

PACKAGE ID - 001083SPARC00 SCORES

KWIC TITLE - Data Analysis for Sequencing by Hybridization
(SBH) Experiments

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LIMITATION CODE -COPY **AUDIENCE CODE** - LIM

COMPLETION DATE - 01/01/1994 **PUBLICATION DATE** - 01/01/1994

DESCRIPTION - SCORES is user friendly software designed to analyze data from SBH (Sequencing By Hybridization) experiments. In these ANL experiments DNA samples are spotted on a nylon membrane and hybridized with radioactivity labeled oligonucleotide probes. An image analysis program (DOTS) calculates a raw value for each DNA dot from images generated by the Molecular Dynamics Phosphorimager. SCORES reads in the DOTS output for each hybridization done for a particular filter. The data for each probe is normalized against a mass probe and scaled properly. These values from 100 or more probes are then used to compute the distance (i.e., degree of similarity) between any two clones on the filter. These calculated distances define clusters of similar clones (cDNA) or contigs (genomic DNA). Histograms of the data at each stage of analysis to establish thresholds for further steps. SCORES generates various statistical tables to evaluate the quality of spotting, hybridization of filters, and of individual dots.

PACKAGE CONTENTS - Media Directory; Software Abstract; Media Includes Source Code;

SOURCE CODE INCLUDED? - Yes

MEDIA QUANTITY - 1 3.5 Diskette

COMPUTER - SUN SPARC

OPERATING SYSTEMS - Unix

PROGRAMMING LANGUAGES - C

SOURCE CODE AVAILABLE (Y/N) - Y

RELATED SOFTWARE - SCORES reads the output produced by the DOTS program. X-Windows and Motif are implemented to provide the user-friendly interface.

HARDWARE REQS - Sun SPARCstation

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SOFTWARE ABSTRACT

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SUBJECT CLASS CODE - Y

KEYWORDS -

COMPUTER PROGRAM DOCUMENTATION
S CODES
STATISTICS
DATA ANALYSIS
GENOME MUTATIONS
DNA SEQUENCING
HUMAN POPULATIONS
OLIGONUCLEOTIDES

EDB SUBJECT CATEGORIES -
990200 550200

SPONSOR - DOE/EH

PACKAGE TYPE - AS - IS