



Introduction

EPMA: Typical problem of coupled electron-photon transport

- Focused monoenergetic e⁻ beam
 - → x-ray generation and transport within the sample
 - → measured x-ray energy spectrum

Quantitative analysis (x-ray intensities → element concentrations) usually based on approximate semi-empirical algorithms

Difficulties for samples with complex geometries (multilayers, particles, rough surfaces, ...) and for unconventional conditions (low voltages, grazing-angle incidence, ...)

Alternative: Monte Carlo simulation methods (MC)

• Components of a Monte Carlo algorithm Interaction model (set of cross sections for the different interaction mechanisms and atomic relaxation data) Determines the reliability of the results Analytical approximations may not be sufficiently accurate (screened Rutherford DCS, Kirkpatrick-Wiedman-Statham DCS, ...) Transport algorithm Must be as faithful as possible (preferably detailed, interaction by interaction, simulation) The continuous slowing-down approximation, CSDA, and other multiple scattering approximations, ... should be avoided Geometry tools Ability to handle systems (samples) with complex geometrical structures Some existing codes use simplifications in the description of photon transport (e.g., exponential attenuation) which limit the accuracy of calculated fluorescence corrections

• The simulation code PENELOPE

PENetration and Energy LOss of Positrons and Electrons (... and photons)

A general-purpose Monte Carlo code system for the simulation of coupled electron-photon transport in arbitrary geometries

Distributed by the OECD-NEA Data Bank (Paris) (~600 registered users, thoroughly checked... in specific energy ranges)

A very detailed description of the code system (including physical interaction models, sampling and transport algorithms) is given in a NEA report. The PDF file can be downloaded from the web site

http://www.nea.fr/lists/penelope.html

The calculations presented here have been performed using the version 2006 of the code, which was released a few weeks ago

Main features

 All kinds of interactions (except nuclear reactions) in the energy range

from 10⁹ eV down to, nominally, 50 eV (covered by the database)

- Implements the most accurate physical models available (limited only by the required generality)
- Simulates electrons and positrons (tunable mixed scheme) and photons (detailed, interaction by interaction)
- Simulates fluorescent radiation from K, L and M-shells
- Includes a flexible geometry package (constructive quadric geometry)
- Electron and positron transport in <u>external</u> magnetic and electric fields (in matter)

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Atomic relaxation

• Ionization of inner shells (K, L1-L3, M1-M5)

The atoms in the sample can be ionized by electron impact, by photoelectric absorption and by Compton scattering of photons

PENELOPE follows all secondary radiations emitted in the relaxation of ions with vacancies in the K shell and in L and M subshells

Transition probabilities from LLNL's Evaluated Atomic Data Library (Perkins et al., 1991), which are calculated using **approximate** theoretical models

X-ray energies from compilations by Deslattes at al (2003) (K and L shells) and Bearden (1967) (M shells)

 \Rightarrow Simulated characteristic lines have the "correct" energies

Variance reduction Oirect MC simulation is very inefficient... The next slide shows 50 simulated trajectories of 30-keV electrons in gold. Only one photon is generated





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PENEPMA: simulation of EPMA spectra

- No programming work is required. The program provides a complete description of electron transport and x-ray generation (including fluorescence)
- You can define the energy, direction and position of the electron beam
- The geometry of the sample (and its environment) is defined by using PENGEOM
- PENEPMA implements interaction forcing
- Allows the simulation of up to 25 photon detectors simultaneously
- Provides the x-ray spectrum for each detector, as well as the spectrum of characteristic x-rays (with the fluorescence contribution given separately)

































Execute "gnusetup.b	at"	
Go to directory c:\g770	and execute	
g77 -Wall -O myt	est1.f -o mytest1.exe	
😂 C:\g77d		_ 🗆 🗵
Archivo Edición Ver	Favoritos Herramientas Ayu	da 🥂
Nombre 🔺	Tamaño Tipo	
Cibin	File Folder	
🚞 doc	File Folder	
🛅 lib	File Folder	
📤 mytest1.f	5 KB ffile	
🕅 prof77.ps	701 KB PostScript	
	17 KB Documento de	e texto
🖲 readme1.txt		











\tables: auxiliary main program tables to generate numerical tables of radiation transport properties (cross sections, mean free paths, stopping powers, ...) for arbitrary materials. It allows the user to access the physics models underlying the simulations.

ENELOPE 6







Most of the information flux between the main program and the simulation and geometry subroutines is through the common block	The simulation parameters, which are needed to initialize PENELOPE, are provided through the common block
which contains the following quantities:	COMMON/CSIMPA/EABS(3,MAXMAT),C1(MAXMAT),C2(MAXMAT), WCC(MAXMAT),WCR(MAXMAT)
KPAR kind of particle (1=electron, 2=photon, 3=positron) E current particle's energy (eV)	For each material MAT the required parameters are
X,Y,Z position coordinates (cm) U,V,W direction cosines WGHT particle's weight (used only with variance reduction) IBODY index of body where the particle is moving MAT corresponding material ILB(5) describes origin of secondary particles (pp. 215-216)	EABS(3,MAT) Absorption energies C1(MAT) Average angular deflection C2(MAT) Maximum average energy loss WCC(MAT) Cutoff energy loss of hard inelastic collisions WCR(MAT) Cutoff energy loss of hard bremsstrahlung emission NOTE: The number label of each material is determined by its position in
In the I/O of the PENELOPE and PENGEOM routines, all energies are in eV and all lengths are in cm	the input material-data file.
To start the simulation of a particle, its initial state variables must be set by the main program. PENELOPE modifies the energy and direction cosines only when the particle undergoes an interaction. The position coordinates are updated by PENGEOM.	To allow repeatability of the simulation, the seeds of the random-number generator (L'Ecuyer) are specified by the main program. COMMON/RSEED/ISEED1,ISEED2 PENELOPE 6



Simula comm DE ICO	ates the next interaction on TRACK (energy and (output) depose DL (output) type of	n event and modifies the I direction) sited energy in the mate of interaction	e state variables in rial
ICOL	electrons (KPAR=1)	photons (KPAR=2)	positrons (KPAR=3)
1	artificial soft event (random hinge)	coherent (Rayleigh) scattering	artificial soft event (random hinge)
2	hard elastic collision	incoherent (Compton) scattering	hard elastic collision
3	hard inelastic collision	photoelectric absorption	hard inelastic collision
4	hard bremsstrahlung emission	electron-positron pair production	hard bremsstrahlung emission
5	inner-shell impact ionisation		inner-shell impact ionisation
6			annihilation
7	delta interaction	delta interaction	delta interaction
8	auxiliary interaction	auxiliary interaction	auxiliary interaction

SUBROUTIN	E SECPAR(LEFT)
This subround during the p from the sec	tine delivers the initial state of a secondary particle produced revious simulation of the shower. This particle is removed condary stack
LEFT	output, number of particles in secondary stack at calling time. When LEFT= 0, the simulation of the shower is completed.
The particle	state variables are directly loaded in
COMMON/TR	ACK/E,X,Y,Z,U,V,W,WGHT,KPAR,IBODY,MAT,ILB(5)
◆ ILB(1)	generation of the particle (1=primary, 2=direct descendants,)
◆ ILB(2)	kind KPAR of the parent particle, only if ILB(1)>1
◆ ILB(3)	Interaction mechanism ICOL that originated the particle
◆ ILB(4)	$\ldots = Z \cdot 10^6 + \mathtt{IS1} \cdot 10^4 + \mathtt{IS2} \cdot 100 + \mathtt{IS3}$, when applicable
◆ ILB(5)	can be defined by the user; it is transferred to all descendants of the particle
-	

label	:	shell	label		shell	label		shell
1	Κ	$(1s_{1/2})$	11	N2	$(4p_{1/2})$	21	O5	$(5d_{5/2})$
2	L1	$(2s_{1/2})$	12	N3	$(4p_{3/2})$	22	O6	$(5f_{5/2})$
3	L2	$(2p_{1/2})$	13	N4	$(4d_{3/2})$	23	O7	$(5f_{7/2})$
4	L3	$(2p_{3/2})$	14	N5	$(4d_{5/2})$	24	P1	$(6s_{1/2})$
5	M1	$(3s_{1/2})$	15	N6	$(4f_{5/2})$	25	P2	$(6p_{1/2})$
6	M2	$(3p_{1/2})$	16	N7	$(4f_{7/2})$	26	P3	$(6p_{3/2})$
7	M3	$(3p_{3/2})$	17	O1	$(5s_{1/2})$	27	P4	$(6d_{3/2})$
8	M4	$(3d_{3/2})$	18	O2	$(5p_{1/2})$	28	P5	$(6d_{5/2})$
9	M5	$(3d_{5/2})$	19	O3	$(5p_{3/2})$	29	Q1	$(7s_{1/2})$
10	N1	$(4s_{1/2})$	20	O4	$(5d_{3/2})$	30	out	er shells



PENGEOM subroutines						
SUBROUTINE GEOMIN(PARINP,NPINP,NMAT,NBOD,IRD,IWR)						
Reads geometry data from the input file, initializes the geometry package and prints the files geometry.rep and pengeom-tree.rep						
SUBROUTINE LOCATE						
Determines the body IBODY that contains a point of coordinates (X,Y,Z) and its material MAT (values delivered though common TRACK)						
SUBROUTINE STEP(DS,DSEF,NCROSS)						
Performs the geometrical part of the track simulation. Moves the particle and changes body and material numbers as necessary. New values of the variables X,Y,Z,IBODY,MAT are delivered though common TRACK						
DS path length to travel DSEF travelled path length before leaving the initial material or completing the jump NCROSS number of interfaces crossed						

















• Practical simulation

Let's assume that your problem can be solved by using the example main program ${\tt penmain}$

- Prepare your geometry definition file. Check that the geometry is properly defined using the viewing-debugging programs gview2d and gview3d
- Run the program material to generate the material data file. It must include all the materials present in your geometry, in the order assumed in the geometry definition file
- Edit the penmain input file. Assign tentative values to the simulation parameters for each material
- Perform preliminary short simulations, and check that the results do make sense
- Consider the possibility of applying variance reduction techniques
 Run the simulation. Make sure that statistical uncertainties are small enough

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Reduced form			Indic	es		Quadric
z - 1 = 0	0	0	0	1	-1	plane
$z^2 - 1 = 0$	0	0	1	0	-1	pair of parallel planes
$x^2 + y^2 + z^2 - 1 = 0$	1	1	1	0	$^{-1}$	sphere
$x^2 + y^2 - 1 = 0$	1	1	0	0	$^{-1}$	cylinder
$x^2 - y^2 - 1 = 0$	1	$^{-1}$	0	0	-1	hyperbolic cylinder
$x^2 + y^2 - z^2 = 0$	1	1	-1	0	0	cone
$x^2 + y^2 - z^2 - 1 = 0$	1	1	$^{-1}$	0	$^{-1}$	one sheet hyperboloid
$x^2 + y^2 - z^2 + 1 = 0$	1	1	$^{-1}$	0	1	two sheet hyperboloid
$x^2 + y^2 - z = 0$	1	1	0	$^{-1}$	0	paraboloid
$x^2 - z = 0$	1	0	0	$^{-1}$	0	parabolic cylinder
$x^2 - y^2 - z = 0$	1	-1	0	-1	0	hyperbolic paraboloid

Non-planar quadrics in reduced form				
	V y	1,1,0,0,-1	1,-1,0,0,-1	
	1,1,-1,0,0	1,1,-1,0,-1	1,1,-1,0,1	
PENELOPE 0	1,1,0,-1,0	1,0,0,-1,0	1,-1,0,-1,0	10













Modules

 ♦ Module = Connected volume limited only by quadrics The particle can enter or leave the module only through the limiting surfaces (this is not true for bodies)
♦ A module may contain bodies and other modules (daughters). These have to be fully contained in the parent module The "cavities" of a module can be filled with a given material
♦ A module cannot overlap other modules or bodies other than its daughters
♦ A module can be rotated/translated as a whole
00000000000000000000000000000000000000
OMEGA=(+0.00000000000000000000000000000000000
PHI=(+0.00000000000000000000000000000000000
X-SHIFT=(+0.00000000000000E+00, 0) (DEFAULT=0.0)
Y-SHIFT=(+0.00000000000000E+00, 0) (DEFAULT=0.0)
Z-SHIFT=(+0.00000000000000E+00, 0) (DEFAULT=0.0)
ENELOPE 0



















Debugging

- GVIEW generates a debugging file named "geometry.rep", as well as an auxiliary file "pengeom_tree_rep" that contains details on the genealogical tree structure
- GVIEW stops when a syntax error or an obvious inconsistency is found The offending input datum usually appears in the last printed lines of the debugging file
- ♦ Errors or inconsistencies in the definition of the geometry are usually identified by visual inspection of the images created by GVIEW

WARNING: PENGEOM assigns its own labels to all geometry elements. To specify a body or module, we need to know its "internal" label.

The surface and body labels used by PENGEOM during simulation are printed in file "geometry.rep". The body labels can also be identified by running GVIEW2D with display mode = 2

ENELOPE 0

The subroutine package PENGEOM

User-callable routines

SUBROUTINE GEOMIN(PARINP,NPINP,NMAT,NBOD,IRD,IWR)

Reads geometry data from the input file, initializes the geometry package and prints the files geometry.rep and pengeom_tree.rep

SUBROUTINE LOCATE

Determines the body that contains a point of given coordinates and its material

SUBROUTINE STEP(DS,DSEF,NCROSS)

Performs the geometrical part of the track simulation. Moves the particle and changes body and material numbers as necessary

PENELOPE 0





• Limitations of PENGEOM

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 \blacklozenge To avoid being caught in an endless loop, STEP does not leave the particle exactly on the surface, but some 10-8 cm farther.

 \blacklozenge Consequently, geometrical details smaller than ~10 7 cm (i.e. 10 Å) are not guaranteed to be described correctly.

◆ PENGEOM admits up to 10,000 surfaces and 5000 bodies (and modules). The maximum number of bodies in a module or the number of surfaces defining a body is set to 250. These parameters can be changed by editing the source file **pengeom.f** (but with extreme care!).

♦ Note that the speed of the simulation depends strongly on the structure of the genealogical tree. The responsibility of setting it appropriately rests with the user.

• Example of "optimized" modular tree **Repetitive structure** $\stackrel{\mathrm{clone}}{\longrightarrow}$ clone group (2)3(1)(1) $\mathbf{2}$ (1)(1)(2) (4)(5)2)3 2 3 group (3)6 5 6 56 7Each step duplicates the existing tree and adds a common root module PENELOPE 0