Literature Databases

Introduction to Bioinformatics
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Exercises:
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Overview

1. Databases
2. Publications in Science
3. PubMed and Entrez (literature DB)
4. ISI Web of Science (citation DB)

Data and Information

- Data :=
  everything that can be collected, stored, and read again.
  Data, by itself, is uninterpreted.

- Information, Knowledge :=
  facts derived from data,
  interpretation of data

Database

- DB := structured collection of data

- customer DBs
- address DBs
- movie DBs
- literature DBs (PubMed)
- sequence DBs for DNA, RNA, proteins
- protein structure DBs (PDB)
- pathway DBs

DBMS – Database Management System

- DBMS :=
  piece of software to access, modify, delete, add data in a database,
  may have a graphical user interface (GUI)

- MS Access
- OpenOffice.org Base
- mySQL

- Entrez at NCBI (“meta access”)

Database System

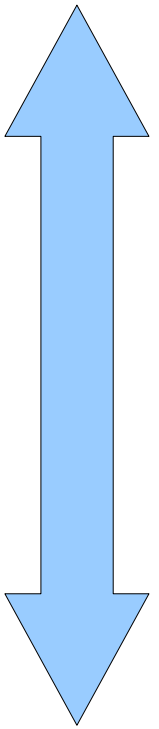
- Database(s) (DB(s))
  + Database Management System (DBMS)
  = Database System (DBS)

Database vs. Flat File

- Even a simple text file can be a “database”
  - tab- or newline-delimited lists of numbers or words
- Flat file
  - requires no special software to access or modify (just a plain text editor)
  - access (searching) is often inefficient
  - integrity and security are difficult to maintain
- Database
  - requires a DBMS
  - allows indexing for efficient complex searches
  - DBMS maintains integrity and security

Publications

- New research results are communicated to the scientific community via
  - conference proceedings ("conference papers")
  - research articles in journals ("journal papers")
  - review articles in journals
  - chapters in edited books
  - student theses
  - textbooks



new
rapid publication

older
slower publication

Who's paying?

- Publications are good for the whole community, even the whole world in the long run
- (Patents are good for one company)
- Who's paying for publications? Two models:
  - classic: the reader (journal subscription)
  - new: the author (open access model)
    sometimes via institutional flat rate
- Who's making money?
  - the publisher (not the scientist or funding agency)

Quality in Publications

- Publishing research results means progress
- But what if something wrong gets published?
- Quality assurance: **peer review**
- Other scientists reads an comment on articles before they are published (anonymously)
- Important part of the job
- Not fail-safe, but no one has a better idea

Not all papers are equal

- Write-only papers
  - no one ever reads them
  - waste of resources and money
  - they still add to the publication list of the author
- Small advances
  - frequent, low-risk
- Big advances
- Papers opening a new research field
  - quite rare, high risk

Literature Search

- Important before starting a new project
- Avoids duplicating existing work
- If articles cannot be found (efficiently), they become write-only papers

- We need DBs of research articles

MEDLINE, PubMed, Entrez

- MEDLINE :=
  database of biomedical journal citations and abstracts, ca. 5,000 journals; is the largest component of
- PubMed :=
  freely accessible online system containing MEDLINE, allows advanced queries
- PubMedCentral :=
  free digital archive of biomedical and life sciences journal literature.
- Entrez :=
  links PubMed to other databases; common interface

Who's behind it?

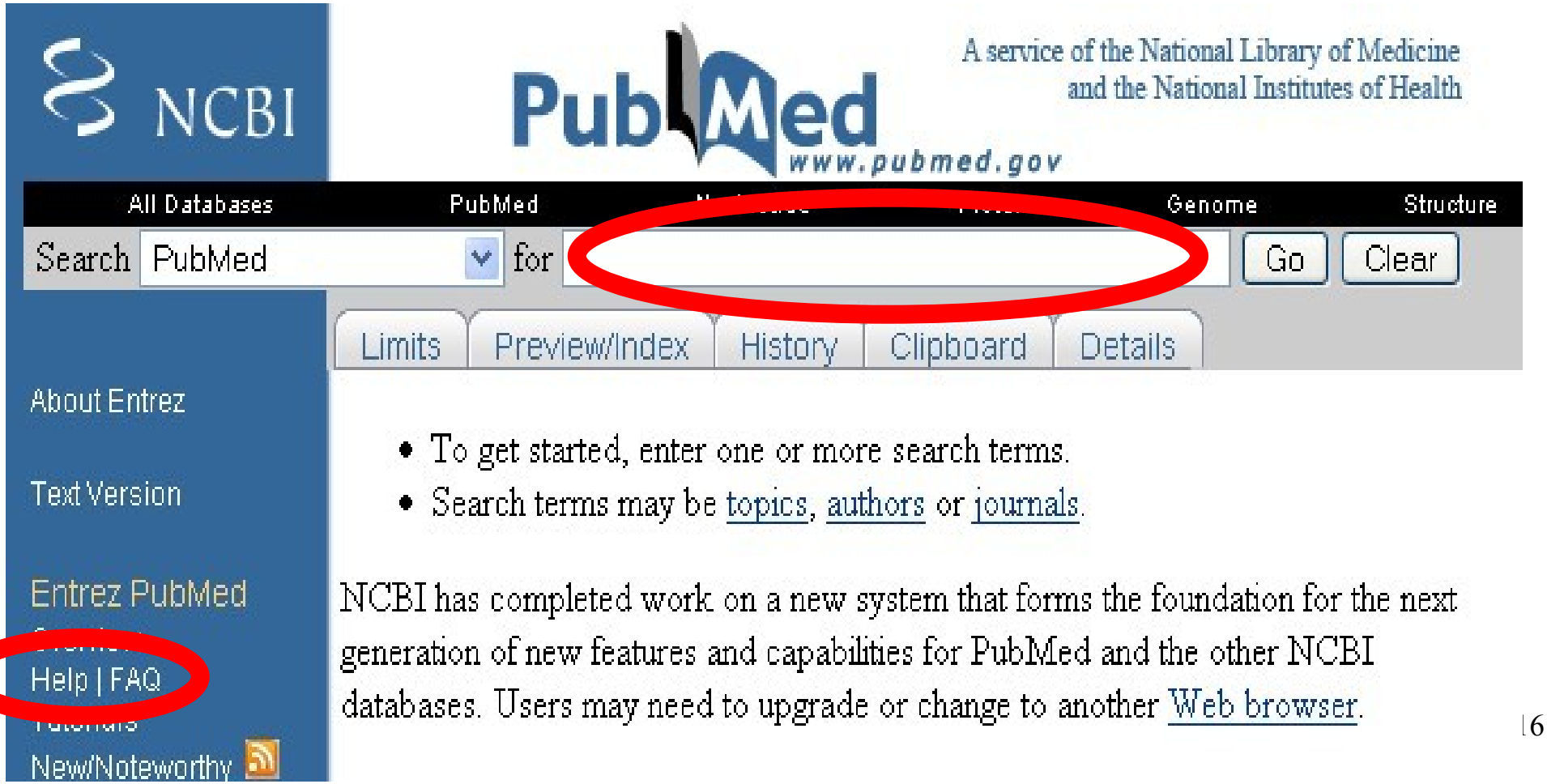
- National Institute of Health (NIH)
  - founded 1887, located in Bethesda, Maryland
  - focal point for medical research in the U.S.
- U.S. National Library of Medicine (NLM)
  - world's largest biomedical library
- National Center for Biotechnology Information (NCBI)
  - creates public databases
  - conducts research in computational biology
  - develops software tools for analyzing genome data
  - disseminates biomedical information

NCBI Website

- URL: http://www.ncbi.nlm.nih.gov/

Searching PubMed

- Access MEDLINE and PubMed via Entrez at http://www.ncbi.nlm.nih.gov/sites/entrez/



Simple Search

- Simply enter key words into the “for” field
- Default:
  - key words are connected by AND,
  - refer to author OR title OR abstract ...,
  - case insensitive;
  - quotes fix the order of terms
- Examples:
  - `Rahmann Microarray`
  - `Rahmann “Microarray Design”`
- Use the 'Help' button!

Search Results

PubMed | Protein | Genome | Structure | OMIM | PMC | Journals | Books

rahmann microarray | Go | Clear | Save Search

Limits | Preview/Index | History | Clipboard | Details

Display Summary | Show 20 | Sort by | Send to

All: 4 | Review: 0

Items 1 - 4 of 4 — One page.

1: Baumbach J, Brinkrolf K, Czaja LF, Rahmann S, Tauch A. — Related Articles, Links

CoryneRegNet: An ontology-based data warehouse of corynebacterial transcription factors and regulatory networks.
BMC Genomics. 2006 Feb 14;7(1):24 [Epub ahead of print]
PMID: 16478536 [PubMed - as supplied by publisher]

2: Schliep A, Torney DC, Rahmann S. — Related Articles

Group testing with DNA chips: generating designs and decoding experiments.
Proc IEEE Comput Soc Bioinform Conf. 2003;2:84-91.
PMID: 16452782 [PubMed - indexed for MEDLINE]

3: Rahmann S. — Related Articles

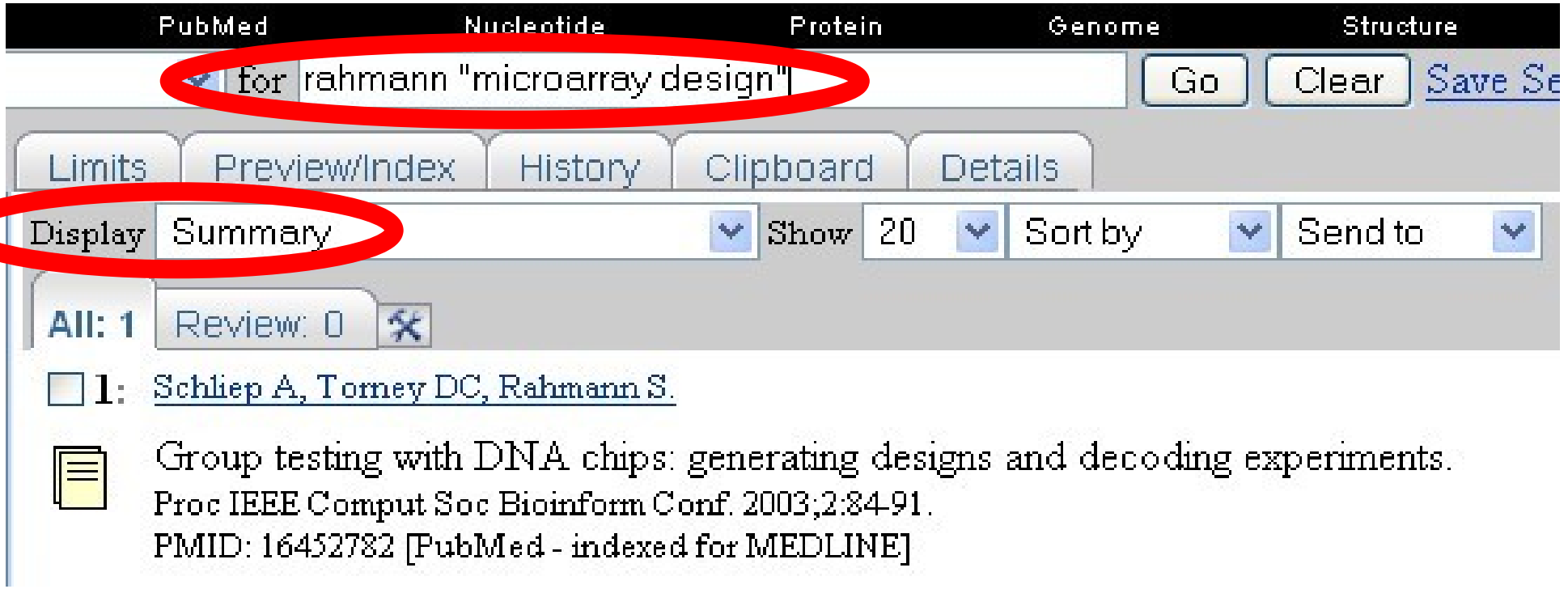
Rapid large-scale oligonucleotide selection for microarrays.
Proc IEEE Comput Soc Bioinform Conf. 2002;1:54-63.
PMID: 15838123 [PubMed - indexed for MEDLINE]

4: Rahmann S. — Related Articles, Links

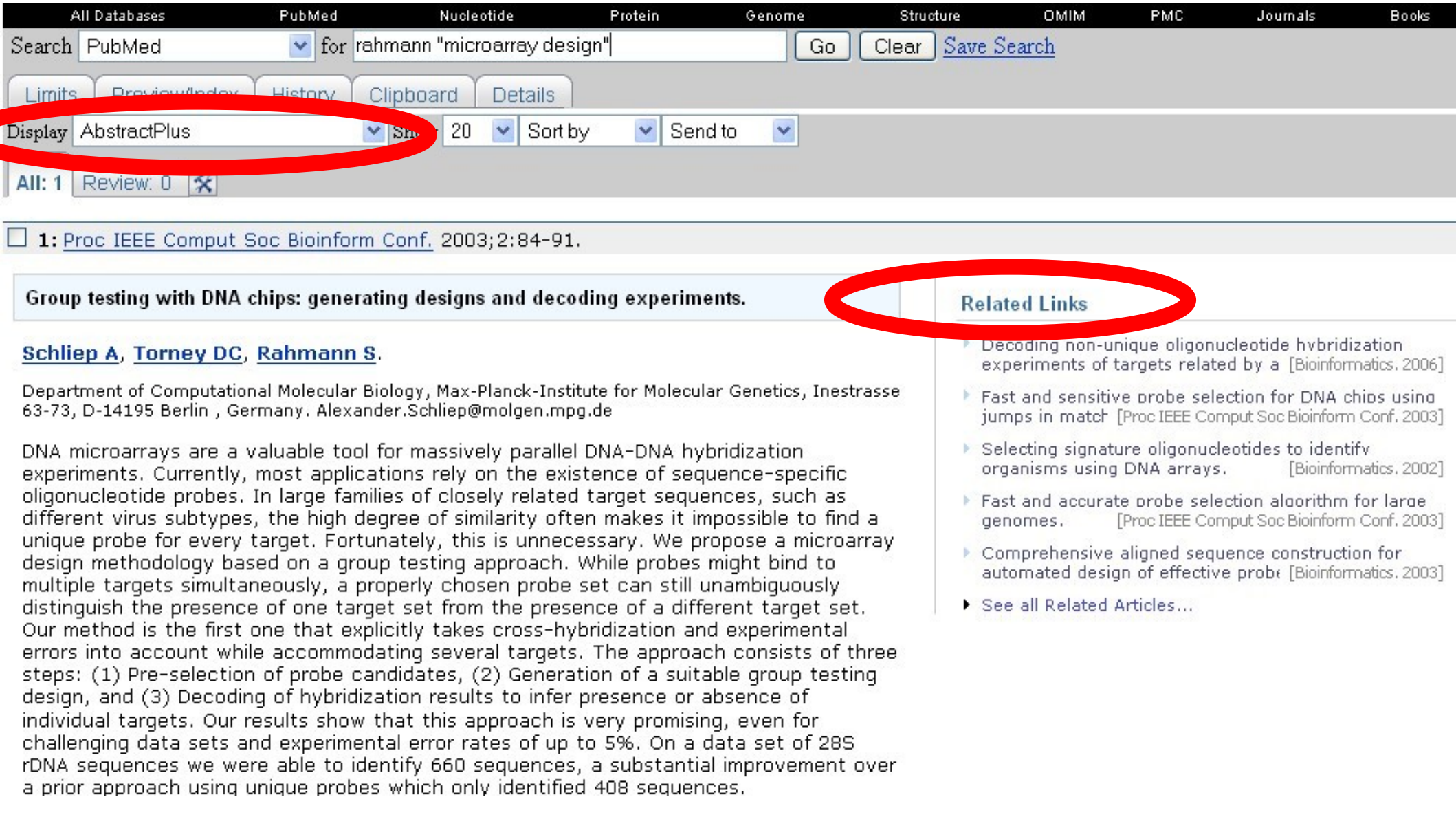
Fast large scale oligonucleotide selection using the longest common factor approach.
J Bioinform Comput Biol. 2003 Jul;1(2):343-61.
PMID: 15290776 [PubMed - indexed for MEDLINE]

Search Results

- Note: If there is exactly one hit, you usually see immediately the abstract.



Displaying more information



Structure of MEDLINE Entries

```
PMID- 16452782
OWN - NLM
STAT- MEDLINE
DA  - 20060202
DCOM- 20060808
PUBM- Print
IS  - 1555-3930 (Print)
VI  - 2
DP  - 2003
TI  - Group testing with DNA chips: generating designs and decoding experiments.
PG  - 84-91
AB  - DNA microarrays are a valuable tool for massively parallel DNA-DNA
      hybridization experiments. Currently, most applications rely on the
      existence of sequence-specific oligonucleotide probes. In large families
      of closely related target sequences, such as different virus subtypes, the
      high degree of similarity often makes it impossible to find a unique probe
      for every target. Fortunately, this is unnecessary. We propose a
      microarray design methodology based on a group testing approach. While
      probes might bind to multiple targets simultaneously, a properly chosen
      probe set can still unambiguously distinguish the presence of one target
      set from the presence of a different target set. Our method is the first
      one that explicitly takes cross-hybridization and experimental errors into
      account while accommodating several targets. The approach consists of
      three steps: (1) Pre-selection of probe candidates, (2) Generation of a
      suitable group testing design, and (3) Decoding of hybridization results
      to infer presence or absence of individual targets. Our results show that
      this approach is very promising, even for challenging data sets and
      experimental error rates of up to 5%. On a data set of 28S rDNA sequences
      we were able to identify 660 sequences, a substantial improvement over a
      prior approach using unique probes which only identified 408 sequences.
AD  - Department of Computational Molecular Biology, Max-Planck-Institute for
      Molecular Genetics, Inestrasse 63-73, D-14195 Berlin , Germany.
      Alexander.Schliep@molgen.mpg.de
```

Field name: PMID (unique PubMed ID)
Value: a unique number identifying the article

Field Restrictions

- Down Syndrome:
  - finds, e.g., articles by Dr Down on any syndrome
- “Down Syndrome”
  - using quotes is much better
- Down [ti]
  - restricts to articles with 'Down' in the title
- Down [au]
  - articles whose author is Dr Down
- [pmid]: unique PubMed identifier
  - always remember it for any interesting article

Fields

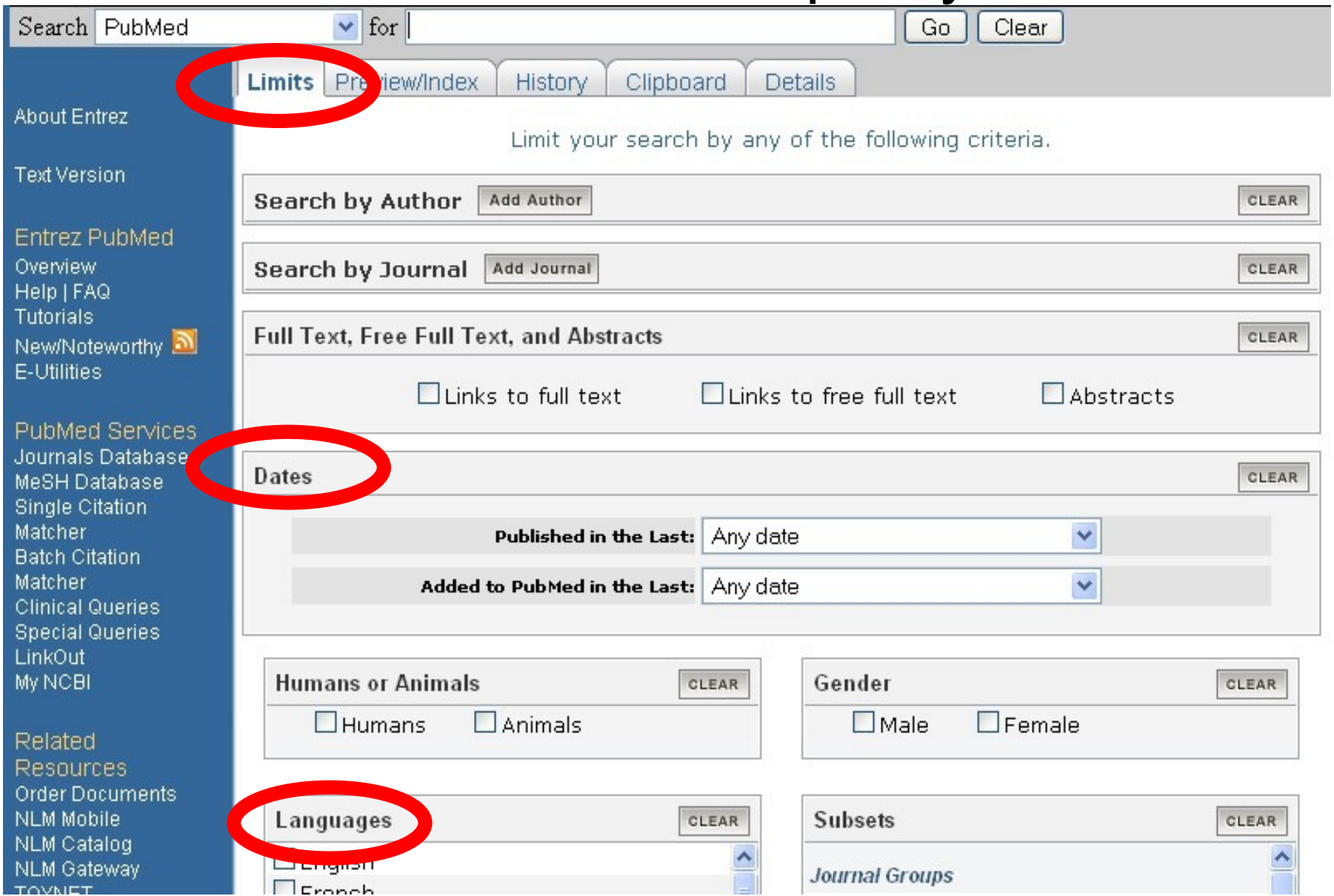
- PMID: PubMed ID
- TI: Title
- AB: Abstract
- AD: Address
- FAU: Full author name
- AU: author (Last name + Initials)
- SO: Journal abbreviation
- ...

Boolean Operations

- AND (default)
- OR
- NOT
- Example
  - Find microarray experts in Dortmund
    microarray [ti] AND Dortmund [ad]
  - Find (many) microarray papers not by Rahmann
    microarray [ab] NOT Rahmann S [au]

Using the “Limits” Tab

- Convenient alternative to specify restrictions



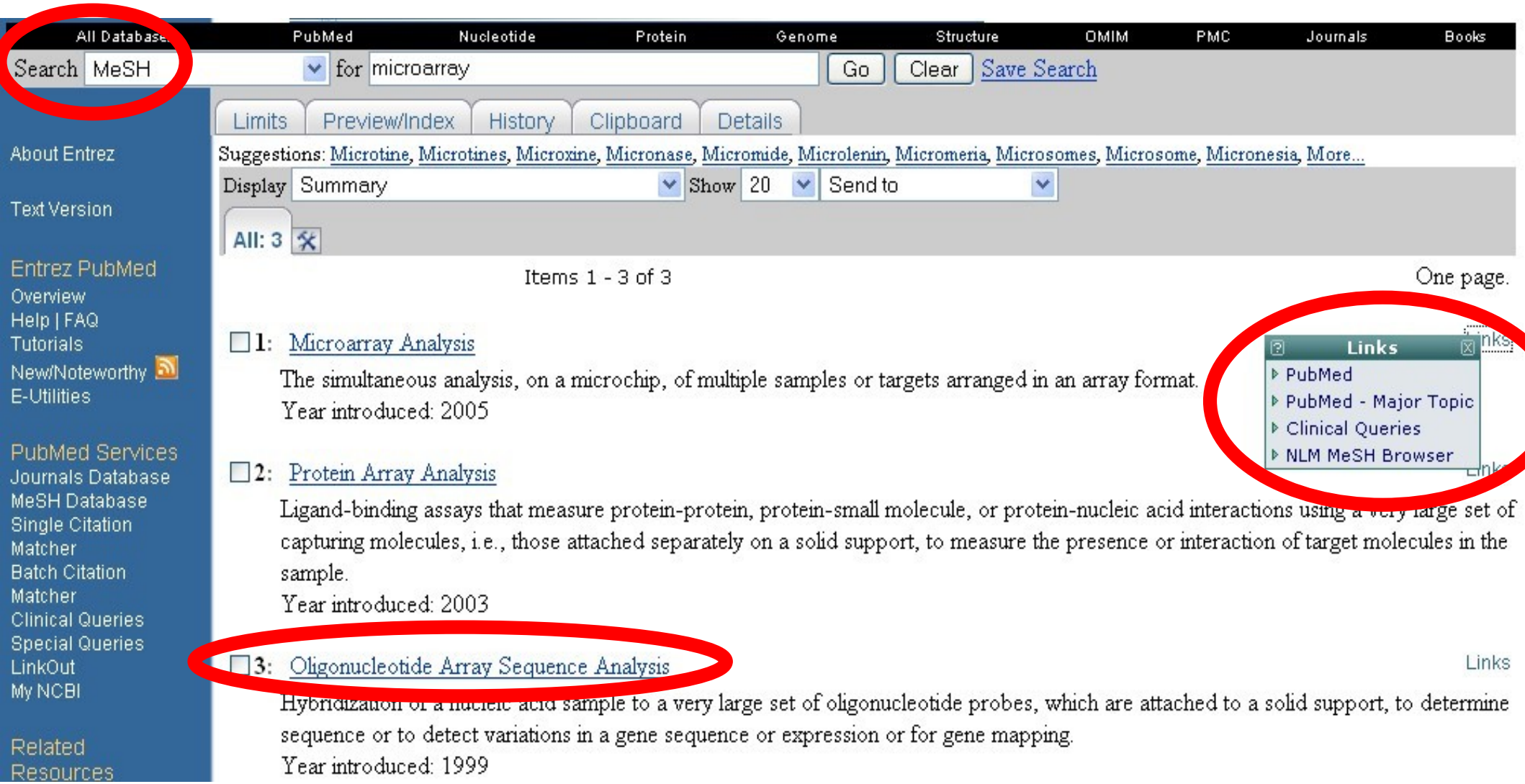
A Few Hints

- Use quotes
- Add initials to author names
- Write down the PMID
- If you find too many results, restrict your search
- If you find too few (or no) results, broaden your search.
- (Use synonyms)
  Problem: The same “idea” or “concept” is often represented by several different terms.

MeSH Terms

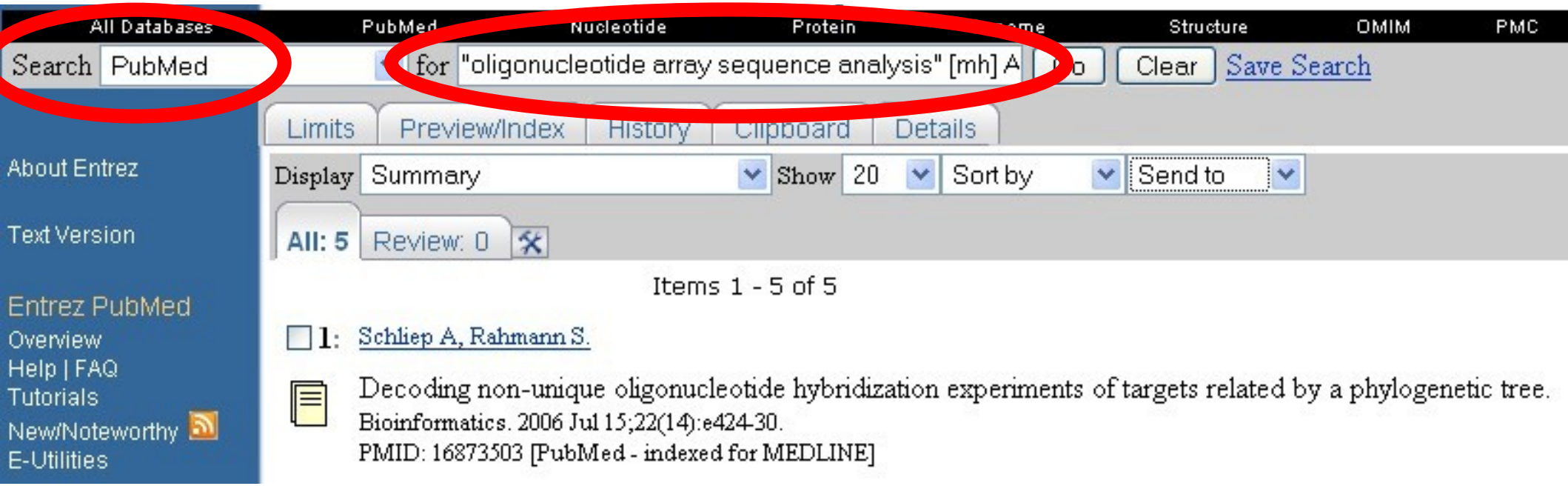
- MeSH = Medical Subject Headings
- MeSH is a controlled vocabulary used for indexing articles for MEDLINE/PubMed.
- MeSH terminology provides a consistent way to retrieve information that may use different terminology for the same concepts.

Example: Microarray



MeSH Terms in a PubMed Search

- Directly enter a [MH] field
- Or “build” the query interactively using the GUI



ISI Web of Science

- Commercial (Thomson Scientific) citation database http://isiknowledge.com/
- Access to journal articles in the sciences, social sciences and arts and humanities.
- Web of Science also provides a unique search method, cited reference searching.
- Access to the Science Citation Index® (1900-present)

Explanations

- New research builds on past research.
- Newer papers **cite** older papers they refer to.
- Interesting question:
  How influential is a paper (how often cited)?
- [The papers of] which journals are influential?
  => “Impact factor”
- Science Citation Index provides this information
- A fair basis for evaluating researchers?