RAM-SCB Species Information

All information regarding the species in RAM-SCB has been moved to the ModRamSpecies.f90 file. A species is defined by the SpeciesType fortran construct;

```
type SpeciesType
  character(len=8)    :: s_name       ! Sets the species name
  character(len=2)    :: s_code       ! Sets the species unique code
  real(DP)            :: s_mass       ! Sets the species mass as a multiple of the proton mass
  real(DP)            :: s_comp       ! Sets the species composition ratio
  integer             :: s_charge     ! Sets the charge state of the species
  logical             :: SCB          ! Sets whether the species is used in the pressure balance
  logical             :: WPI          ! Sets whether the species uses wave particle interactions
  logical             :: CEX          ! Sets whether the species charge exchanges
  character(len=100)  :: cross_section ! File name for cross sections (or na)
end type SpeciesType
```

Declaring species to run in the PARAM file

To pick the species to run in RAM we use the #SPECIES declaration in the PARAM file. Below is the default settings

```
#SPECIES
4                    nS              ! Number of species to run
"_H _O He _e"        NameVar         ! The species codes of the species to run
F                    FixedComp       ! Whether to use Young et. al. or a fixed composition
```

If FixedComp is set to True, then the ratios should be listed below, for example, if we wish to run electrons, protons, and oxygen with a 90-10 ratio for protons to oxygen we would use

```
#SPECIES
3                    nS              ! Number of species to run
"_H _O _e"           NameVar         ! The species codes of the species to run
T                    FixedComp       ! Whether to use Young et. al. or a fixed composition
0.9                  Fraction        ! Species fraction of first species in NameVar
0.1                  Fraction        ! Species fraction of second species in NameVar
1.0                  Fraction        ! Species fraction of third species in NameVar
```

Default species included

RAM-SCB includes electrons, protons, He+1 and O+1 as default species, with species codes of "_e", "_H", "He", and "_O" respectively. By default all four species are run and composition is chosen based on the Young et. al. model.

How to add additional species

To add a new species to RAM you simply increase nSpecies in the ModRamSpecies module and add a new entry to the DefineSpecies subroutine. Each entry MUST be filled in and the species code MUST be unique. As an example, if we wanted to run a species of Nitrogen that didn't impact the SCB force balance equation we would

1. Change nSpecies = 4 to nSpecies = 5
2. Add

```
RAMSpecies(5)%s_name = "Nitrogen"
RAMSpecies(5)%s_code = "_N"
RAMSpecies(5)%s_comp = 1.0
RAMSpecies(5)%s_mass = 14.0
RAMSpecies(5)%s_charge = 1
RAMSpecies(5)%SCB = .false.
RAMSpecies(5)%WPI = .false.
RAMSpecies(5)%CEX = .true.
RAMSpecies(5)%cross_sections = 'NitrogenCrossSections.dat'
```

Note that to use charge exchange for a species that is not Hydrogen, HeliumP1, or OxygenP1 you must provide a charge exchange cross section file with that contains a list of velocities and their corresponding cross section with Hydrogen (charge exchange with Hydrogen is currently the only supported charge exchange interaction). An example file is included in the input directory.