Saturday, 31 July 2021 19:22

SEROTYPE:

DISTINCT VANIATION WITHIN SPECIES OF BACTERIAS, VINUS ON INDIVIDUALS

CLASSI PICATION BASED ON CELL-SUNFACE ANTIGEN

EPIDEMIDLOGIC CLASSIFICATION

SALMONEULA SELDTYPE IDENTIFICATION

SEQSERD TOOL

METHOLS BEHIND VALIDATION DATA HOW TO USE THE TOOL OUTPUT DATA

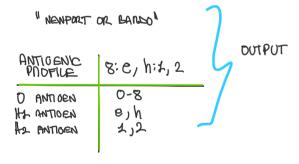
| DINECT | LOCATING GENE THAT ENCODES FOR PHENOTYPE | SEQ SENO |
|----------|--|----------|
| INDINECT | MANKENS WE EXPECT TO FOLLOW SENOTYPE | MLST |

RAW DATA BWA COMPATIBLE WITH BOTH

CUNATED DATABASE

GENOTYPE & PHENOTYPE
IF THE GENE IS NOT EXPIRESED

USE RAW DATA IF POSSIBLE



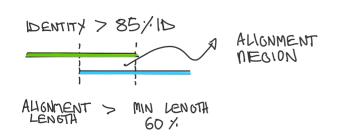
IF 2 SENOTYPE THEN MLST SOLVING AMELICUITY

E. COLI SEROTYPE IDENTIFICATION Senotype Finder Tool

SENDTYPING FROM SEQUENCING DATA

· MARCT VS INDINECT

ASSEMBLED BASED TOOL (BLAST) 4



- GENE LENGTH
- GENE NAME
- / IDENTITY

- WINTE INVITE
- WHERE GENE WAS FOUND
- POSITION IN CONTIG - PREDICTED SENOTYPE

PLASMID FINDER

PLASMID TYPING

DEF

DOUBLE STRANDED CINCULAR OR LINEAR DNA MOLECULES

VERTICAL & HOMZONTAL THANSFERT

THEY CONFER PHENOTYPE, POSITIVE TO NATURAL SELECTION

(MICHOBIAL NESISTANCE)

IMPORTANT TO STUDY BACTERIA EPIDEMIOLOGY

PLASMID FINDER

(MEPLICON) IN SLUCON DETECTION OF PLASMIDS

PMLST

ANALYSIS & TYPING OF PLASMIDS (ST TYPE)

PLASMID 1. IDENTITY QUERY & HSP LENGTH

HSP LENGTH OF ALIGNMENT LESTWEEN THE LEST MATCHING ALELE AND THE COMMESPONDING SER IN GENOME

535/534 - 1 POSITION THAT CANNOT BE ALIGNED WITH NEPLICON

TCG ATTGGA C CA TCG ATTGGA CCG

CONFIGURATION, WHAT PLASMID?

PMLST BO PLASMIDFINDER BEFORE

Y. IDENTITY

MOBILE ELEMENT PINDER

WAY AME WE INTERESTED?

IMPORTANT FOR GACTERIAL EVOLUTION

HOMIZONTAL GENE TRANSPER

- TRANSPORTATION (PHAGE TRANSMISSION)
 TRANSPORTATION (WA FROM ENVIRONMENT) · CONSUCATION (TRANSPOSONS & PLASMICS)

MOBILE ELEMENTS

CAMNES CELLILAR MACHINERY TO PENFORM CONSUMATION CONSUGATORY PLASMILLS (NEEDS TO BE) MOBILIZABLE BLEMONTS

WHAT FUNCTION SO THEY PROVIDE?

FUNCTION WITHIN CEUS VS BETWEEN CEUS

MOVING GENES DETWEEN PLASMIDS & CHROMOSOMES

DESEMBATE GENES MGE USEFUL FON EVOLUTION

NAPID GENE-REAMANGEMENTS CAN BE DELETENAL TO ONGANISM

PREDICTION OF MOBILE ELEMENTS

ASSEMBLED SEQUENCE DATA
WE ARE INTERESTED IN CONTEXT

FULLY ALIGNMENT PARTIAL ALIGNMENT STOUCTURAL VARIATIONS

COVERAGE
SEQ. IDENTITY
LEVEL OF THUNCATION

MODEL QUALITY
PARAMETERS

NESULT INDEX PAGE

| CONTIG | PLASMID | #MGE | NEUSTANCE | VANVANCE |
|--------|---------|------|-----------|----------|
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