

Concept

Spreadsheet Column

Example

	<div>INVESTIGATION<div><div>- Name (ID)</div><div>- Institution</div><div>- Description</div><div>- Metadata: Value</div><div>- Category</div></div></div>	<div><div>investigation_id</div><div>investigation_institution</div><div>investigation_description</div></div>	<div>A survey of oil wells</div> <div>Dalhousie University</div> <div>A genomics analysis of microbial organisms.affecting oil wells</div>	
		<div>investigation_category</div>	<div>oil; well;</div>	
	<div>PROCESS<div><div>- Name (ID)</div><div>- Description</div><div>- Citation</div><div>- Metadata: Value</div><div>- Parameter: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div>PROCESS<div><div>- Name (ID)</div><div>- Description</div><div>- Citation</div><div>- Metadata: Value</div><div>- Parameter: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div><div>process_id</div><div>process_description</div><div>process_citation</div></div>	<div>QIIME2 2019.7 Standard Workflow</div> <div>Default ASV workflow for QIIME2</div> <div>Caporaso et al.</div>
.....		<div>process_category</div>	<div>computational</div>	
		<div>upstream_process</div>	<div>16S V3-V4 Sequencing Protocol</div>	
	<div>STEP<div><div>- Name (ID)</div><div>- Description</div><div>- Processes</div><div>- Metadata: Value</div><div>- Parameter: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div>STEP<div><div>- Name (ID)</div><div>- Description</div><div>- Processes</div><div>- Metadata: Value</div><div>- Parameter: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div><div>step_id</div><div>step_description</div><div>process_id</div></div>	<div>qiime2_dada2_denoise</div> <div>Denoise sequences into ASVs with DADA2 wrapped by QIIME2</div> <div>QIIME2 2019.7 Standard Workflow</div>
.....		<div>step_category</div>	<div>clustering</div>	
		<div>upstream_step</div>	<div>qiime2_quality_filter</div>	
	<div>ANALYSIS<div><div>- Name (ID)</div><div>- Location</div><div>- Date</div><div>- Process</div><div>- Step (if not in Process)</div><div>- Metadata: Value</div><div>- Parameter: Value</div><div>- Category</div></div></div>	<div><div>analysis_id</div><div>analysis_location</div><div>analysis_date</div><div>process_id</div><div>step_id</div></div>	<div>QIIME2, loosened quality filter</div> <div>researchserver12</div> <div>09/09/2019</div> <div>QIIME2 2019.7 Standard Workflow</div> <div>qiime2_different_quality_filter</div>	
		<div>analysis_category</div>	<div>complete</div>	
	<div>RESULT<div><div>- UUID (ID)</div><div>- Type</div><div>- Source</div><div>- Analysis</div><div>- Source Step</div><div>- Samples</div><div>- Metadata: Value</div><div>- Parameter: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div>RESULT<div><div>- UUID (ID)</div><div>- Type</div><div>- Source</div><div>- Analysis</div><div>- Source Step</div><div>- Samples</div><div>- Metadata: Value</div><div>- Parameter: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div><div>result_id</div><div>result_type</div><div>result_source</div><div>analysis_id</div><div>step_id</div><div>sample_id</div></div>	<div>b413fffa-2d5f-4ab0-9243-df36dedc6de6</div> <div>pcoa</div> <div>vegan</div> <div>QIIME2, loosened quality filter</div> <div>qiime2_diversity_pcoa</div> <div>14AB-12C_Z_16S</div>
.....		<div>result_category</div>	<div>ordination</div>	
		<div>upstream_result</div>	<div>f18acf7f-dbbd-46d7-a713-259df4a3888a</div> <div>(points to a distance matrix artifact)</div>	
	<div>SAMPLE<div><div>- Name (ID)</div><div>- Investigation</div><div>- Process</div><div>- Metadata: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div>SAMPLE<div><div>- Name (ID)</div><div>- Investigation</div><div>- Process</div><div>- Metadata: Value</div><div>- Category</div><div>- Upstream</div></div></div>	<div><div>sample_id</div><div>investigation_id</div><div>process_id</div></div>	<div>14AB-12C_Z_16S</div> <div>A survey of oils wells</div> <div>16S V3-V4 Sequencing Protocol</div>
.....		<div>sample_category</div>	<div>16S</div>	
		<div>upstream_sample</div>	<div>14AB-12C_Z</div>	
	<div>FEATURE<div><div>- Name (ID)</div><div>- Results</div><div>- Sequence</div><div>- Annotations</div><div>- Samples</div><div>- Metadata: Value</div><div>- Category</div></div></div>	<div><div>feature_id</div><div>result_id</div><div>result_sequence</div></div>	<div>c2792ae7f98ac74ef7381520d7da90fb</div> <div>54777bb6-bfb3-48d4-b15d-fab01ef97c37</div> <div>ATGCAGCTAGCTACGATCGTTGCAGCGGGC...</div>	
		<div>sample_id</div>	<div>14AB-12C_Z_16S</div>	
		<div>feature_category</div>	<div>bacteria; amplicon; 16S</div>	