises nucleic acid sequence information, is generated according to a schedule, and is determined by a method comprising collecting two or more samples from the one or more surfaces according to the schedule and analysing the two or more samples to determine the relatedness of the two or more samples.

2. A computer-implemented method for source attribution of a contaminant at a site and displaying a representation thereof, the method comprising

generating, receiving or storing an electronic representation of the site in electronic memory, the representation comprising respective location information about one or more surfaces within the site,

generating or receiving in the electronic memory contamination status information about a surface of the one or more surfaces,

modifying the representation to associate or link the location information with the contamination status information of the corresponding surface, and

transmitting the modified representation to a display device for display to a user,

wherein the contamination status information comprises nucleic acid sequence information, is generated according to a schedule, and is determined by a method comprising collecting two or more samples from the one or more surfaces according to the schedule and analysing the two or more samples to determine the relatedness of the two or more samples;

optionally further comprising generating the representation by a method comprising

generating or receiving an initial representation of the site comprising a digital plan of the site, a 3D digital model of the site, or one or more images of the site, or any combination of any two or more thereof,

generating or receiving location information about respective one or more surfaces within the site,

storing the initial representation and the location information in a database, and

associating or linking the initial representation with the location information, such that a surface of the one or more surfaces can be identified by its respective location information.

3. A computer-implemented method for source attribution of a contaminant at a site and displaying a representation thereof, the method comprising

generating, receiving or storing in electronic memory respective location information about one or more surfaces within the site,

generating or receiving in the electronic memory contamination status information about a surface of the one or more surfaces,

transmitting the location information and the contamination status information to remote electronic memory comprising an electronic representation of the site,

receiving a modified electronic representation where the location information has been associated or linked with the contamination status information of the corresponding surface, and

displaying the modified electronic representation to a user,

wherein the contamination status information comprises nucleic acid sequence information, is generated according to a schedule, and is determined by a method comprising collecting two or more samples from the one or more surfaces according to the schedule and analysing the two or more samples to determine the relatedness of the two or more samples;

optionally wherein one or more of either or both of the generating steps and the transmitting step are carried out using a point of use hardware device.

4. The computer-implemented method of any one of claims 1 to 3, wherein:

a) the contamination status information further comprises amino acid sequence information, microbiological assay information, chemical assay information, or biochemical assay information, or any combination of any two or more thereof.

b) the nucleic acid sequence information comprises one or more partial or whole genome sequences or mixed genome sequences;

c) the nucleic acid sequence information comprises ribosomal RNA sequence information, single nucleotide polymorphism (SNPs) information or metagenomic information and/or

d) the contamination status information comprises information about a nucleic acid containing material, including but not limited to a bacteria, a virus, a protozoa, a plant, or an animal, or any combination of any two or more thereof.

5. The computer-implemented method of claim 4, wherein the nucleic acid sequence information is generated using nucleic acid sequencing methods including but not limited to Sanger sequencing, whole genome sequencing (WGS), or next generation sequencing (NGS) or wherein the microbiological assay information comprises mass spectrometry information.

6. The computer-implemented method of any one of claims 1 to 5, wherein the site is a food production site, a food handling site, a food preparation site, a food logistics site, a food consumption site, an agricultural site, an animal handling site, a medical facility, a building, a vehicle, or a structure.

7. The computer-implemented method of any one of claims 1 to 6, wherein:

a) the representation comprises a 3D digital model, a point cloud, or one or more images of the site, or any combination thereof; and/or

b) the representation comprises unique identifiers linked to the one or more surfaces.

8. The computer-implemented method of claim 7, wherein the point cloud is:

a) generated by photogrammetrically processing the one or more images of the site; or

b) generated by laser, radar or sonar distance measurement of the site.

9. The computer-implemented method of any one of claims 1 to 8, wherein the contamination status information is determined by a method comprising collecting one or more samples from the one or more surfaces and analysing the one or more samples.

10. The computer-implemented method of claim 9, wherein the one or more samples are obtained according to a sampling plan and wherein optionally the sampling plan provides a first sampling location, a second sampling location, and an n^{th} sampling location, wherein each sampling location is determined by one or more statistically-based sampling methods.

11. The computer-implemented method of claim 10, wherein the sampling plan provides a first sampling location, a second sampling location, and an n^{th} sampling location, wherein each sampling location is determined by one or more statistically-based sampling methods, wherein the statistically-based method is:

a) simple random sampling, the method comprising selecting within the site a first random sampling location, a second random sampling location, and an n^{th} random sampling location; or

b) systematic sampling, the method comprising defining a grid within the site, selecting a first sampling location on the grid, selecting a second sampling location on the grid, and selecting an n^{th} random location on the grid.

c) adaptive cluster sampling, the method comprising randomly selecting within the site a first set of primary sampling locations, determining whether each primary sampling location contains a contaminant, and selecting a second set of secondary sampling locations, each secondary sampling location being adjacent to a primary sampling location that contains a contaminant.

12. The computer-implemented method of claim 9 to 11, wherein the one or more samples are collected by swabbing, wiping, vacuuming, or blotting or any combination thereof.

13. The computer-implemented method of claim 9, wherein analysis of the one or more samples comprises determining the presence of microbial contaminants using an assay to identify nucleic acid or amino acid information, or a microbiological assay, a chemical assay, or a biochemical assay, or any combination thereof.

14. The computer-implemented method of any one of claims 9 to 13, wherein analysis of the one or more samples comprises:

a) determining the identity of a contaminant;

b) determining the relatedness of two or more samples; and/or

c) determining the movement of a contaminant within a site by a method comprising

obtaining assay information from each of two or more samples obtained from different locations within the site,

determining the relatedness of the samples by analysing the assay information,

identifying potential vectors of contamination, and

determining the movement of the contaminant within the site by comparing the relatedness of the samples with the potential vectors.

15. The computer-implemented method of any one of claims 9 to 13, wherein analysis of the one or more samples comprises determining the identity of a microorganism contaminant by a method comprising

obtaining a first nucleic acid sequence from the one or more samples,

providing a second nucleic acid sequence from a reference microorganism,

defining a threshold of sequence similarity for establishing the identity of a microorganism in the one or more samples, and

determining whether the sequence similarity between the first and second nucleic acid sequences meets the threshold.

16. The computer-implemented method of claim 15, wherein:

a) the threshold for establishing identity is a sequence similarity of at least about 60, 70, 80, 90, 95, or 99 percent;

b) the method is repeated for 10, 100, or 100 or more nucleic acid sequences from the one or more samples; and/or

c) the identity of the microorganism comprises genus, species and/or strain information.

17. The computer-implemented method of any one of claims 15 to 16, further comprising determining a level of risk associated with the microorganism contaminant by comparing the identity of the microorganism contaminant to a database comprising microorganism identifiers and associated risk or hazard information, and associating a risk or hazard to the microorganism contaminant.

18. The computer-implemented method of any one of claims 9 to 13 and 15 to 17, wherein the analysis of the one or more samples comprises determining the relatedness of two or more samples by a method comprising

obtaining a first nucleic acid sequence from a first sample,

obtaining a second nucleic acid sequence from a second sample or from a reference source, and

comparing the first and second nucleic acid sequences to determine the relatedness of the samples.

19. The computer-implemented method of claim 18, wherein comparing the first and second nucleic acid sequences to determine the relatedness of the samples comprises

identifying one or more SNPs between each of the first and second nucleic acid sequences, and

comparing the SNPs from the first and second nucleic acid sequences to determine the relatedness of the samples.

20. The computer-implemented method of any one of claims 9 to 13 and 15 to 19, wherein the analysis of the one or more samples comprises determining the movement of a microorganism contaminant within a site by a method comprising

obtaining nucleic acid sequence information from each of two or more samples obtained from different locations within the site,

determining the relatedness of the samples by analysing the nucleic acid sequence information,

identifying potential vectors of contamination, and

determining the movement of the microorganism contaminant within the site by comparing the relatedness of the samples with the potential vectors.