ENCODE Phase 2: Participants and Projects

ENCODE Production Scale Effort

Research Group	Institution	Research Goals
Bradley Bernstein	Broad Institute of MIT and Harvard	Map histone modifications using chromatin immunoprecipitation followed by high-throughput sequencing.
Gregory Crawford	Duke University	Identify and characterize regions of open chromatin using DNaseI hypersensitivity assays, formaldehyde-assisted isolation of regulatory elements, and chromatin immunoprecipitation.
Morgan Giddings	University of North Carolina, Chapel Hill	Produce large-scale proteomic data sets on ENCODE cell lines using mass spectrometry.
Thomas Gingeras	Affymetrix, Inc.	Identify protein-coding and non-protein coding RNA transcripts using microarrays, high-throughput sequencing, sequence paired-end tags, and sequenced cap analysis of gene expression tags.
Timothy Hubbard	Wellcome Trust Sanger Institute	Annotate gene features using computational methods, manual annotation, and targeted experiments.
Richard Myers	HudsonAlpha Institute for Biotechnology	Identify transcription factor binding sites using chromatin immunoprecipitation followed by high-throughput DNA sequencing; Pilot effort to determine the methylation status of CpG-rich regions.
Michael Snyder	Stanford University	Identify transcription factor binding sites using chromatin immunoprecipitation followed by high-throughput DNA sequencing.
John Stamatoyannopoulos	University of Washington, Seattle	Map and functionally classify DNaseI hypersensitive sites by digital DNaseI and histone modification mapping using high-throughput sequencing.
Thomas Tullius	Boston University	Develop high-throughput methods for collecting hydroxyl radical cleavage data; locate structural features in human genome that are under selective evolutionary pressure, but for which the exact nucleotide sequence is not under selection.
Kevin White	University of Chicago	Epitope tag transcription factors for chromatin immunoprecipitation using BAC recombineering.

Mouse ENCODE Production Scale Effort

Research Group	Institution	Goals
Ross Hardison	Pennsylvania State University	Identify molecular events retained by both mouse and human since divergence using genome-wide assays; analyze how conservation of biochemical features relates to conservation of DNA sequence and conservation of regulated gene expression.
Bing Ren	Ludwig Institute for Cancer Research	Conduct a genome-wide analysis of active promoters, enhancers and insulator elements in embryonic and adult mouse tissue using high throughput experimental strategy.
Michael Snyder	Stanford University	Map the binding sites of transcription factors in mouse cell lines orthologous to well-studied human cell lines.
John Stamatoyannopoulos	University of Washington, Seattle	Produce comprehensive maps of mouse regulatory DNA marked by DNaseI hypersensitive sites using ultra-deep sequencing.

ENCODE Pilot Scale Effort

Research Group	Institution	Research Goals
Job Dekker	University of Massachusetts Medical School	Map long-range gene regulatory elements using 5C (Chromosome Conformation Capture carbon-copy)
Laura Elnitski	National Human Genome Research Institute	Map silencer and enhancer blocker elements using transient transfection assays; Study bidirectional promoters that map across species.
Eric Green	National Human Genome Research Institute	Generate and analyze BAC-based sequence data.
Elliott Margulies	National Human Genome Research Institute	Develop and implement analytical methods for identifying and characterizing evolutionarily constrained sequences.

Scott Tenenbaum	University at Albany-State University of New York	Identify sites that are targets for RNA-binding proteins using immunoprecipitation followed by microarrays or high-throughput sequencing.
Zhiping Weng	University of Massachusetts Medical School	Predict transcription factor binding sites that determine active promoters using computational methods.

ENCODE Data Coordination Center

Research Group	Institution	Research Goals
W. James Kent	University of California, Santa Cruz	Collect, organize, store, manage, and provide access to data from ENCODE and related projects

ENCODE Data Analysis Center

Research Group	Institution	Research Goals
Ewan Birney	European Bioinformatics Institute	Coordinate and assist in the integrative analysis of data produced by the ENCODE Consortium

ENCODE Technology Development Effort

Research Group	Institution	Research Goals
Howard Chang	Stanford University	Develop high-throughput methods to predict functional motifs in RNA, to map RNA structure, and to assign biological functions to RNA motifs.
Michael Dorschner	University of Washington, Seattle	Develop an *in vivo* method for identifying sites of protein-DNA interaction using cleavage sensitivity with UV light, dimethylsulfate, and DNaseI followed by single molecule sequencing.
John Greally	Albert Einstein College of Medicine	Develop high-throughput methods to analyze cytosine methylation and map histone modifications.
Xiaoman Li	University of Central Florida	Develop computational methods for identifying conserved cis-regulatory modules in non-protein coding regions.
Marcelo Nobrega	University of Chicago	Develop tagged DNA binding proteins that are recognizable by tag-specific antibodies; Develop platforms to test predicted enhancers, silencers and insulators.
Yijun Ruan	Genome Institute of Singapore	Develop methods that use high-throughput sequencing to characterize long-range chromatin interactions involved in transcription.

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