

An Integrated Computer Simulation Program for Plasma and Gas Processes

- The simulation program facilitates cost reductions in the development of plasma process technologies -

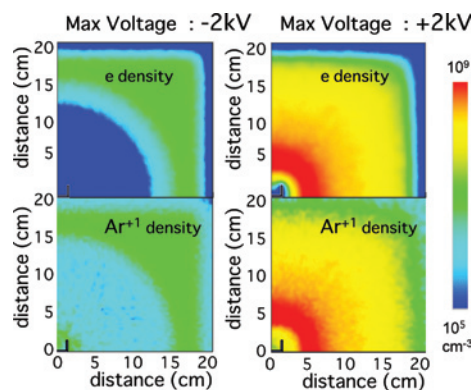
Yoshiko MIYAGAWA

Institute for Structural
and Engineering
Materials
e-mail:
y.miyagawa@aist.go.jp
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Materials processing technologies using plasma have progressed rapidly in recent years. In collaboration with PEGASUS software incorporated, an integrated computer program for the analysis of plasma processes and rarefied gases has been developed by combining the dynamic-SASAMAL code, which was developed in AIST for analyzing the interactive behavior of energetic ions with a solid surface. The program enables computer analysis of the interactions between the vacuum chamber inner wall or a workpiece surface and the plasma, in terms of gas flow, plasma behavior, sputter etching, and other factors. The program can be used for process analysis in a wide range of equipment, including that used in plasma enhanced chemical vapor deposition, etching, plasma display panels, magnetron sputtering, ion injection devices, and various vacuum equipment.

Spatial distribution of plasma density generated when a positive pulsed voltage (maximum voltage: 2 kV, pulse length: 5 μ s) was applied to the work-

piece (H shape in cross section; 4cm \times 4cm). The results show that a high-density region of plasma was generated around the workpiece.



Ar gas : 0.1 mTorr,
Initial plasma density : 10⁷ cm⁻³
Length of pulsed voltage : 5 μ sec

Example of simulation :

Comparison of plasma generation by a positive and a negative pulsed voltage which is applied to the target.

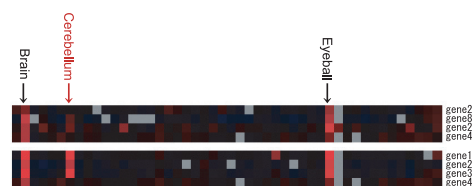
It is clearly shown that a plasma is not generated by a negative pulsed voltage but an intense plasma is generated by a positive pulsed voltage.

Detection of Genes with Tissue-Specific Expression Patterns using AIC

Koji KADOTA

Computational Biology
Research Center
e-mail:
koji-kadota@aist.go.jp
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We applied a method based on Akaike's Information Criterion (AIC) to detect tissue-specific genes whose expression profile is considerably different in target tissue(s) than in others¹⁾. Such observations are detected as outliers and the method we used was originally developed to detect outlier(s). Our analysis showed that it is specifically applicable to the extraction of specific expression patterns from arbitrarily selected tissues under the condition of co-existing similar tissues because of those detected as outliers. This method is currently employed in other analyses³⁾ and appears to be readily utilizable in various fields of expression analysis.



Detection of genes specifically up-regulated in brain and eyeball.

The AIC based method (upper) detects 4 genes whose expression profiles meet our expectation. However, among the top 4 genes identified by the conventional pattern-matching method (lower), the detection of 3 is disappointing they manifest up-regulated signatures in the cerebellum, contrary to the expectation that the expression profile be similar to that of objective tissues.