

Semiconductor Device Modelling and Simulations
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Lecture - 60
Atlas Silvaco

Hello welcome to lecture number 60. In this lecture we will discuss about a simulation tool Atlas from Silvaco.

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In previous lecture we have discussed about the need for commercial simulation tool and what are the different requirements and then we give some overview. Now we will discuss the syntax of the tool how to use for different simulating different devices. Then in next couple of lectures we will consider different devices and how we actually solve the equations and the models that we have discussed theoretically to apply to real devices.

Because solving a differential equation requires lot of expertise and a lot of time to develop those codes and all. So, one way is of course to use these commercial tools. So, we will introduce Atlas Silvaco in this lecture so how to run Atlas Silvaco tool.

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RUNNING ATLAS SILVACO

Interactive mode with Deckbuild

- `deckbuild -as <input filename> -outfile <output filename>`

Batch mode with Deckbuild

- `deckbuild -run -as <input filename> -outfile <output filename>`

No window Batch mode with Deckbuild

- `deckbuild -run -ascii -as <input filename> -outfile <output filename>`

Running Atlas inside Deckbuild

- `go atlas`

Starting Parallel Atlas

- `go atlas simflags="-V 5.14.0.R -P 4"`

Batch Mode Without DeckBuild

- `atlas <input filename> -logfile <output filename>`

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So, there are two ways basically, one of course you can open the deck build directly and write your code and there is a run button on it you run and it will run basically. Then you will have runtime log here and then if you specify any log file such as the structure file log file, they will be the output of this code. Another way you can run this drag build in interactive mode by using a command.

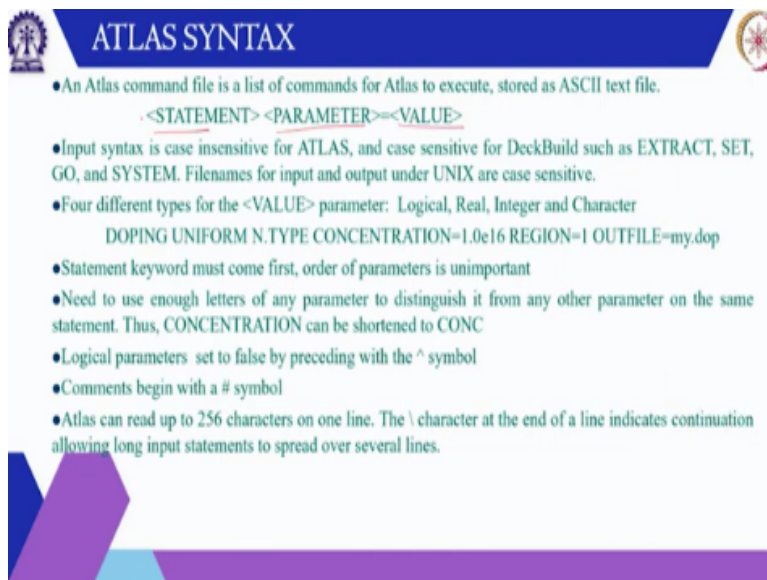
So, on a command prompt you can write deck build and mention the file name with dot dash as script. You can also run this deck build in batch mode by using dash run command and if you want to run this one without deck build window is directly deck build but without opening the deck window itself. Then you can put this dash run dash **(()) (02:23)**. You can also run directly Atlas simulator which is basically a device simulator.

Because there are different tools in Silvaco one is of course deck build which is kind of interface GUI interface then you have Atlas simulator for device simulation you have Athena simulator for process simulation and so on. So, you can directly write go Atlas inside the deck build to run Atlas simulator or you can also run this one from the command line you write Atlas the file name then this out file name you can also mention at runtime log.

So, this will be batch mode without deck will as such and you can also mention if you want to use some parallel processor. So, here in example there are four processors are mentioned with

DSP command and this is the version number if you have different versions, you can use that particular version.

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ATLAS SYNTAX

- An Atlas command file is a list of commands for Atlas to execute, stored as ASCII text file.
- `<STATEMENT> <PARAMETER>=<VALUE>`
- Input syntax is case insensitive for ATLAS, and case sensitive for DeckBuild such as EXTRACT, SET, GO, and SYSTEM. Filenames for input and output under UNIX are case sensitive.
- Four different types for the <VALUE> parameter: Logical, Real, Integer and Character
- `DOPING UNIFORM N.TYPE CONCENTRATION=1.0e16 REGION=1 OUTFILE=my.dop`
- Statement keyword must come first, order of parameters is unimportant
- Need to use enough letters of any parameter to distinguish it from any other parameter on the same statement. Thus, CONCENTRATION can be shortened to CONC
- Logical parameters set to false by preceding with the ^ symbol
- Comments begin with a # symbol
- Atlas can read up to 256 characters on one line. The \ character at the end of a line indicates continuation allowing long input statements to spread over several lines.

So, now Atlas syntax mainly consists of statements. So, you have a statement name and then you mention the parameter name and its value first it statement name has to appear. So, what is a basically for example doping. So, doping is the command it has to appear here the rest of the parameters their order is not important. So, you can write uniform first or you can write n dot type fast so this is a general rule for any statement **(()) (03:53)**.

Now input syntax does not depend on the case of the letter. So, you can write this doping as a small letter or capital letter does not really matter. But the command which are executed by deck build they are cash sensitive such as extract command or set command or some system command. And of course, if there is a unique system and if there are command related to Unix then they are also case sensitive.

Now the values they are typically of four types it can be logical value a real value or integer or a character. So, here one statement is given is called doping. So, doping we have this parameter uniform. So, uniform is basically logic parameter. So, it simply means the doping that we are specifying is uniform you can specify gaussian or other type of doping also. Then you can also say N type or P type then you can especially the value it can be real or integer.

For example, consultation is specified which is a real value so, this means 10 raised to power 16 per cubic centimetre is a concentration. Then the region number so because the device structure consists of different regions so starting from one. So, this doping is assigned to region number so whole of the region one is doped with n-type doping with a concentration 10 is to power 16 per cubic centimetre.

And then file name is mentioned so it is a kind of the name of the file. So, this is again a character so all four parameters are present in this example. Then statement keyword which is a doping here it must come first an order of parameters is not important. Now it is also okay if you do not use full name, you can use only the name as long as it distinguishes from other command. For example, concentration this is a big word.

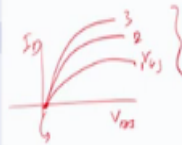
There is no command having these four letter CONC. So, that means you can shorten it to CONC so you can write CONC so up to CONC you can shorten it and because it is unique it will take it as a concentration only. Now logical parameters if you put a cap symbol before the logical parameter then it is set to false basically. So, that means if you specify that you want to simulate electrons only then you can put cap there then you are not simulating electrons you are only simulating the whole characteristic and so on.

So, you can set this parameter to false by putting this cap symbol and any line starting with hash symbol is a comment. So, that line is ignored. Now Atlas can read up to 256 characters on a one line. Now sometime it is possible that your command may be long enough then you can continue that command using backward slash character. So, you have command here put a backward slash then continue the command.

So, then this command can spread over several lines. So, if you put this backwards less than that means it is a continuation of the previous statement.

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ORDER OF ATLAS COMMANDS	
Group	Statements
Structure specification	MESH REGION ELECTRODE DOPING
Material Models Specification	MATERIAL MODELS CONTACT INTERFACE
Numerical Method Selection	METHOD
Solution Specification	LOG SOLVE LOAD SAVE
Results Analysis	EXTRACT TONYPLOT



Now these are different groups we will go from through them one by one. So, you especially the mass the reason the electrode the doping then especially the material parameters. So, material their models the contact properties interface properties then select the numerical method then for solution you can specify the log file name then different solve statement. You can also use this load function this is basically used to set the initial solution.

Let us say you are solving for different ID VDS curve for different values of VGS. So, this is one curve this is second curve this is a third curve so, this is VGS 1 VGS 2 VGS 3 and so on. So, what you will do less you start with VGS = VGS 1 and VGS 0 to some value you scan it. Then this because the previous solution is used as a initial guess for the next solution. So, if you directly jump from here to here it may not converge.

So, what you can do you can save this structure file and then load it basically. So, then that will become the initial solution and you can again continue another different curves. So, this family of curves can be plotted then of course you can save the structure file log file and so on. That to analyse the result it offers the function such as extract and TONYPLOT. So, in extract you can extract the parameters from the log file.

Let us say you want to extract the current voltage cap strains conductance and so on. So, those can be extracted you can also extract the carrier consultation in the device structure the field

distribution. So, all those parameters can be extracted then TONYPLOT is used to plot basically so you can also plot the terminal characteristic from the log file or you can also plot the device properties carry a consultation and so on from the structure file itself.

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DEFINING A STRUCTURE

Three ways to define a device structure in Atlas.

- Read an existing structure from a file. A MESH statement loads in the mesh, geometry, electrode positions, and doping of the structure. `MESH INFILE=<filename>`
- Automatic Interface feature from DeckBuild to transfer the input structure from Athena or DevEdit.
- Create a structure by using the Atlas command language.
 - The first statement must be: `MESH SPACE.MULT=<VALUE>`
 - Followed by a series of X.MESH and Y.MESH statements.
`X.MESH LOCATION=<VALUE> SPACING=<VALUE>`
`Y.MESH LOCATION=<VALUE> SPACING=<VALUE>`
 - Parameter, `SPACE.MULT > 1` will create a globally coarser mesh for fast simulation.

• statements: `MESH`, `REGRID`, `ELIMINATE`

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So, defining the structure, there are three ways to define a structure. One it can read an existing structure file. So, that structure file can be generated from the Dev Edit or you may have previously generated that file. So, you can read that structure file and the syntax is MESH INFILE and write the file name. File name usually as a extension.str. Another one is automatic interfacing with the Athena simulation.

So, you can have Athena simulation or the Dev Edit simulation. So, you write go Athena and you have created your structure then you can go at last and the at the end whatever structure file is there it is automatically passed to the second program or the device simulator. Or third way is you can create a structure file filed by the Atlas command itself. So, to specify the structure first of all you have to specify the MESH.

So, it is a MESH then space multi is a parameter which can control you know whether you want to have a coercive MESH or you want to have fine MESH. So, a small parameter so space mode less than one MESH whatever MESH you have specified will be finer basically. So, the gap will be reduced by that factor or if you make it 2, 3, 4 so on. That means your MESH will become

coercer in comparison to what you have described through this series of XMESH and YMESH statements.

So, this XMESH statement is basically in the X direction so, you can specify the location and you can also especially the spacing. So, at this location what is the spacing so this is let us say X 1 and there is some spacing you can spend then the X 2 you can here also specify the spacing. So, let us say here X 1 is let us say one micron and let us say this is 10 micron and here spacing is let us say 0.1 here let us say 0.01.

So, then what it will do? It will gradually change spacing from 0.1 to 0.01 so, it will come finer MESH as you approach location X 2 so this is what it will do. If you specify space dot MULT S 2 then this will become coarse. So, this will come half of the MESH element will be there and so on. Then there are other commands also you can use REGRID command or you can use ELIMINATE command.

REGRID command is used when you have a structure let us say from the process simulation from Athena you get a structure and then the MESH size the MESH is typically different for the process simulation in the device simulation. So, you would like to REGRID the MESH. So, that command can be used so it generates a fresh grid for the structure or then you can let us say (O) (12:18) somewhere and you can make it cost then you can eliminate some of the grid points.

So, for that eliminate command is used. The syntax of these commands that we discussed in this lecture can be found in the last chapter of this manual at an hour Atlas manual.

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SPECIFYING REGIONS AND MATERIALS



- Every part of mesh must be assigned a material type with REGION statements.
 - REGION number=<integer> <material_type> <position parameters>
- Region numbers must start at 1 and can go up to 1000
- Composition-dependent material Defined with x and y composition fractions
- Position parameters are (in microns): X.MIN, X.MAX, Y.MIN, and Y.MAX
- Overlap between two REGION statement, assigned as material type of the new region
- Entire mesh and doping definition before any MATERIAL statements, to specify the material properties
- Cylindrical Mesh
 - MESH NX=20 NY=20 CYLINDRICAL [X=0 is axis of symmetry]
 - MESH INF=mesh0.str CYLINDRICAL [imports a cylindrical mesh]



Then specifying the regions and material. So, it is important that if every part of mesh must be assigned a material type with a REGION statement. So, region can be you know one two three so on you can go up to thousand and then for region your displacement this is a region number and what is a number it must start with one and it will have material parameter and the position parameter.

And once you have defined the mesh then all the regions should have with all the mesh points whatever reason associated with them. Let us say if there is no device in that region then you can simply specify this as air. So, this is your air basically but it must be specific reason. You can also define the composition dependent material. So, let us say you have this indium gallium arsenate. So, you can this is on the gallium as in a substrate.

So, then you have to especially what is enzyme composition. So, that also can be specified using these reasons and materials. So, they can specify with X composition Y composition fractions by default these positions are in micron. So, X minimum X maximum Y minimum and Y maximum all these values are in micron. So, if you use these four parameters so you can especially region number 1 X minimum is some value X maximum sub value.

So, this is your X minimum this is your X maximum this is your Y minimum now this is your Y maximum. So, this whole rectangular region will be this number one or whatever number you

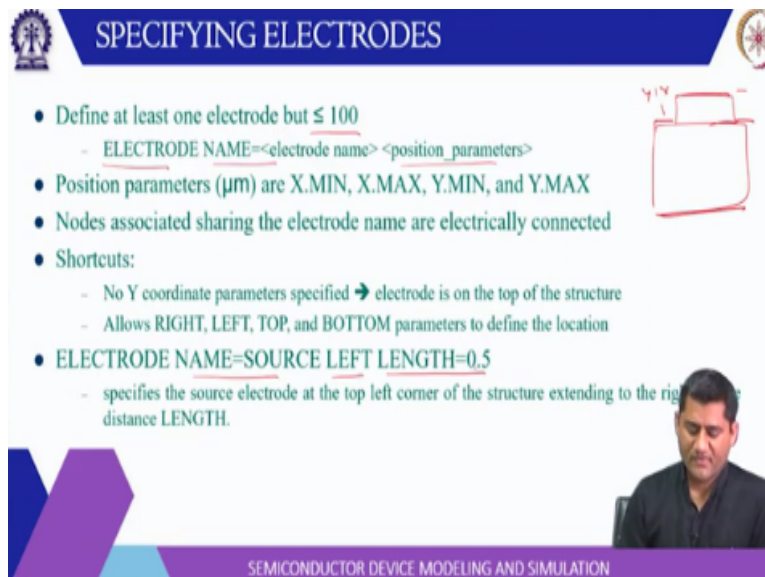
specify here. Now if it so happens that you have two consecutive regions statement and there is overlap between the two mesh points then the newer statement. So, material type of a newer region will take a precedence.

So, the overlap region will be treated as a second material type then entire mesh and doping has to be defined before you specify the material statement and this allows you to especially the material properties. Now Atlas Silvaco also allows you to use cylindrical mesh so in the cylindrical mesh the syntax is slightly different. So, you have this $X = 0$ which is the axis of symmetry and then you go to x this thing and this becomes your Y .

So, along the radial direction you can define this X points basically $x \ 0 \ 1 \ 2 \ 3$ and so on and this is vertical is Y axis. So, $X = 0$ is the axis of symmetry if you load this mesh file then also the cylindrical has to be mentioned because when the file is saved it does not restore this parameter. So, from a store file you do not know whether it is cylindrical or rectangular. So, you can also load a mesh in file so mesh 0.str so dot str is a default extension.

And then with cylindrical parameter so it will mean that the mesh that is stored here it will be imported as a cylindrical mesh.

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SPECIFYING ELECTRODES

- Define at least one electrode but ≤ 100
 - ELECTRODE NAME=<electrode name> <position_parameters>
- Position parameters (μm) are X.MIN, X.MAX, Y.MIN, and Y.MAX
- Nodes associated sharing the electrode name are electrically connected
- Shortcuts:
 - No Y coordinate parameters specified \rightarrow electrode is on the top of the structure
 - Allows RIGHT, LEFT, TOP, and BOTTOM parameters to define the location
- ELECTRODE NAME=SOURCE LEFT LENGTH=0.5
 - specifies the source electrode at the top left corner of the structure extending to the right distance LENGTH.

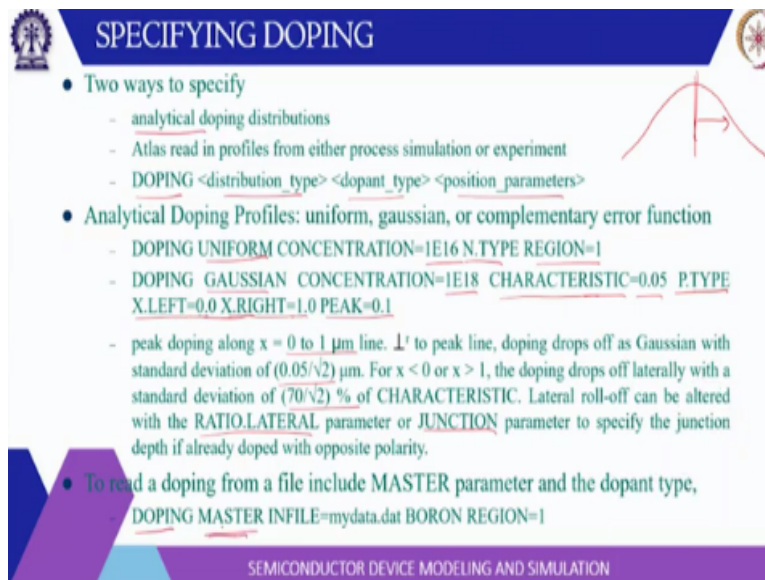
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Then specifying the electrode, so again at least one electrode has to be specified and it will also be integer one and so 1, 2, 3 like that up to 100 you can specify. So, electrode name then mention the name and then the position parameters. So, position parameters again you can specify X MIN, X MAX, Y MIN, Y MAX so this is your structure. So, you can specify so this is X MIN this is Y MIN and Y MAX and so on.

There are some shortcut also. So, you do not have to stretch a parameter in those case so you can write top bottom and so on then left right. So, these are the shortcuts that are used to define the location of the electrode. So, for example electrode name is the source it is on the left side and the length is .05. So, it will on the left side so another property of or another way the syntax works is that if you do not specify a parameter it is assumed to be 0.

So, you have specified the left and the length so Y is 0 so Y 0 will be the top so this basically specially the source electrode at the top left corner of the structure and then is length is 0.5 micron and so on.

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SPECIFYING DOPING

- Two ways to specify
 - analytical doping distributions
 - Atlas read in profiles from either process simulation or experiment
 - `DOPING <distribution_type> <dopant_type> <position_parameters>`
- Analytical Doping Profiles: uniform, gaussian, or complementary error function
 - `DOPING UNIFORM CONCENTRATION=1E16 N.TYPE REGION=1`
 - `DOPING GAUSSIAN CONCENTRATION=1E18 CHARACTERISTIC=0.05 P.TYPE X.LEFT=0.0 X.RIGHT=1.0 PEAK=0.1`
 - peak doping along $x = 0$ to $1 \mu\text{m}$ line. \perp to peak line, doping drops off as Gaussian with standard deviation of $(0.05/\sqrt{2}) \mu\text{m}$. For $x < 0$ or $x > 1$, the doping drops off laterally with a standard deviation of $(70/\sqrt{2}) \%$ of CHARACTERISTIC. Lateral roll-off can be altered with the `RATIO.LATERAL` parameter or `JUNCTION` parameter to specify the junction depth if already doped with opposite polarity.
- To read a doping from a file include MASTER parameter and the dopant type,
 - `DOPING MASTER INFILE=mydata.dat BORON REGION=1`

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Then to specify doping there are two ways you can do you can specify the analytical doping distribution or it can read some input file so if doping profile is stored in file. So, it can read that profile from that file which might have been obtained through some process simulation or from

experiment it can read that file. So, you can use the command doping then the distribution type dopant type and the position parameter.

So, for example these are the examples of analytical doping profile. So, this is uniform doping then concentration is 10 raised to power 16 per cubic centimetre and it is N type doping and it is in the region number one or you can especially the gaussian doping. So, it is a gaussian concentration is 10 to the power 18. Now there are some characteristic of the gaussian because gaussian is this type characteristic.


So, it will basically define the property of this gaussian function and this is P type doping then from left $x = 0$ x right is 10 and peak is 0.1 so, that means the peak doping is along the line $x = 0$ to 1 micron line and the perpendicular to the peak line doping drop of gaussian. So, this is a peak line and perpendicular to that peak line the dropping will drop off his gaussian profile with the gaussian parameters related to this characteristic.

So, this characteristic is 0.05 so standard deviation will be 0.05 by root 2 micrometre and for x less than 0 and greater than 1. So, that means outside this range this doping will drop off laterally with a deviation of 70 by root 2 percent of this characteristic. So, that will be 70 by root 2 times 0.05 percent. And lateral roll-off can be altered with the ratio dot lateral parameter. So, there are other parameters also.


You can also show the junction parameter to specify the junction depth. So, all the details of these statement can again be found at the end of the chapter end of the manual there is a chapter called statement. So, there you can find all the details. Now to read a doping profile from a file you can write doping and you have to use this parameter master. So, this is recommended for reading a file and file is a data file so my data dot data extension is used.

Then it is boron and it is read to the reason number 1. So, this data file will have the you know the concentration profile in the related coordinates.

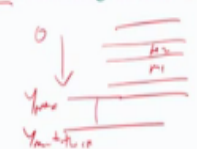
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AUTO MESHING



- Auto-meshing is particularly suited for epitaxial structures including devices with many layers.
 - MESH AUTO [AUTO parameter in the MESH statement]
 - X.MESH LOCATION=-1.0 SPACING=0.1
 - X.MESH LOCATION=1.0 SPACING=0.1
 - Y.MESH statements is optional
- Y mesh lines determined by the parameters of the REGION statements
 - REGION BOTTOM THICKNESS=0.1 MATERIAL=AlGaAs NY=5 DONOR=1E17 X.COMP=0.2
 - NY = evenly spread Y mesh lines contained in the region
 - SY = spacing in microns between Y mesh lines in the region
- For material discontinuities such as etching out a region
 - REGION MATERIAL=Air X.MIN=0.0 Y.MAX=0.0
- Auto-meshing with an absolute value of Y, arrange structure s.t. discontinuity is at Y=0





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You can also use automation which is particularly useful for epitaxial structures because epitaxial structure you have to get you have to consider these different interfaces. So, this will automatically consider these interfaces from material 1 to material 2 and so on. Usually, the multi-layer structures like distributed drag reflectors big cells and so on. So, you can use the command mesh auto so auto parameter is there in the message statement.

Then of course you can specify that just X location and Y mesh statement is optional. You can specify or you need not to specify now Y mesh lines are determined by the parameters of the region statement. For example, this is a reason at the bottom so it is added at the bottom is for Y coordinate loop goes like this from 0 to Y max so, bottom is it is added at Y max so, this will come Y max + Y max + the thickness.

So, this becomes your region so, at the bottom this is a thickness material is aluminium gallium nitride number of grid points in vertical direction are five and it is doped with donor concentration ten to the power of 17 and X composition is 0.2. So, if the substrate is let us say gallium nitride then aluminium composition will be 0.2 and so on. So, NY is a evenly spread Y mesh line contained in the region and SY is the specific in micron between the mesh lines in the region.

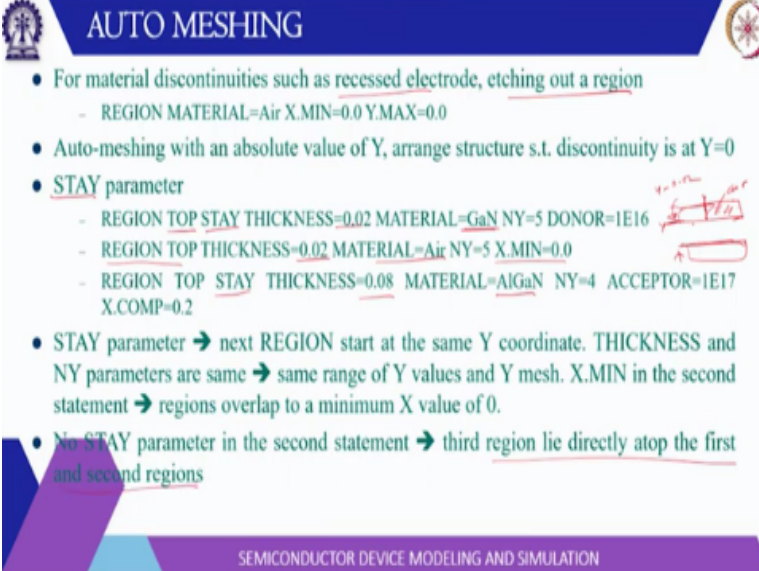
So, either you can especially NY or you can specify SY for material discontinuities. For example, if you etching out a reason then you can write region material name air because you

have etch out. So, nothing is there then you can write air there and then you can switch the region X MAX 0, Y MAX 0 and so on. Automation meshing with an absolute value of Y then you have to arrange the structure that this continuity occurs at Y = 0.

Now why that is important, because let us say this is your structure and the at Y = 0 there may not be a let us say Y = Y 0 there may not be a grid point. So, if you specify the discontinuity at Y = 0 where there is no grid point then your restructure will align in such a way that it will correspond to the grid point basically. So, it will be different from Y = 0. So, in this case what you can do? You can align or restructure that this discontinuity falls at Y = 0.

And then use the mesh accordingly so that is why it is important that when you use automation with some absolute value of Y then arrange the descriptive at Y = 0.

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AUTO MESHING

- For material discontinuities such as recessed electrode, etching out a region
 - REGION MATERIAL=Air X.MIN=0.0 Y.MAX=0.0
- Auto-meshing with an absolute value of Y, arrange structure s.t. discontinuity is at Y=0
- STAY parameter
 - REGION TOP STAY THICKNESS=0.02 MATERIAL=GaN NY=5 DONOR=1E16
 - REGION TOP THICKNESS=0.02 MATERIAL=Air NY=5 X.MIN=0.0
 - REGION TOP STAY THICKNESS=0.08 MATERIAL=AlGaN NY=4 ACCEPTOR=1E17 X.COMP=0.2
- STAY parameter → next REGION start at the same Y coordinate. THICKNESS and NY parameters are same → same range of Y values and Y mesh. X.MIN in the second statement → regions overlap to a minimum X value of 0.
- No STAY parameter in the second statement → third region lie directly atop the first and second regions

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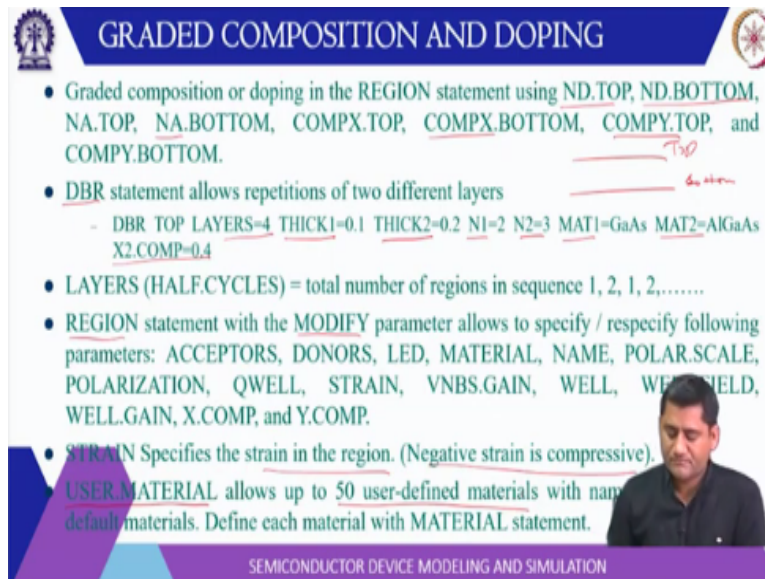
So, for material discontinuities such as recessed electrode or etching out a region you can specify this region number. Then there is another way called stay parameter. So, stay parameter what this does let us say you have this top surface this bottom surface then you put another layer. And if you mesh on the stay parameter then next material will also be specified on the top of previous value of Y so, that means this will overlap with this material is specified.

So, for example here region at top you have this material gallium nitride thickness and you put a stay parameter. So, that means let us say this is some Y and this will be the top layer will be Y - 0.02 so, there is a thickness. The next material will also be deposited here so this is a region top thickness 0.02 now this material is air and this is $X_{MIN} = 0$. So, that means this region will be now air because two successive region statement this is overlapping.

So, this will not be galinated but this will be air basically. Similarly, at the bottom stay parameter allows that you know next statement start with the previous interface basically. So, here if you try the top stay parameter again it is at the top. So, this algon will be on the top of the top surface and the thickness will be 0.08 so, if there is no stay parameter it will start from the top of the region now.

No stay parameter is the second which third region lies directly atop the first and second regions. So, this means this will be AlGaAs.

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GRADED COMPOSITION AND DOPING

- Graded composition or doping in the **REGION** statement using **ND.TOP**, **ND.BOTTOM**, **NA.TOP**, **NA.BOTTOM**, **COMPX.TOP**, **COMPX.BOTTOM**, **COMPY.TOP**, and **COMPY.BOTTOM**.
- DBR** statement allows repetitions of two different layers
 - DBR TOP LAYERS=4 THICK1=0.1 THICK2=0.2 N1=2 N2=3 MAT1=GaAs MAT2=AlGaAs X2.COMP=0.4
- LAYERS (HALF.CYCLES)** = total number of regions in sequence 1, 2, 1, 2,.....
- REGION** statement with the **MODIFY** parameter allows to specify / respecify following parameters: **ACCEPTORS**, **DONORS**, **LED**, **MATERIAL**, **NAME**, **POLAR.SCALE**, **POLARIZATION**, **QWELL**, **STRAIN**, **VNBS.GAIN**, **WELL**, **WELL.FIELD**, **WELL.GAIN**, **X.COMP**, and **Y.COMP**.
- STRAIN** Specifies the strain in the region. (Negative strain is compressive).
- USER.MATERIAL** allows up to 50 user-defined materials with names different from default materials. Define each material with **MATERIAL** statement.

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So, you can also especially a graded composition doping. So, graded composition you can especially in the **REGION** statement. So, there is a **ND dot TOP**, **ND dot BOTTOM** **TOP** **BOTTOM**. So, there is a layer here you can mention it that top this is a top and this is the bottom. So, you can define the donor concentration receptor concentration composition X composition or Y composition.

So, you can also there is a command called DBR also which allows you to specify multiple layers. So, you can name the layer, layer 1 thickness 1 layer 2 which has thickness 2 and number of such layers two and three then material corresponding to this layer calcium gallium arsenide and aluminium arsenate and the composition. So, this is your aluminium composition that is 0.4 then layers is basically number of layers is four that means total number of half cycles.

So, two gallium layer and two AlGaIn's layer will be deposited and the sequence will be 1, 2 and so on. Now region statement with the modify parameter allows to specify or re-specify these parameters. So, if you have already defined a region you want to change some properties of the region then you can again write the region statement with modify parameters. So, that allows you to change all these parameters like ACCEPTOR, DONORS, MATERIAL, POLAR, POLARIZATION and so on.

Strain specify the strain in the region so, negative strain by definition is a compressive strength you can also have your user materials. So, it allows up to 50 user defined materials. So, you have to start with some existing material and change the properties battery basically. And it has to be defined with the material statement.

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REGRID


- REGRID creates a fine mesh in localized region where specified quantity varies rapidly.
 - `REGRID LOGARITHM DOPING RATIO=2 SMOOTH.KEY=4 DOPFILE=<filename1> OUTFILE=<filename2>`
- This statement is used after the MESH, REGION, MATERIAL, ELECTRODE, and DOPING. Can be used before any solution is obtained.
- SMOOTH.KEY selects a smoothing algorithm [Default = 4]
- REGRID on solution variables [High voltage power devices often regrid on potential]
 - only be used after a solution has been obtained.
 - After a regrid, the solution must be re-solved at the same bias in Atlas.
 - `REGRID POTENTIAL RATIO=0.2 MAX.LEVEL=1 SMOOTH.K=4 DOPFILE=<filename1>`
 - SOLVE PREV
- Advised to quit and restart Atlas between regrids on electrical quantities. You can use the go atlas statement followed by a MESH statement, loading the output file of the REGRID command, and a re-setting of all material and model parameters.

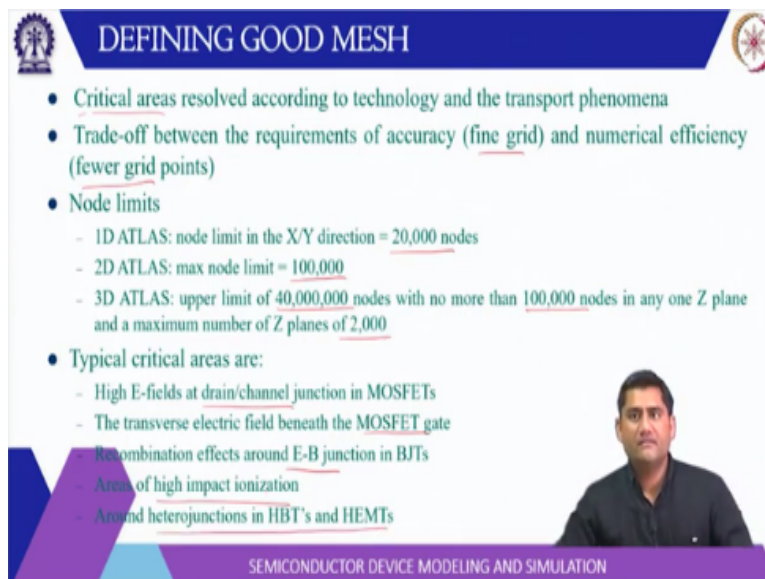
SEMICONDUCTOR DEVICE MODELING AND SIMULATION

REGRID creates a fine mesh in a localized region where the specified quantities varies rapidly. So, for example you have a PN junction so at the interface the carrier concentration varies with a grid slope. So, then you would like to have a fine mesh there and by chance you have not defined that mesh you can REGRID it basically. And then you can write logarithmic scale with doping ratio two. So, this is basically used to REGRID the mesh.

So, that it resolves this parameter variation nicely and this statement is used after MESH, REGION, MATERIAL, ELECTRODE and DOPING. SMOOTH dot KEY is basically you know you can select smoothing algorithm default value of this parameter is 4. You can also REGRID on the solution variables. For example, you can solve get this thing with respect to the carrier concentration with respect to the electric field so these are basically solution parameters.

So, potential REGRID POTENTIAL, RATIO 0.2, MAX LEVEL, DOPFILE, SMOOTH dot K. Now once you REGRID it is advised to quit and restart the atlas between the REGRID on electrical quantities. So, you can use the go (()) (28:08) statement followed by the mesh command. So, it will basically restart the you know Atlas simulator.

(Refer Slide Time: 28:15)



DEFINING GOOD MESH

- Critical areas resolved according to technology and the transport phenomena
- Trade-off between the requirements of accuracy (fine grid) and numerical efficiency (fewer grid points)
- Node limits
 - 1D ATLAS: node limit in the X/Y direction = 20,000 nodes
 - 2D ATLAS: max node limit = 100,000
 - 3D ATLAS: upper limit of 40,000,000 nodes with no more than 100,000 nodes in any one Z plane and a maximum number of Z planes of 2,000
- Typical critical areas are:
 - High E-fields at drain/channel junction in MOSFETs
 - The transverse electric field beneath the MOSFET gate
 - Recombination effects around E-B junction in BJTs
 - Areas of high impact ionization
 - Around heterojunctions in HBT's and HEMTs

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

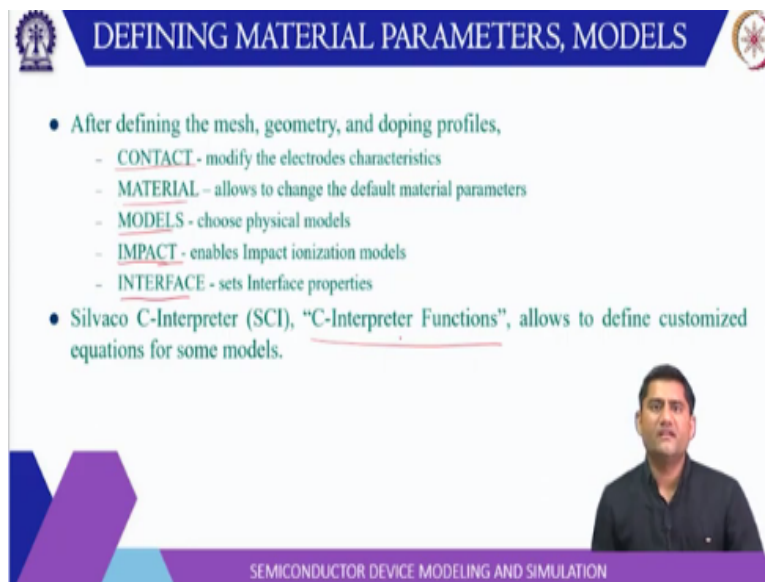
Then defining a good mesh. So, these are the summary of defining good mesh critical areas should be resolved according to the technology and the transport phenomena then trade-off between the accuracy and the efficiency. So, fine grid means it will have greater accuracy and

but then it will take a lot of time in simulation or you can use fewer grid points it will be fast in terms of numerical simulation but accuracy will be slightly reduce.

So, initially if you want to solve some structure you can start with the coarse mesh. Now once you are sure that this is working fine and you want to get a solution then you can go ahead with a fine grid and solve it. Node limit is basically you can use 20,000 nodes in one day and 100,000 node in 2D and 40 million nodes in 3D with a Z plane having around 2,000 planes and in each plane about hundred thousand nodes are allowed.

And for critical areas that are where you need to resolve the mesh you can use this high field at the drain channel junctions or between the MOSFET gates there is a transverse electric field at the oxide and MOSFET. Then emitter based junction in BJT when it is forward wise there is a lot of recombination. So, that need to resolve or high impact ionization in case of reverse biased junctions in HBT I and HEMTs.

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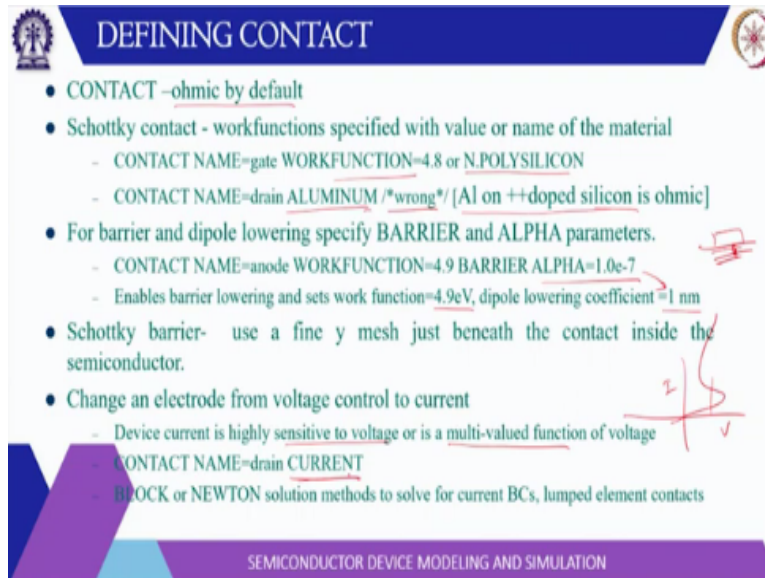
The slide is titled "DEFINING MATERIAL PARAMETERS, MODELS" in a blue header bar. It contains a bulleted list of simulation commands and their functions. A presenter is visible in the bottom right corner of the slide area.

- After defining the mesh, geometry, and doping profiles,
 - CONTACT - modify the electrodes characteristics
 - MATERIAL - allows to change the default material parameters
 - MODELS - choose physical models
 - IMPACT - enables Impact ionization models
 - INTERFACE - sets Interface properties
- Silvaco C-Interpreter (SCI), "C-Interpreter Functions", allows to define customized equations for some models.

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

Then we are defining the material parameters and the models. So, there are statements here CONTACT, MATERIAL, MODELS, IMPACT and INTERFACE. So, most of the models are specified using the model command and only the impact ionization based models are enabled using impact statement. Then you can also have your own C file to define a customized equation for some model that Silvaco also allows.

(Refer Slide Time: 30:22)



DEFINING CONTACT

- CONTACT –ohmic by default
- Schottky contact - workfunctions specified with value or name of the material
 - CONTACT NAME=gate WORKFUNCTION=4.8 or N.POLYSILICON
 - CONTACT NAME=drain ALUMINUM /*wrong*/ [Al on ++doped silicon is ohmic]
- For barrier and dipole lowering specify BARRIER and ALPHA parameters.
 - CONTACT NAME=anode WORKFUNCTION=4.9 BARRIER ALPHA=1.0e-7
 - Enables barrier lowering and sets work function=4.9eV, dipole lowering coefficient =1 nm
- Schottky barrier- use a fine y mesh just beneath the contact inside the semiconductor.
- Change an electrode from voltage control to current
 - Device current is highly sensitive to voltage or is a multi-valued function of voltage
 - CONTACT NAME=drain CURRENT
 - BLOCK or NEWTON solution methods to solve for current BCs, lumped element contacts

Handwritten notes: A red arrow points from the text "Enables barrier lowering and sets work function=4.9eV, dipole lowering coefficient =1 nm" to the parameter "ALPHA=1.0e-7". Another red arrow points from the text "Device current is highly sensitive to voltage or is a multi-valued function of voltage" to the parameter "CURRENT". There are also some scribbles and a small diagram of a Schottky barrier.

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

So, regarding the CONTACT it is ohmic by default. So, if you write a contact name then it will be assume to be ohmic but if we specify the work function or the name of the material. So, which has some associated electron affinity then that contact will deteriorate Schottky contact. But in case of aluminium to a highly doped region the contact will be ohmic only it will not be Schottky.

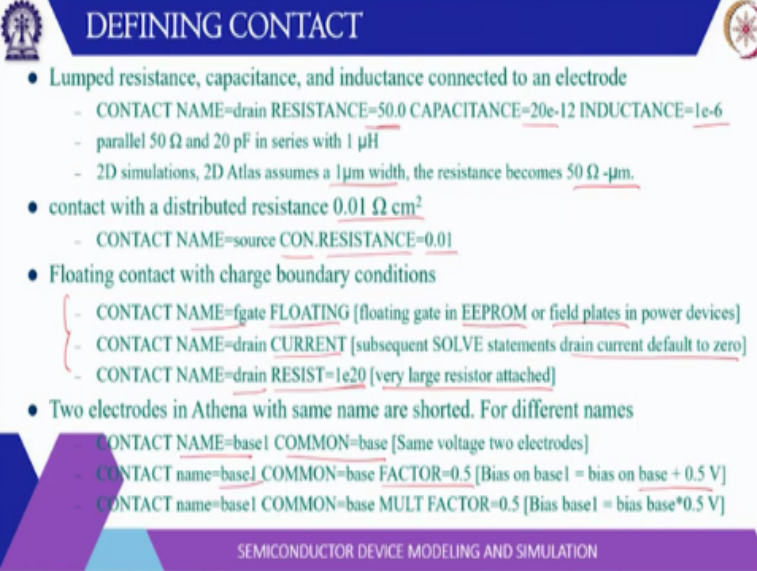
So, for a highly doped region if you put aluminium there then that will be wrong basically. Because for highly doped region aluminium doping is highly dope region aluminium contact is ohmic basically. So, for barrier and dipole lowering especially the barrier and alpha parameters so again you can specify this alpha parameter 1×10^{-7} here so, this enables the barrier lowering and set the lower function to 4.9 electron volt and the dipole lowering coefficient is 1 nanometre which is 1×10^{-10} this one is 7 centimetre.

Now Schottky barrier it uses a fine and y mesh just beneath the contact inside the semiconductor. So, it is requirement for a Schottky barrier because all the activities taking place here this metal and there is a semiconductor here. So, all the activities taking place here so here you need to have a final mesh. Then change an electrode from voltage control to current control so then you have to write this name CURRENT here.

So, by default a contact is a voltage controlled if you especially the parameter current then this contact becomes current controlled. And this is used in case a device is a sense it very sensitive to voltage or it is a multi-valued function of voltage. For example, SCR if you see here so, it have some characteristic like this so, this is voltage. Then now for a given voltage you have two current values.

So, in this case you would like to have a contact as a current contact rather than a voltage contact. Then you can especially the methods BLOCK on NEWTON method. So, these are used to solve for current boundary condition and lumped element contacts.

(Refer Slide Time: 32:37)



DEFINING CONTACT

- Lumped resistance, capacitance, and inductance connected to an electrode
 - CONTACT NAME=drain RESISTANCE=50.0 CAPACITANCE=20e-12 INDUCTANCE=1e-6
 - parallel 50 Ω and 20 pF in series with 1 μ H
 - 2D simulations, 2D Atlas assumes a 1 μ m width, the resistance becomes 50 Ω - μ m.
- contact with a distributed resistance 0.01 Ω cm²
 - CONTACT NAME=source CON.RESISTANCE=0.01
- Floating contact with charge boundary conditions
 - CONTACT NAME=fgate FLOATING [floating gate in EEPROM or field plates in power devices]
 - CONTACT NAME=drain CURRENT [subsequent SOLVE statements drain current default to zero]
 - CONTACT NAME=drain RESIST=1e20 [very large resistor attached]
- Two electrodes in Athena with same name are shorted. For different names
 - CONTACT NAME=base1 COMMON=base [Same voltage two electrodes]
 - CONTACT name=base1 COMMON=base FACTOR=0.5 [Bias on base1 = bias on base + 0.5 V]
 - CONTACT name=base1 COMMON=base MULT FACTOR=0.5 [Bias base1 = bias base*0.5 V]

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

Now lumped elements can also be specified along with the contact name so, you can especially that like RESISTANCE 50 ohm CAPCITANCE 20 into e is 12 so that is 20 picofarad inductance 1e - 6 and 3. So, it is micro Henry. So, in 2D simulation your Atlas assumes one micro meter bits in the third dimension. So, the resistance will become 50 ohm micrometre you can also specify the distributed resistance.

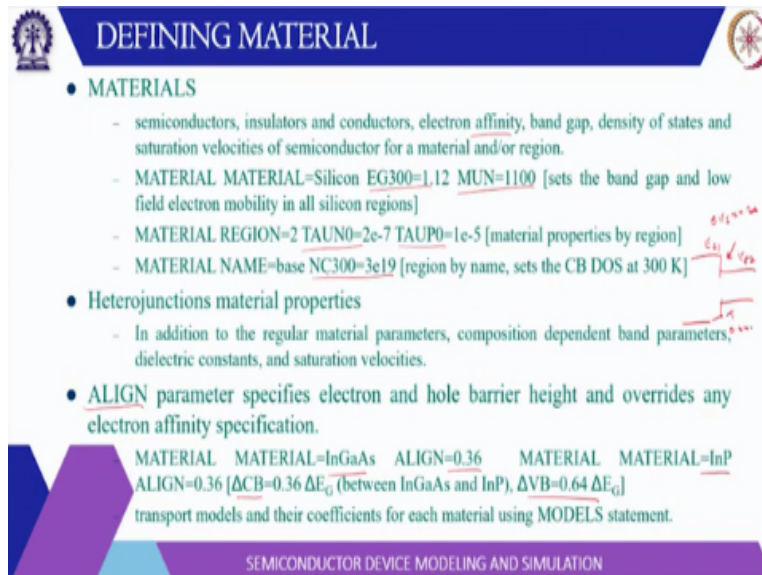
So, that is basically CON dot RESISTANCE which is 0.01 ohm centimetre square. You can also define the floating contact. So, you can write name and the floating so these are used in EEPROM and field plates in power devices. You can specify the contact as a current source so

this is basically drain current at default to zero here unless you space the value of the current it will be zero or you can connect a resistance to the drains so it is $1e20$ that is very large resistor.

So, again it is open basically. So, these are three ways you can define a floating contact. So, either you include the term floating or you make it as a current electrode and current is zero or you connect a very high resistance. Then the two electrode in Athena with same name are sorted. So, for different names if you want to connect the two electrode with different names then you can use this command CONTACT NAME, base 1 then COMMON.

So, now this base 1 is connected to the electrode base and then you can use basically some factor also if there is some bias so this is a base voltage plus 0.5 voltage is connected to base 1 and you can also have this factor can be multiplicative. So, instead of adding 0.5 you can multiply 0.5 so that is also possible you can define like this.

(Refer Slide Time: 34:36)



DEFINING MATERIAL

- MATERIALS**
 - semiconductors, insulators and conductors, electron affinity, band gap, density of states and saturation velocities of semiconductor for a material and/or region.
 - MATERIAL MATERIAL=Silicon EG300=1.12 MUN=1100 [sets the band gap and low field electron mobility in all silicon regions]
 - MATERIAL REGION=2 TAUN0=2e-7 TAUP0=1e-5 [material properties by region]
 - MATERIAL NAME=base NC300=3e19 [region by name, sets the CB DOS at 300 K]
- Heterojunctions material properties**
 - In addition to the regular material parameters, composition dependent band parameters, dielectric constants, and saturation velocities.
- ALIGN** parameter specifies electron and hole barrier height and overrides any electron affinity specification.

MATERIAL MATERIAL=InGaAs ALIGN=0.36 MATERIAL MATERIAL=InP
 ALIGN=0.36 [$\Delta CB=0.36 \Delta E_g$ (between InGaAs and InP), $\Delta VB=0.64 \Delta E_g$]
 transport models and their coefficients for each material using MODELS statement.

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

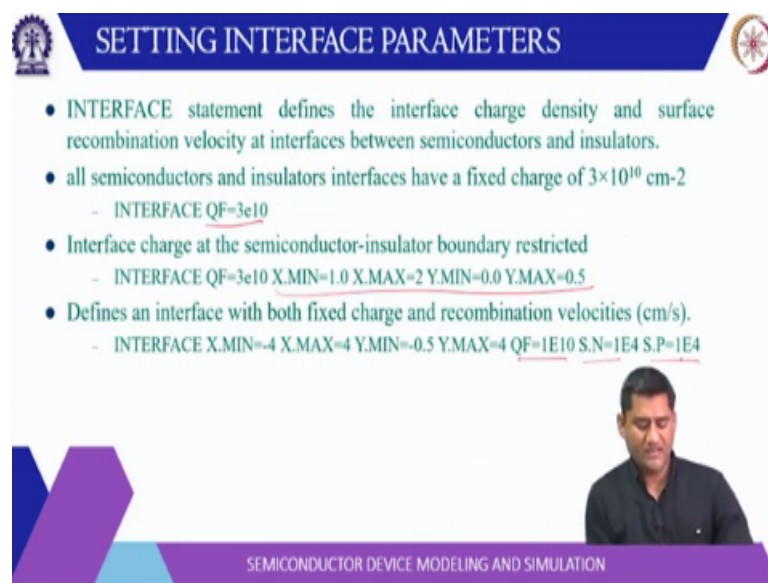
Then defining the materials, semiconductor insulator conductors they can be defined and you can change their properties such as electron affinity, band gap, density of a state for conduction band balance band saturation velocities mobilities. So, all these parameters can be modified under the material statement. So, you write the material then the name and the band gap and then this MUN which is basically electron mobility, this is a band gap 300 at 300 Kelvin.

You can specify the TAUN 0 TAUP 0 this is basically the carrier lifetime and then this is the density of a state at 300 Kelvin for the conduction band see. Heterojunction materials properties in addition to regular material parameters composition dependent band parameters dielectric constant and the saturation velocities can also be specified. A line parameter is basically let us say there are two materials with different band gap.

So, now how to align these things so this ALIGN parameter takes care of this alignment. So, for example here material indium gallium arsenide align is 0.36 and it is aligned to multi-indium phosphide. So, that means 36 percent of the band gap will appear across as the conduction band and remaining 64 percent will appear across a band gap. So, this will be let us say this is $E_g 1$ this is $E_g 2$ so ΔE_g is $E_g 1 - E_g 2$ so ΔE_g into 0.36 will be this and 0.64 will be this.

So, this is using the align parameter or you can also especially the electron affinity then this is electron affinity. So, then they will be aligned according to the electron affinity.

(Refer Slide Time: 36:27)



SETTING INTERFACE PARAMETERS

- INTERFACE statement defines the interface charge density and surface recombination velocity at interfaces between semiconductors and insulators.
- all semiconductors and insulators interfaces have a fixed charge of $3 \times 10^{10} \text{ cm}^{-2}$
 - INTERFACE QF=3e10
- Interface charge at the semiconductor-insulator boundary restricted
 - INTERFACE QF=3e10 X.MIN=1.0 X.MAX=2 Y.MIN=0.0 Y.MAX=0.5
- Defines an interface with both fixed charge and recombination velocities (cm/s).
 - INTERFACE X.MIN=-4 X.MAX=4 Y.MIN=-0.5 Y.MAX=4 QF=1E10 S.N=1E4 S.P=1E4

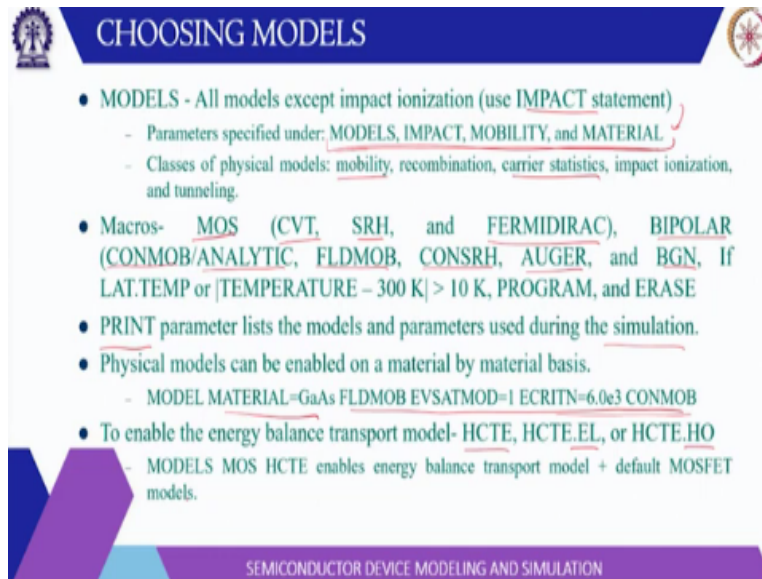
SEMICONDUCTOR DEVICE MODELING AND SIMULATION

Interface statement it defines the interface charge density the surface recombination velocity how the recombination takes place at the surface. So, for example interface fixed charge is 3 into 10 so 10 per square centimetre. So, this many electrons per square centimetres are there electronic charge. The interface charge at the semiconductor insulator boundary. So, you can specify the

region in which it applies basically or you define an interface with both fixed charges and the recombination velocities.

So, this is a fixed charge then these are the recombination parameter for electron and hole and these are the coordinates of the interface.

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CHOOSING MODELS

- **MODELS** - All models except impact ionization (use **IMPACT** statement)
 - Parameters specified under: **MODELS**, **IMPACT**, **MOBILITY**, and **MATERIAL**.
 - Classes of physical models: **mobility**, **recombination**, **carrier statistics**, **impact ionization**, and **tunneling**.
- **Macros**- **MOS** (**CVT**, **SRH**, and **FERMIDIRAC**), **BIPOLAR** (**CONMOB/ANALYTIC**, **FLDMOB**, **CONSRH**, **AUGER**, and **BGN**, If **LAT.TEMP** or $|\text{TEMPERATURE} - 300 \text{ K}| > 10 \text{ K}$, **PROGRAM**, and **ERASE**)
- **PRINT** parameter lists the models and parameters used during the simulation.
- Physical models can be enabled on a material by material basis.
 - **MODEL MATERIAL=GaAs FLDMOB EVSATMOD=1 ECRITN=6.0e3 CONMOB**
- To enable the energy balance transport model- **HCTE**, **HCTE.EL**, or **HCTE.HO**
 - **MODELS MOS HCTE** enables energy balance transport model + default MOSFET models.

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

Then choosing the models. Models are chosen so all the models are especially around the model statement except the impact ionization. So, this impact ionization and models are specified using the impact statement. So, for example mobility material parameter they specify the parameters for these models. So, mobility and material parameters they are specified under the separated statement.

But these parameters can be specified any of these four commands basically and it depends basically the syntax you know how to define those parameters that is mentioned basically. Now there are classes of physical models, mobility models, recombination, carrier statistics such as you can use FERMIDIRAC distribution or the Boltzmann distribution then impact ionization and tunnelling models. Apart from these models they are macros also.

So, you can use one name let us say MOS then these four three four models are included there CVT, SRH this is (0) (38:21) recombination CVT is for perpendicular field dependence

mobility. Then Fermi Dirac then for bipolar again it is a macro it includes the field mobility concentration dependent SRH **(()) (38:36)** recombination band gap narrowing and concentration dependent mobility.

But if temperature is so this is used for $T = 300$ Kelvin but if temperature is more than or less than 300 by 10 Kelvin then the analytical model is used instead of consultation dependent mobility. There is another parameter called print. If you include this one under model statement then it will list out all the models and parameter that are used in the simulation. Now physical models can be enabled on a material by them for different materials you can use different models.

So, you can write a model then the material name then you basically enable these models. For example, field mobility is enabled then this is basically the model related to the particular material. So, for example energy balance transport you can use HCT, HCT for electron HCT for hole and models most HCT enables energy balance transport and the default is MOSFET models. So, you can enable different models and very specific to the particular material you can enable those models.

You can enable the critical electric field you can enable the velocity saturation of a gallium arsenide you have this negative thing. So, there is a negative mobility here so this when you increase the field this mobility goes down. So, that can also be enabled so, this EVSAT parameters basically controls some of the models basically.

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CHOOSING METHOD



- Atlas solve up to six equations. Three types of solution techniques: (a) decoupled (GUMMEL), (b) fully coupled (NEWTON) and (c) BLOCK.
- CLIMIT or CLIM.DD = minimal values of concentrations resolved by the solver.
 - CLIMIT= $1e-4$ recommended for all simulations of breakdown
- DVMAX = maximum update of potential per iteration of Newton's method.
- CLIM.EB = cut-off carrier concentration below which the program wont consider error in the carrier temperature.
 - energy balance simulations to avoid excessive calculations of the carrier temperature at locations in the structure where the carrier concentration is low.
- METHOD NEWTON CARRIERS=2 to be set for isothermal drift diffusion simulations for cases
 - current boundary conditions, distributed or lumped external elements, AC analysis, impact ionization
- Both BLOCK or NEWTON or both are permitted for lattice heat and energy balance.

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

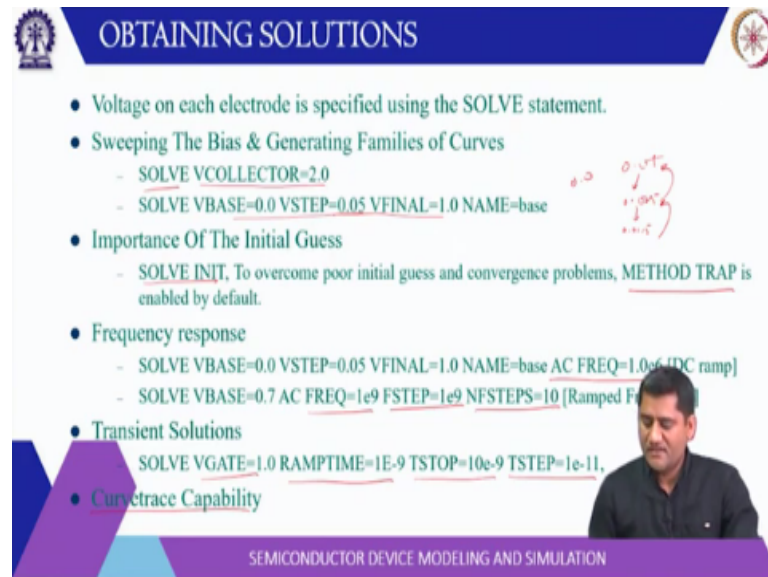
Then choosing the method, you can there are three methods that are available. If the equations are decoupled then you can go with the GUMMEL model and for coupled you can use NEWTON or the BLOCK method. For all the equations that are coupled then you can use Newton method and it is also default. Then the parameters also can be changed for example if you are doing simple PN junction simulation or device simulation you are okay to ignore some carrier consultation which is below certain limit.

But let us say if you are simulating a reverse bias PN junction where there is a positive avalanche breakdown. Then a single carrier is important. So, then you can reduce the limit of consultation which is ignored. So, for example default is some value and you can use smaller than that resistance $1e-4$. So, then this value is used for breakdown simulations then you can also mention the maximum update for potential perpetration in Newton methods.

So, that is DVMAX then CLIM EB so this is basically cut off carry consultation below which the program will not consider error in the carrier temperature. So, energy balance simulation the avoid excessive calculation of the carry temperature at locations in the structure where the carrier concentration is low. Then you can set for number of carriers one or two so that is for isothermal diffusion simulation of cases, current boundary condition, distributed lumped external element, AC analysis, impact ionization.

So, both block and Newton both are permitted for lattice heat and energy balance. So, that means if you have lattice heat energy balance then you can use this both the simulator. In Newton they are coupled with the you know drift diffusion model. In block they are decoupled with the drift diffusion model. So, these two equations are solved separately.

(Refer Slide Time: 42:11)



OBTAINING SOLUTIONS

- Voltage on each electrode is specified using the SOLVE statement.
- Sweeping The Bias & Generating Families of Curves
 - SOLVE VCOLLECTOR=2.0
 - SOLVE VBASE=0.0 VSTEP=0.05 VFINAL=1.0 NAME=base
- Importance Of The Initial Guess
 - SOLVE INIT, To overcome poor initial guess and convergence problems, METHOD TRAP is enabled by default.
- Frequency response
 - SOLVE VBASE=0.0 VSTEP=0.05 VFINAL=1.0 NAME=base AC FREQ=1.0e6 [DC ramp]
 - SOLVE VBASE=0.7 AC FREQ=1e9 FSTEP=1e9 NFSTEPS=10 [Ramped Freq]
- Transient Solutions
 - SOLVE VGATE=1.0 RAMPTIME=1E-9 TSTOP=10e-9 TSTEP=1e-11,
- CurveTrace Capability

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

Then obtain their solutions you can write the command solve statement mention the internal name and especially the voltage or if it is a current contact then especially the current. The contacts that are not specified any value by default they are zero. So, you can solve VBASE and VSTEP it from 0 to 1 and the VSTEP size of 0.05 so, solvent is another command to create an initial guess. So, it basically to overcome poor initial cases and converges problem METHOD TRAP is enabled by default.

So, trap is basically what it does? Let us say you specify zero volts you simulate let us say it converge then you go to 0.05 let us say it does not converge then it will half it. So, it will come 0.025 it still does not cover then it will become 0.0125 so, I think four times it goes then it traces back. So, this is basically the importance of the TRAP parameter. You can also obtain a frequency response by mentioning this AC parameter so mention the AC parameter and the frequency.

You can also ramp up the frequency so start with 1 e 9 FSTEP size of 1 e 9 and you have 10 steps basically. You can also obtain the transient solution so these are the solution with respect to the time. So, you apply this voltage the ramp time is nanosecond and stop time is 10 nanosecond and initial step is 0.01 nanosecond. So, there is another capability called the curve trace where if your IV curve is not smooth you have some variation then you can do the curve trace.

Because for single current or single voltage it is possible that you know there are multiple solutions. So, then in that case this curve trace capability can be used.

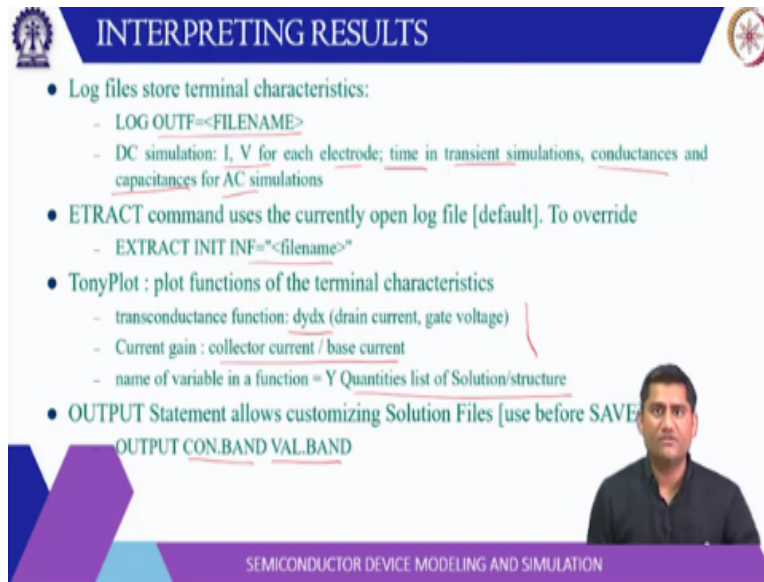
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INTERPRETING RESULTS									
proj	psi	n	p	psi	n	p			
direct	x	x	x	rhs	rhs	rhs			
i	j	m							
1	N			-5.00*	-5.00*	-5.00*	-26.0*	-17.3*	-17.3*
2	N			-0.006	-0.006	-1.106	-28.7*	-4.817	-6.390
3	N			0.230	0.669	-0.553	-28.7*	-5.188	-6.744
4	N			-1.016	-1.023	-1.423	-28.6*	-7.038	-10.29
5	N			-3.369	-3.049	-4.298	-28.8*	-11.13	-15.26
Electrode	Va(V)	Jn(A/um)	Jp(A/um)	Jc(A/um)	Jt(A/um)				
cathode	-3.123e-015	-9.322e-033	-1.566e-019	-1.566e-019	-1.566e-019				
anode	0.000e+000	0.000e+000	1.254e-031	1.254e-031	1.254e-031				
Total			-1.566e-019						

Now if you look at the typical output file you have this thing running runtime output you have these different i, j, m so, these are basically different iterations 1, 2, 3, 4 this method is Newton here so, it can be gummel block or Newton or Newton with autonr or couple Schrodinger Poisson. So, these may appear here and this i j m will represent the number of loops and these are the parameters for the convergence.

So, 10 is over minus 5 10 is over minus 1 10 is over minus 26 10 is over minus 17 and so on. So, that means these are converged basically you can see here and it is less than the convergence criteria. So, this is a voltage this is a current density this is a conduction current density this is a total current density. So, you can see this one and the runtime output is very important to find out whether if there is any error or if there is warning you can find from the runtime output.

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The slide is titled "INTERPRETING RESULTS" in a blue header. It contains a list of bullet points explaining how to interpret simulation results. A presenter's video feed is visible in the bottom right corner of the slide area.

- Log files store terminal characteristics:
 - LOG OUTF=<FILENAME>
 - DC simulation: I, V for each electrode; time in transient simulations, conductances and capacitances for AC simulations
- ETRACT command uses the currently open log file [default]. To override
 - EXTRACT INIT INF=<filename>
- TonyPlot : plot functions of the terminal characteristics
 - transconductance function: dydx (drain current, gate voltage)
 - Current gain : collector current / base current
 - name of variable in a function = Y Quantities list of Solution/structure
- OUTPUT Statement allows customizing Solution Files [use before SAVE]
 - OUTPUT CON.BAND VAL.BAND

SEMICONDUCTOR DEVICE MODELING AND SIMULATION

Then interpreting the results, the log file you can write the log out file name then in the DC simulation you will get the I, V characters for each electrode in transient simulation time is added and in AC simulation you also get the conductance and capacitance for each terminal. Then extract command you can extract the parameters from the log file or the structure file. Then Tony Plot basically it plots the IV characteristic.

You can also get these dragged parameters such as trans conductance which is dy/dx of 10 current and the gate voltage. You can also get the current gain the ratio of this thing. So, these things can also be plotted in the Tony plot. So, name of variable in a function is Y and quantities in the list of solution structures so you can be plot it. So, output statement usually specified before the solve. So, it allows to customizing the solution.

So, you can write the output con band and valence band so that means in the structure file the conduction band and valence band energy will also be included. By default, they are not included.

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INTERPRETING RESULTS



- PROBE - Save Quantities from the Structure at each Bias Point
- Structure files provide all data from the structure at a single bias point.
- Log files provide terminal characteristics for a set of bias points.
- PROBE statement to combine these and allow certain structural quantities to be saved at each bias point. value from the PROBE at each bias point in DC or timestep in transient mode is saved to the log file.
 - PROBE NAME=mycarriers N.CONC X=1 Y=0.1
- Re-initializing Atlas at a Given Bias Point. To begin a solution at a previously solved bias point, re-load the structure file saved at that point.
 - LOAD INFILE=<filename> MASTER




SEMICONDUCTOR DEVICE MODELING AND SIMULATION


Then there is a probe command which allows the quantities to be probed at that particular position. So, from save quantities from the structure at each bias point you can have these quantities. So, structure file provides all the data at a single bias point. So, this is the effect of probe statement and log files provide the terminal characteristic for a set of bias points. And probe statements combine these two and allow certain structural quantity to be saved at each bias point.

So, value from the probe at each bias point in DC or time step in transient mode is need saved to the log file. So, you can syntax you can see here probe name it then electron concentration at $X = 1$ and $Y = 0.1$ so, this will basically along with the solution file the thermal characteristic it will also have this concentration obtained from these grid points. So, reason I reinitializing Atlas at a given bias point to begin a solution previously solved bias point and reload the structure file saved at that point. So, for that you can use this master command.


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CONCLUSION



- Discussed about general structure and syntax of ATLAS SILVACO



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So, in conclusion we have discussed all the general structure and syntax of Atlas Silvaco. Thank you very much.