

```

{
  "id": "obj.1276",
  "name": "Healthy human [taxID:9606] fecal [UBERON:0001988] metagenomic
diversity",
  "version": "1.2",
  "createdby": "hadley_king@gwmail.gwu.edu",
  "created": "Jan 26, 2017 16:35:29",
  "modified": "Mar 02, 2017 19:00:33",
  "digital_signature": "QSEQa6HNzERVIMONZWEj",
  "verification_status": "unreviewed",
  "publication_status": "draft",
  "usability_domain": [
    "Identify the most common organism present in a human[taxID:9606]
fecal[UBERON:0001988] sample",
    "Identify the general community composition of organisms in a
human[taxID:9606] fecal[UBERON:0001988] sample"
  ],
  "authors": [
    {
      "orchid": "0000-0003-1409-4549"
    },
    {
      "orcid": "0000-0002-8138-8312"
    }
  ],
  "description_domain": {
    "keywords": [
      "metagenome",
      "metagenomic analysis"
    ],
    "xref": [
      "UBERON:0001988",
      "taxID:9606"
    ],
    "pipeline_steps": [
      {
        "tool_name": "HIVE_CensuScope",
        "tool_desc": "Detect taxonomic composition of a metagenomic data
set.",
        "tool_version": "1.3",
        "tool_package": "null",
        "step_number": "1",
        "input_uri_list": [
          "hive://nuc-read/514683",
          "hive://nuc-read/514682",
          "hive://genome/513957"
        ],
        "output_uri_list": [
          "hive:///data/524669/dnaAccessionBasedResult.csv"
        ]
      ]
    ]
  ]
}

```

```

    },
    {
        "tool_name": "HIVE_hexagon",
        "tool_desc": "Alignment of reads to a set of references",
        "tool_version": "1.3",
        "tool_package": "null",
        "step_number": "2",
        "input_uri_list": [
            "https://www.ncbi.nlm.nih.gov/nuccore/CP000139.1",
            "https://www.ncbi.nlm.nih.gov/nuccore/FP929042.1",
            "https://www.ncbi.nlm.nih.gov/nuccore/FP929046.1",
            "https://www.ncbi.nlm.nih.gov/nuccore/FP929045.1",
            "https://www.ncbi.nlm.nih.gov/nuccore/FP929043.1",
            "https://www.ncbi.nlm.nih.gov/nuccore/FP929048.1",
            "hive:///data/524669/dnaAccessionBasedResult.csv"
        ],
        "output_uri_list": [
            "hive:///data/524569/alCount-Unaligned0524569-alCount--1.csv"
        ]
    }
]
},
"execution_domain": {
    "script": "hive://workflows/human_gut_metagenomic_diversity.py",
    "pipeline_version": "2.0",
    "platform": "HIVE",
    "driver": "Python2.7.10",
    "prerequisites": [
        {"name": "HIVE_censuscope", "version": "1.3"},
        {"name": "HIVE_hexagon", "version": "1.3"}
    ],
    "env_parameters": [
        "HIVEv1.3"
    ]
},
"parametric_domain": {
    "complexityRefEntropy": "1.2 - reluctant",
    "maximumPercentLowQualityAllowed": "15",
    "keepMarkovnikovMatches": "0n",
    "storeAlignments": "Yes",
    "keepAllMatches": "All equally best alternative matches",
    "selfStopping": "No",
    "CensuslimitIterations": "5",
    "sample": "2500",
    "acceptNNNQuaTrheshold": "filter Ns only",
    "complexityRefWindow": "30",
    "taxDepth": "leaf",
    "minMatchLen": "45"
},
"io_domain": {
    "reference_uri_list": [

```

```

        "https://www.ncbi.nlm.nih.gov/nuccore/CP000139.1",
        "https://www.ncbi.nlm.nih.gov/nuccore/FP929042.1",
        "https://www.ncbi.nlm.nih.gov/nuccore/FP929046.1",
        "https://www.ncbi.nlm.nih.gov/nuccore/FP929045.1",
        "https://www.ncbi.nlm.nih.gov/nuccore/FP929043.1",
        "https://www.ncbi.nlm.nih.gov/nuccore/FP929048.1",
        "hive://genome/513957"
    ],
    "input_uri_list": [
        "https://hive.biochemistry.gwu.edu/nuc-read/514683",
        "https://hive.biochemistry.gwu.edu/nuc-read/514682"
    ],
    "output_uri_list": [
        "https://hive.biochemistry.gwu.edu/data/524669/dnaAccessionBasedResult.csv",
        "https://hive.biochemistry.gwu.edu/data/524569/Unaligned Reads (HIVE_ID).fasta",
        "https://hive.biochemistry.gwu.edu/data/524569/alCount-Unalignedo524569-alCount--1.csv"
    ]
},
    "error_domain": [
        "false negative discovery < 0.000001"
    ]
}

```