UMN Genetic Analysis Facilities
www.umn.edu/agac
Biomedical Genomic Core Facilities

• **Goal:**
  – Enable and foster the development of the world’s leading program in Biomedical (structural, functional and comparative) genomics at the University of Minnesota

• **Objective:**
  – Develop the requisite infrastructure to support faculty initiatives and research in Biomedical genomics at the University of Minnesota and provide services at competitive prices
Biomedical Genomic Core Facilities

• **Seamless Operations**
  – Integration of genetic analysis facilities within the AHC
    • AGAC, MCF, and BIPL’s genetic analysis activities will be a single ISO administered by the BMGC
      – in place by July 1, 2000
    – Coordination with other complementary facilities through the auspices of the GPCC
Today’s Situation
Key Core Facilities

• **DNA Sequencing / Genotyping at the U**
  – 4 ABI model 377 DNA sequencers
    • Theoretical capacity of 750 reads/day
  – Target >2,500 reads/day to enable medium / high throughput projects that are coming online / projected
    • One ABI 3700 96-well capillary machine order in process
  – Price support for internal users
    • when provided in 96-well format and 96 samples - $5 each
    • when provided in single tubes - $7 each
Today’s Situation
Key Core Facilities

- Microarray technology:
  - Recently installed 1st generation technology at the University of Minnesota
  - web-pages with protocols established www.umn.edu/agac
  - Human 40k unigene set for arraying in-place
    - First set of ~ 4k genes will be available by month end
    - Priced at $50 each slide
  - near-term upgrades in consideration
    - Will be housed at Mpls node
  - Discussions in progress regarding Affymetrix system

- Proteomic technology:
  - In collaboration with Mass Spec Facility in St. Paul
    - immediate installation of 2-d gel apparatus in progress

6/19/00
Today’s Situation
Key Core Facilities

• Bioinformatics
  – All activities in collaboration with Bioinformatics Center (Ernest Retzel, Director)
  – LIMS in place for high-throughput analysis
  – Microarray analysis
    • Quantarray
    • Shareware clustering programs
    • Spotfire